

DR WPI: 1996-443187/44.
 DR N-PSDB; AAT39039.
 XX
 PT Neisseria meningitidis antigen, highly conserved between different
 PT strains - useful for prodn. of antibodies for immunisation against,
 PT or diagnosis of, N. meningitidis infection
 XX
 PS Claim 7; Fig 1; 117pp; English.
 XX
 CC A proteinase K resistant surface protein has been isolated
 CC from 4 strains of N. meningitidis (AAT39039 to AAT39042). The isolated
 CC 22 kD antigen, antigenic fragments of antibodies can be used
 CC in a vaccine for the prevention of infection by N. meningitidis or
 CC by N. gonorrhoeae in humans. The antibodies may also be used
 CC diagnostically to detect N. meningitidis infection. The antigen
 CC may also be used to detect antibodies specific to N. meningitidis
 CC antigen.
 CC DNA sequences encoding the antigen, or their fragments, can be used
 CC as probes for the detection of pathogenic Neisseria bacteria.
 CC
 XX
 SQ Sequence 174 AA:
 Query Match 100.0%; Score 868; DB 17; Length 174;
 Best Local Similarity 100.0%; Pred. No. 4,1e-87;
 Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKKALATLIALALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 DB 1 MKKALATLIALALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 QY 61 FAVDYTRYKKNYKAPSTDPEKLYSIGASAIYDFDTQSPVKPYLGARLSINRASVDLGSDSF 120
 DB 61 FAVDYTRYKKNYKAPSTDPEKLYSIGASAIYDFDTQSPVKPYLGARLSINRASVDLGSDSF 120
 QY 121 SQTSLGLVLTGVSAYAVTPNVDLDAGYRYNYIGKVNTRYKNVRSSELSVGVRKF 174
 DB 121 SQTSLGLVLTGVSAYAVTPNVDLDAGYRYNYIGKVNTRYKNVRSSELSVGVRKF 174
 RESULT 2
 AAM04893
 ID AAM04893 standard; Protein; 174 AA.
 AC AAM04893;
 XX
 DT 22-DEC-1996 (first entry)
 XX
 DE Proteinase K resistant N. meningitidis 22 kD surface protein.
 XX
 KW Proteinase K resistant; Neisseria meningitidis;
 KW Neisseria gonorrhoeae; antibody; detection; probe; surface protein.
 XX
 OS Neisseria meningitidis strain 24063.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT /label= sig_peptide
 FT Protein 20..174
 FT /label= mat_protein
 XX
 PN W09629412-A1.
 PD 26-SEP-1996.
 XX
 PF 15-MAR-1996; 96WO-CA00157.
 XX
 PR 04-AUG-1995; 95US-0001983.
 PR 17-MAR-1995; 95US-0406362.
 XX
 PA (IAFB-) IAF BIO VAC INC.
 XX
 PI Brodeur BR, Hamel J, Martin D, Rioux C;
 XX

DR WPI: 1996-443187/44.
 DR N-PSDB; AAT39041.
 XX
 PT Neisseria meningitidis antigen, highly conserved between different
 PT strains - useful for prodn. of antibodies for immunisation against,
 PT or diagnosis of, N. meningitidis infection
 XX
 PS Claim 7; Fig 9; 117pp; English.
 XX
 CC A proteinase K resistant surface protein has been isolated
 CC from 4 strains of N. meningitidis (AAT39039 to AAT39042). The isolated
 CC 22 kD antigen, antigenic fragments of antibodies can be used
 CC in a vaccine for the prevention of infection by N. meningitidis or
 CC by N. gonorrhoeae in humans. The antibodies may also be used
 CC diagnostically to detect N. meningitidis infection. The antigen
 CC may also be used to detect antibodies specific to N. meningitidis
 CC antigen.
 CC DNA sequences encoding the antigen, or their fragments, can be used
 CC as probes for the detection of pathogenic Neisseria bacteria.
 CC
 XX
 SQ Sequence 174 AA:
 Query Match 98.4%; Score 854; DB 17; Length 174;
 Best Local Similarity 98.3%; Pred. No. 1,4e-85;
 Matches 171; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MKKALATLIALALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 DB 1 MKKALATLIALALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 QY 61 FAVDYTRYKKNYKAPSTDPEKLYSIGASAIYDFDTQSPVKPYLGARLSINRASVDLGSDSF 120
 DB 61 FAVDYTRYKKNYKAPSTDPEKLYSIGASAIYDFDTQSPVKPYLGARLSINRASVDLGSDSF 120
 QY 121 SQTSLGLVLTGVSAYAVTPNVDLDAGYRYNYIGKVNTRYKNVRSSELSVGVRKF 174
 DB 121 SQTSLGLVLTGVSAYAVTPNVDLDAGYRYNYIGKVNTRYKNVRSSELSVGVRKF 174
 RESULT 3
 AAM04894
 ID AAM04894 standard; Protein; 174 AA.
 AC AAM04894;
 XX
 DT 22-DEC-1996 (first entry)
 XX
 DE Proteinase K resistant N. meningitidis 22 kD surface protein.
 XX
 KW Proteinase K resistant; Neisseria meningitidis;
 KW Neisseria gonorrhoeae; antibody; detection; probe; surface protein.
 XX
 OS Neisseria meningitidis strain b2.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT /label= sig_peptide
 FT Protein 20..174
 FT /label= mat_protein
 XX
 PN W09629412-A1.
 PD 26-SEP-1996.
 XX
 PF 15-MAR-1996; 96WO-CA00157.
 XX
 PR 04-AUG-1995; 95US-0001983.
 PR 17-MAR-1995; 95US-0406362.
 XX
 PA (IAFB-) IAF BIO VAC INC.
 XX
 PI Brodeur BR, Hamel J, Martin D, Rioux C;
 XX

DR WPI: 1996-443187/44.
 DR N-PSDB; AAT39042.
 XX
 PT Neisseria meningitidis antigen, highly conserved between different
 PT strains - useful for prodn. of antibodies for immunisation against,
 PT or diagnosis of, N. meningitidis infection
 XX
 PS Claim 7; Fig 10; 117pp; English.
 XX
 CC A proteinase K resistant surface protein has been isolated
 CC from 4 strains of N. meningitidis (AAT39039 to AAT39042). The isolated
 CC 22 kd antigen, antigenic fragments of antibodies can be used
 CC in a vaccine for the prevention of infection by N. meningitidis or
 CC by N. gonorrhoeae in humans. The antibodies may also be used
 CC diagnostically to detect N. meningitidis infection. The antigen
 CC may also be used to detect antibodies specific to N. meningitidis
 CC antigen.
 CC DNA sequences encoding the antigen, or their fragments, can be used
 CC as probes for the detection of pathogenic Neisseria bacteria.
 XX
 SQ Sequence 174 AA:
 Query Match 95.0%; Score 825; DB 17; Length 174;
 Best Local Similarity 94.3%; Pred. No. 2,1e-82;
 Matches 164; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
 QY 1 MKKALATLIALPALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 DB 1 MKKALATLIALPALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 QY 61 FAVDYTRYKNKAPSTDEPKLISGASAIYDPTDQSPVKPYLGARLSINRASVLDGSGDSF 120
 DB 61 FAVDYTRYKNKAPSTDEPKLISGASAIYDPTDQSPVKPYLGARLSINRASVLDGSGDSF 120
 QY 121 SQSTIGLGLVLTGVSAYTPNVLDAGYRNYIGKVTNKVNSGELSAGYRVKF 174
 DB 121 SQSTIGLGLVLTGVSAYTPNVLDAGYRNYIGKVTNKVNSGELSAGYRVKF 174
 RESULT 4
 AAM04892
 ID AAM04892 standard; Protein; 175 AA.
 AC AAM04892;
 XX
 DT 22-DEC-1996 (first entry)
 XX
 DE Proteinase K resistant N. meningitidis 22 kd surface protein.
 XX
 KW Proteinase K resistant; Neisseria meningitidis;
 KW Neisseria gonorrhoeae; antibody; detection; probe; surface protein.
 XX
 OS Neisseria meningitidis strain MCH88.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT /label= sig_peptide
 FT Protein 20..175
 FT /label= mat_protein
 XX
 PN W09629412-A1.
 XX
 PD 26-SEP-1996.
 PD
 XX
 PF 15-MAR-1996; 96MO-CA00157.
 PF
 XX
 PR 04-AUG-1995; 95US-0001983.
 PR 17-MAR-1995; 95US-0406362.
 XX
 PA (IAFB-) IAF BIO VAC INC.
 PA
 PI Brodeur BR, Hamel J, Martin D, Rioux C;
 XX

DR WPI: 1996-443187/44.
 DR N-PSDB; AAT39040.
 XX
 PT Neisseria meningitidis antigen, highly conserved between different
 PT strains - useful for prodn. of antibodies for immunisation against,
 PT or diagnosis of, N. meningitidis infection
 XX
 PS Claim 7; Fig 8; 117pp; English.
 XX
 CC A proteinase K resistant surface protein has been isolated
 CC from 4 strains of N. meningitidis (AAT39039 to AAT39042). The isolated
 CC 22 kd antigen, antigenic fragments of antibodies can be used
 CC in a vaccine for the prevention of infection by N. meningitidis or
 CC by N. gonorrhoeae in humans. The antibodies may also be used
 CC diagnostically to detect N. meningitidis infection. The antigen
 CC may also be used to detect antibodies specific to N. meningitidis
 CC antigen.
 CC DNA sequences encoding the antigen, or their fragments, can be used
 CC as probes for the detection of pathogenic Neisseria bacteria.
 XX
 SQ Sequence 175 AA:
 Query Match 95.0%; Score 824.5; DB 17; Length 175;
 Best Local Similarity 95.4%; Pred. No. 2.4e-82;
 Matches 167; Conservative 0; Mismatches 7; Indels 1; Gaps 1;
 QY 1 MKKALATLIALPALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 DB 1 MKKALATLIALPALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 QY 61 FAVDYTRYKNKAPSTDEPKLISGASAIYDPTDQSPVKPYLGARLSINRASVLDGSGDS 119
 DB 61 FAVDYTRYKNKAPSTDEPKLISGASAIYDPTDQSPVKPYLGARLSINRASVLDGSGDS 120
 QY 120 FSQSTIGLGLVLTGVSAYTPNVLDAGYRNYIGKVTNKVNSGELSAGYRVKF 174
 DB 121 FSQSTIGLGLVLTGVSAYTPNVLDAGYRNYIGKVTNKVNSGELSAGYRVKF 175
 RESULT 5
 AAB19895
 ID AAB19895 standard; Protein; 155 AA.
 AC AAB19895;
 XX
 DT 19-MAR-2001 (first entry)
 XX
 DE Neisseria meningitidis NspA protein.
 XX
 KW NspA; infection; diagnosis; therapy; vaccine; meningococcal B.
 KW Neisseria meningitidis.
 XX
 FH Key Location/Qualifiers
 FT Region 6..17
 FT /note= "transmembrane beta-strand"
 FT Region 18..26
 FT /note= "surface-exposed connecting loop"
 FT Region 27..37
 FT /note= "transmembrane beta-strand"
 FT Region 40..50
 FT /note= "transmembrane beta-strand"
 FT Region 51..62
 FT /note= "surface-exposed connecting loop"
 FT Region 63..74
 FT /note= "transmembrane beta-strand"
 FT Region 78..88
 FT /note= "transmembrane beta-strand"
 FT Region 89..104
 FT /note= "surface-exposed connecting loop"
 FT Region 105..114
 FT /note= "transmembrane beta-strand"
 FT Region 118..130

```

FT      /note= "transmembrane beta-strand"
DE      131..145
FT      /note= "surface-exposed connecting loop"
FT      146..155
FT      Region
FT      /note= "transmembrane beta-strand"
PN      WO200071725-A2.
XX
XX      30-NOV-2000.
XX
XX      19-MAY-2000; 2000MO-IB00828.
XX
XX      19-MAY-1999; 99GB-0011692.
XX      19-AUG-1999; 99GB-0019705.
XX      09-MAR-2000; 2000GB-0005730.
XX
XX      (CHIR-) CHIRON SPA.
XX
XX      Giuliani MM, Pizsa M, Rappuoli R;
XX      WPI; 2001-025167/03.
XX
XX      Novel composition comprising first and second biological molecules from
XX      a Neisseria bacterium, useful as vaccines or immunogenic compositions
XX      for treating Neisserial infections
XX
XX      Example 12; Fig 32; 126pp; English.
XX
XX      The present sequence is that of the Neisseria meningitidis NspA
XX      protein, which contains 8 transmembrane beta-strands and 4
XX      surface-exposed connected loops. Recombinant NspA is being
XX      developed as a vaccine for the prevention of meningococcal
XX      disease caused by all serotypes. The invention provides
XX      combination compositions comprising: (i) 2 or more Neisserial
XX      proteins, (ii) 2 or more different Neisserial nucleic acids; or
XX      (iii) mixtures of 1 or more Neisserial protein and 1 or more
XX      Neisserial nucleic acid. The proteins and nucleic acids are
XX      preferably from different Neisseria spp., especially Neisseria
XX      meningitidis and Neisseria gonorrhoeae, but may be from the same
XX      species. A claimed composition includes the NspA protein,
XX      preferably in mature form. The compositions are used e.g. as
XX      immunogenic compositions, vaccines or diagnostic reagents. They
XX      are used to treat or prevent Neisserial infection, to detect the
XX      presence of Neisserial bacteria or of antibodies raised against
XX      Neisserial bacteria, and/or as reagents which can raise antibodies
XX      against Neisserial bacteria.
XX
XX      Sequence 155 AA:
SQ
XX
XX      Query Match 90.4%; Score 785; DB 22; Length 155;
XX      Best Local Similarity 100.0%; Pred. No. 4.4e-78;
XX      Matches 155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      QY 20 ECASGFYVOADAAHAKASSLSGASGFSPRISAGRIDLPADVITYKKYKAPSTDFK 79
XX      DB 1 ECASGFYVOADAAHAKASSLSGASGFSPRISAGRIDLPADVITYKKYKAPSTDFK 60
XX
XX      QY 80 LYSIGASAIYDFDQSPYKPYLGARLSLNRAASVDIGSDSFSQSTIGLGVLTGVSAVTP 139
XX      DB 61 LYSIGASAIYDFDQSPYKPYLGARLSLNRAASVDIGSDSFSQSTIGLGVLTGVSAVTP 120
XX
XX      QY 140 NVDLNGAGTRINYGKYNVTYKKNRSGELSVGVKVF 174
XX      DB 121 NVDLNGAGTRINYGKYNVTYKKNRSGELSVGVKVF 155
XX
XX      RESULT 6
XX      AAR73911
XX      ID AAR73911 standard; protein; 170 AA.
XX      AC AAR73911;
XX      XX
XX      DT 05-DEC-1995 (first entry)

```

```

XX      Neisseria meningitidis opacity related protein POPM3.
DE      131..145
FT      /note= "surface-exposed connecting loop"
FT      146..155
FT      Region
FT      /note= "transmembrane beta-strand"
PN      WO200071725-A2.
XX
XX      30-NOV-2000.
XX
XX      19-MAY-2000; 2000MO-IB00828.
XX
XX      19-MAY-1999; 99GB-0011692.
XX      19-AUG-1999; 99GB-0019705.
XX      09-MAR-2000; 2000GB-0005730.
XX
XX      (CHIR-) CHIRON SPA.
XX
XX      Giuliani MM, Pizsa M, Rappuoli R;
XX      WPI; 2001-025167/03.
XX
XX      Novel composition comprising first and second biological molecules from
XX      a Neisseria bacterium, useful as vaccines or immunogenic compositions
XX      for treating Neisserial infections
XX
XX      Example 12; Fig 32; 126pp; English.
XX
XX      The present sequence is that of the Neisseria meningitidis NspA
XX      protein, which contains 8 transmembrane beta-strands and 4
XX      surface-exposed connected loops. Recombinant NspA is being
XX      developed as a vaccine for the prevention of meningococcal
XX      disease caused by all serotypes. The invention provides
XX      combination compositions comprising: (i) 2 or more Neisserial
XX      proteins, (ii) 2 or more different Neisserial nucleic acids; or
XX      (iii) mixtures of 1 or more Neisserial protein and 1 or more
XX      Neisserial nucleic acid. The proteins and nucleic acids are
XX      preferably from different Neisseria spp., especially Neisseria
XX      meningitidis and Neisseria gonorrhoeae, but may be from the same
XX      species. A claimed composition includes the NspA protein,
XX      preferably in mature form. The compositions are used e.g. as
XX      immunogenic compositions, vaccines or diagnostic reagents. They
XX      are used to treat or prevent Neisserial infection, to detect the
XX      presence of Neisserial bacteria or of antibodies raised against
XX      Neisserial bacteria, and/or as reagents which can raise antibodies
XX      against Neisserial bacteria.
XX
XX      Sequence 170 AA:
SQ
XX
XX      Query Match 15.6%; Score 135; DB 16; Length 170;
XX      Best Local Similarity 26.3%; Pred. No. 9.4e-07;
XX      Matches 41; Conservative 20; Mismatches 47; Indels 48; Gaps 4;
XX
XX      QY 6 ATLIALALPAAALAEASGFYVOADAAH-----AKASSLSGS-----AKG 45
XX      DB 15 SSLFSSAAQAASEDRSPYVOADLAAERITHDYPOATGANNTSTVSDFRNIRAS 74
XX
XX      QY 46 FSPRISAGYRINDLPADVITYKKYKYN-----KAPSTDFK 79
XX      DB 75 IHPKVSAGYDFGGMRIADADASYRKNNNNKYSYNTRELENNKNNKDLKTENQENGTFFA 134
XX
XX      QY 80 LYSIGASAIYDFDQSPYKPYLGARLSLN--RASVD 113
XX      DB 135 ASSIGLSAIDYDFKLGKFKRYIGARVAYGVHVRHSID 170
XX
XX      RESULT 7
XX      AAM04912
XX      ID AAM04912 standard; protein; 25 AA.
XX      AC AAM04912;
XX      XX
XX      DT 22-DEC-1996 (first entry)
XX      DE N. meningitidis 608B peptide CS-857.
XX      XX
XX      KM Proteinase K resistant; Neisseria meningitidis; epitope; mapping;
XX      KM Neisseria gonorrhoeae; antibody; detection; probe; surface protein.

```



```
XX OS Synthetic.
XX PN MO9629412-A1.
XX PD 26-SEP-1996.
XX PF 15-MAR-1996; 96WO-CA00157.
XX PR 04-AUG-1995; 95US-0001983.
XX PR 17-MAR-1995; 95US-0406362.
XX PA (IAFB-) IAF BIO VAC INC.
XX PI Brodeur BR, Hamel J, Martin D, Rioux C;
XX DR WPI; 1996-443187/44.
XX PT Neisseria meningitidis antigen, highly conserved between different
XX PT strains - useful for prodn. of antibodies for immunisation against,
XX PT or diagnosis of, N. meningitidis infection
XX PS Claim 24; Page 84; 117pp; English.
XX CC Example 9 describes the epitope mapping of the 22 kD
XX CC N. meningitidis protein. Identification was accomplished
XX CC using 18 overlapping synthetic peptides (AAW04895 to AAW04912).
XX SQ Sequence 25 AA;

Query Match 15.3%; Score 133; DB 17; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 FAVDYTRYKNYKAPSTDFKLSIGA 85
DB 1 FAVDYTRYKNYKAPSTDFKLSIGA 25

RESULT 8
AAU34556
ID AAU34556 standard; Protein; 212 AA.
XX AC AAU34556;
XX DT 14-FEB-2002 (first entry)
XX DE E. coli cellular proliferation protein #137.
XX KM Antisense; prokaryotic cellular proliferation protein;
XX KM antibiotic; antibacterial; drug design.
XX OS Escherichia coli.
XX PN MO200170955-A2.
XX PD 27-SEP-2001.
XX PF 21-MAR-2001; 2001WO-US09180.
XX PR 21-MAR-2000; 2000US-191078P.
XX PR 23-MAY-2000; 2000US-206848P.
XX PR 26-MAY-2000; 2000US-207727P.
XX PR 23-OCT-2000; 2000US-242578P.
XX PR 27-NOV-2000; 2000US-253625P.
XX PR 22-DEC-2000; 2000US-257931P.
XX PR 16-FEB-2001; 2001US-269308P.
XX PA (ELIT-) ELITRA PHARM INC.
XX PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GU;
XX PI Yamamoto RT, Xu HH;
```

```
DR WPI; 2001-611495/70.
DR N-PSDB; AAS52415.
XX PT New polynucleotides for the identification and development of
XX PT antibiotics, comprise sequences of antisense nucleic acids -
XX PS Example 3; Seq ID No 10149; 511pp; English.
XX CC The invention relates to antisense inhibitors of genes essential to
XX CC prokaryotic cellular proliferation, their use in identifying the
XX CC genes, their use in the discovery of novel antibiotics, the essential
XX CC genes themselves and the encoded proteins. The prokaryotes used are
XX CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
XX CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
XX CC invention is also useful for the identification of potential new targets
XX CC for antibiotic development. The antisense nucleic acids can also be used
XX CC to identify proteins used in proliferation, to express these proteins,
XX CC and to obtain antibodies capable of binding to the expressed proteins.
XX CC The proteins can be used to screen compounds in rational drug discovery
XX CC programmes. The antisense nucleic acid sequence is also useful to screen
XX CC for homologous nucleic acids which are required for cell proliferation in
XX CC a wide variety of organisms. The present sequence represents an
XX CC essential prokaryotic cellular proliferation protein.
XX CC Note: The sequence data for this patent did not form part
XX CC of the printed specification, but was obtained in electronic
XX CC format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 212 AA;
```

```
Query Match 10.9%; Score 94.5; DB 22; Length 212;
Best Local Similarity 23.3%; Pred. No. 0.035;
Matches 48; Conservative 29; Mismatches 70; Indels 59; Gaps 10;
```

```
QY 1 MKKALTLTALA--LPAALAEASGFYQADAAHAK-----ASSLSGSAKGRSPRTISAGY 54
DB 1 MKKLVYAAALAVTTLLSGSAFAHBAEGEFMRAGSAIVYRPEGAGTLGSGRSV----- 54
QY 55 RINDLRFADVTRYKNYKA-----PSTDFKLYSIGASAIYDF----- 91
DB 55 -TNNTOGLGTF--YMTDNGVELLAATPR-HKITRATGDIAYVNHNPITLAKMW 108
QY 92 ---DTQSPVKPYIGARLS-----LNRAVDLGGSDSFQTSIGLGYLGVSYAVTPN 140
DB 109 YFGDASSKFRPYGAGINTTFEDNGFNHGKEAGLSLDKDSWGAGQVVDYLNRD 168
QY 141 --VDLAGRYRNYIGKVNTPKVRSG 164
DB 169 WLVMMSVWTM-----DIDTTANKIG 189

RESULT 9
AAB47447
ID AAB47447 standard; Protein; 353 AA.
XX AC AAB47447;
XX DT 31-OCT-2001 (first entry)
XX DE MOMP P5.
XX KM surface exposed loop; major outer membrane protein P5; MOMP P5;
XX KM non-typeable H. influenzae; ntlH; LB4(f) peptide; B cell epitope;
XX KM otitis media; sinusitis; conjunctivitis;
XX KM lower respiratory tract infection.
XX OS Haemophilus influenzae.
XX PA Key
XX PA Location/Qualifiers
XX FT 38..57
XX FT /label= Loop 1
XX FT /note= "Extracellular domain"
XX FT 89..100
XX FT Domain
```

```

FT      /label= Loop 2           /note= "Extracellular domain"
FT      136..150
FT      Domain
FT      /label= Loop 3
FT      /note= "Extracellular domain"
FT      181..204
FT      Domain
FT      /label= Loop 4
FT      /note= "Extracellular domain"
PN      W0200161013-A1.
XX      23-AUG-2001.
PD
XX      13-FEB-2001; 2001WO-EP01556.
PF
XX      15-FEB-2000; 2000GB-0003502.
XX
XX      (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX      Berthel FJ, Denoel P, Poolman J, Thonnard J;
XX      WPI; 2001-52259/57.
XX
XX      Recombinant bacterial outer membrane protein where one or more
XX      surface-exposed loops are modified is useful as a vaccine to prevent or
XX      treat Haemophilus influenzae infection or associated disease, e.g.,
XX      otitis media and conjunctivitis -
XX      Disclosure; Fig 1; 29pp; English.
XX
CC      This sequence represents the major outer membrane protein p5 of
CC      non-typable H. influenzae. One or more surface exposed loops of this
CC      protein may be replaced with a modified peptide of the invention. Each
CC      of these peptides contain an LBI(f) peptide which is a 19 amino acid
CC      peptide derived from the sequence of MOMP p5 from strain nrl1128,
CC      representing amino acids Arg17 to Gly135. This peptide represents the
CC      third exposed loop of p5 and is a potential B cell epitope. The loops
CC      of the invention are modified in terms of being in a non-native
CC      environment in the recombinant outer membrane protein. The modified
CC      MOMP p5 may be used to induce an immune response in a mammal to
CC      prevent or treat Haemophilus influenzae infection or associated
CC      disease, e.g., otitis media, sinusitis, conjunctivitis, or lower
CC      respiratory tract infection.
XX
SQ      Sequence       353 AA;
          Query Match             10.8%; Score 94; DB 22; Length 353;
          Best Local Similarity    23.8%; Pred. No. 0.08;
          Matches   51; Conservative 30; Mismatches 93; Indels 40; Gaps
OY      1 MKKALATLIALPAAALAEGA---SGFVQDAADAHAKASSLSGS-----AKGHS 47
        ||| | : | | | | : | | | | | | | | | | | | | | | | | | | |
DB      1 MKKTALVALVAGLAASVAQAAPQENTFYAGVKACQASHDGLRALARYKKGYHRNSTP 60
OY      48 PRISAGYRI--NDLRFAV----DYTRYKNYKA PSTDFKLXYSIGA--SAIDPFTOSPY 97
        : | | : | | | | : | | | | | | | | | | | | | | | | | | | |
DB      61 YGVFGYQIQLNNNTNLGLAVELGYDDPGRAKGKREKTKTVKHNHGHSLSKGSYEVLBE 120
OY      98 KPYLCARLSLNAAVDLGSDSFQSOTSIG-----LGYL-TGVSYAVTPPNVDLDAGY-- 147
        : | | : | | | | : | | | | | | | | | | | | | | | | | | | |
DB      121 DYTGGAGVALNSDKLKLYNENSTLKKLGEHRRARASGFAYAGAERYAVLPDLAVRLEYOW 180
OY      148 -----RYNYIGKVNTPVKNVRS--GELSYGVRYKF 174
        : | | : | | | | : | | | | | | | | | | | | | | | | | | | |
DB      181 LTRVGKYRPQOKPNTALNINPMWIGSINAGISTRF 214
XX
RESULT 10
ID      AAU38252
XX      AAU38252 standard; Protein; 257 AA.
XX      AAU38252;

```

DT	14-FEB-2002	(first entry)
XX		
DE	Salmonella typhi cellular proliferation protein #143.	
XX		
KW	Antisense: prokaryotic cellular proliferation protein;	
XX	antibiotic; antibacterial; drug design.	
XX		
OS	Salmonella typhi.	
XX		
PN	WO200170955-A2.	
XX		
PD	27-SEP-2001.	
XX		
PF	21-MAR-2001; 2001WO-US09180.	
XX		
PR	21-MAR-2000; 2000US-191078P.	
XX		
PR	23-MAY-2000; 2000US-206848P.	
XX		
PR	26-MAY-2000; 2000US-207727P.	
XX		
PR	23-OCT-2000; 2000US-242578P.	
XX		
PR	27-NOV-2000; 2000US-253625P.	
XX		
PR	22-DEC-2000; 2000US-257931P.	
XX		
PR	16-FEB-2001; 2001US-269308P.	
XX		
PA	(ELIT-) ELITRA PHARM INC.	
XX		
PI	Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GU;	
XX		
PI	Yanamoto RT, Xu HH;	
XX		
DR	WPI: 2001-611495/70.	
XX		
DR	N-PSDB; AAS56111.	
XX		
XX		
PT	New polynucleotides for the identification and development of	
XX	antibiotics, comprise sequences of antisense nucleic acids -	
XX		
PS	Example 3; Seq ID No 13845; 511pp; English.	
XX		
CC	The invention relates to antisense inhibitors of genes essential to	
XX	prokaryotic cellular proliferation, their use in identifying the	
CC	genes, their use in the discovery of novel antibiotics, the essential	
XX	genes themselves and the encoded proteins. The prokaryotes used are	
CC	Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella	
XX	pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The	
CC	invention is also useful for the identification of potential new targets	
XX	for antibiotic development. The antisense nucleic acids can also be used	
CC	to identify proteins used in proliferation, to express these proteins,	
XX	and to obtain antibodies capable of binding to the expressed proteins.	
CC	The proteins can be used to screen compounds in rational drug discovery	
XX	programmes. The antisense nucleic acid sequence is also useful to screen	
CC	for homologous nucleic acids which are required for cell proliferation in	
XX	a wide variety of organisms. The present sequence represents an	
CC	essential prokaryotic cellular proliferation protein.	
XX	Note: The sequence data for this patent did not form part	
CC	of the printed specification, but was obtained in electronic	
XX	format directly from WIPO at	
CC	ftp.wipo.int/pub/published_pct_sequences.	
XX		
SQ	Sequence 257 AA;	
XX		
Query Match	10.3%; Score 89.5; DB 22; Length 257;	
Best Local Similarity	21.9%; Pred. No. 0.16;	
Matches 46; Conservative 31; Mismatches 70; Indels 63; Gaps 10;		
QY	1 MKKALATLILAL-LPAALACGAGSYQADAAIAK-----ASSLSGAGSFSPRISAG 54	
DB	27 MKKTYVAALALPTLLLSGSAFAHDAGPFPKRAPPAIVRTGCGATGILHNGFD--VS--- 81	
QY	55 RINDLRFAYDYITTKYKKA-----PSTDFKLYSIGAGAIYDF----- 91	
DB	82 --NNTGGLGFT-----YMATDNIIGVLLAIAFR-HKXGTGATGDIATVILLLEPTLMAQ 134	
QY	92 ----DFOGPAKPYIGARLS-----LNRASVDLGGSDSFQSTIGLGVLTGVSAVT-- 138	
DB	135 YFGSSSSKAPRYGVGVNVTTFEDNDFDNGKTKGLSDLSFKDSDKGAAGVGVDYLLN 194	

QY 139 -----PNVDDAGRYNYIGKNTVK 159
 DB 195 WLIGASVWYMDIDTANYKMGVOOHDSVR 224

RESULT 11
 AAY84612
 ID AAY84612 standard; Protein; 180 AA.
 XX
 AC AAY84612;
 XX
 DT 25-JUN-2000 (first entry)
 XX
 DE The outer membrane protein 21 of strain ATCC49143.
 XX
 KM Outer membrane protein 21; OMP21; strain ATCC49143; bacterial infection;
 XX otitis media; respiratory infection; sinusitis; pneumonia; immunisation.
 XX
 OS Moraxella catarrhalis.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 71
 FT /note- "Ala encoded by CCC"
 XX
 PN MO200018910-A1.
 XX
 PD 06-APR-2000.
 XX
 PE 01-OCT-1999; 99MO-US22918.
 XX
 PR 01-OCT-1998; 98US-0164714.
 XX
 PA (ANTE-) ANTEX BIOLOGICS INC.
 XX
 PI Tucker K, Tillmann UF;
 XX
 DR WPI: 2000-293149/25.
 XX
 DR N-PSDB; AAA12591.
 XX
 PT Isolated outer membrane protein from a Moraxella catarrhalis strain
 PT used for diagnosis treatment and prevention of disease caused by M.
 PT catarrhalis e.g. pneumonia, otitis media and respiratory infections -
 XX
 PS Claim 2; Fig 4; 108pp; English.
 XX
 CC The present sequence represents an outer membrane protein 21 (OMP21)
 CC of Moraxella catarrhalis strain ATCC49143. The OMP21 protein has an
 CC apparent molecular weight of 16-20 kD as determined by sodium
 CC dodecylsulfate polyacrylamide gel electrophoresis (SDS-PAGE). OMP21,
 CC its nucleic acids and antibodies can be used in prophylactic and
 CC therapeutic compositions for treating a M. catarrhalis bacterial
 CC infection, otitis media, respiratory infections, sinusitis and
 CC pneumonia. They are useful as reagents for the clinical or medical
 CC diagnosis of M. catarrhalis infections and for scientific research on
 CC the properties of pathogenicity, virulence and infectivity of
 CC M. catarrhalis and host defence mechanisms. The antibodies, particularly
 CC those that are cytotoxic may be used in passive immunisation to prevent
 CC or attenuate M. catarrhalis infections of animals e.g. humans.
 XX
 SQ Sequence 180 AA;

Query Match 10.2%; Score 88.5; DB 21; Length 180;
 Best Local Similarity 26.7%; Pred. No. 0.13;
 Matches 52; Conservative 29; Mismatches 75; Indels 39; Gaps 13;

QY 3 KALATLIA-----LAUPA-AALAGASGF---YVQADAAHAKSSSLGSKGSPRLISA 52
 DB 2 KTLKTLVAVSSSLIAMSANAPISIGNSADAPYVGARIGVDKKQINGKNTATG--TVA 59
 QY 53 GYRINDLFAVDY-----TRYKNYKAPSTDFK--LYSIGASAIYDPD--TQSPVKPYLGLARL 105
 DB 60 GYNF-DQNFGEVAEVGSDAKEFNAGVSPYAGDVKSGFCAVOTYRYNPLNIDF--YANGKL 116

QY 106 SLNKRASVDLGG-----SDSFQSTSIGLGVLTNGSVATPNVDDAGRYNYIGKNTVK 159
 DB 117 GIAKTQVDYTSRNATYTSNKSXDKTSLAGCV--GVGFKPLANVGVBAS--YNYLSB----- 167

QY 160 NVRSSELSYGVRYKF 174
 DB 168 --DANAISLGAHLAF 180

RESULT 12
 AAY34533
 ID AAY34533 standard; Protein; 204 AA.
 XX
 AC AAY34533;
 XX
 DT 25-AUG-1999 (first entry)
 XX
 DE Porphyromonas gingivalis protein PG64.
 XX
 KM Porphyromonas gingivalis; PG; periodontal disease; gingivitis;
 XX vaccine; antigenic.
 XX
 OS Porphyromonas gingivalis.
 XX
 PN WO9929870-A1.
 XX
 PD 17-JUN-1999.
 XX
 PE 10-DEC-1998; 98MO-AU01023.
 XX
 PR 04-AUG-1998; 98AU-0005028.
 XX
 PR 10-DEC-1997; 97AU-0000839.
 XX
 PR 31-DEC-1997; 97AU-0001182.
 XX
 PR 30-JAN-1998; 98AU-0001546.
 XX
 PR 10-MAR-1998; 98AU-0002264.
 XX
 PR 09-APR-1998; 98AU-0002911.
 XX
 PR 23-APR-1998; 98AU-0003128.
 XX
 PR 05-MAY-1998; 98AU-0003338.
 XX
 PR 22-MAY-1998; 98AU-0003654.
 XX
 PR 29-JUL-1998; 98AU-0004917.
 XX
 PA (CSLC-) CSL LTD.
 XX
 PI Agius CT, Barr IG, Hocking DM, Margetts MB, Patterson MA;
 PI Ross BC, Rothel LJ, Webb EA;
 XX
 DR WPI: 1999-385613/32.
 XX
 DR N-PSDB; AAX91751.
 XX
 PT Antigenic Porphyromonas gingivalis peptides for preventing
 PT gingivitis
 XX
 PS Claim 1; Page 524; 588pp; English.
 XX
 CC AAX91536 to AAX91801 encode two hundred and sixty six antigenic
 CC Porphyromonas gingivalis (Pg) polypeptide sequences given in AAY34318 to
 CC AAY34583. AAX91802 to AAX91989 represent PCR primers used in the
 CC isolation of the Pg polypeptides. The Pg polypeptides have antibacterial
 CC activity with a vaccine mechanism of action. The Pg polypeptides can be
 CC used as vaccines especially against Porphyromonas gingivalis. Probes can
 CC be used to detect Porphyromonas gingivalis in standard hybridisation
 CC assays. Porphyromonas gingivalis is involved in periodontal disease
 CC especially gingivitis.
 XX
 SQ Sequence 204 AA;

Query Match 10.2%; Score 88.5; DB 20; Length 204;
 Best Local Similarity 22.1%; Pred. No. 0.15;
 Matches 40; Conservative 35; Mismatches 65; Indels 41; Gaps 8;

QY 8 LIALALPAAA-LAEGASGYVQADAAHAKASSSIGAKFSR-----ISAGRYINDL 59

Db 51 IGVLRGAAAEAFALNDGFIAPGLAVTMGAKMESLSETTTRHLIQLIPVNAQMRRS-- 108
 QY 60 RFADYTRYKNNKAPSPDFELYSIGASAIYDPTQSPVRYLGLARLSLNRAVDLGSDS 119
 Db 109 -FA-----DNNALISLEAGPYFAYGVAGTIK---TKVAGVTAADAFDGDG 149
 QY 120 FSGTSGIGLVLTGVSAYVTPNVLDAGYRNYIGKVNTK-----NVRSGELSVGRVK 173
 Db 150 YNRFDLGLGLSALSY---DRIYVQIGYEH---GILNMLKADAPKTSIRNHDFFVGLGVR 203
 QY 174 F 174
 Db 204 F 204

RESULT 13
 AAY34400
 ID AAY34400 standard; Protein; 221 AA.
 AC AAY34400;
 DF 25-AUG-1999 (first entry)
 DE Porphyromonas gingivalis protein PG64.
 KM Porphyromonas gingivalis; PG; periodontal disease; gingivitis;
 OS vaccine; antigenic.
 XX Porphyromonas gingivalis.
 XX WO9929870-A1.
 PN 17-JUN-1999.
 PD 10-DEC-1998; 98WO-AU01023.
 PR 04-AUG-1998; 98AU-0005028.
 PR 10-DEC-1997; 97AU-0000839.
 PR 31-DEC-1997; 97AU-0001182.
 PR 30-JAN-1998; 98AU-0001546.
 PR 10-MAR-1998; 98AU-0002264.
 PR 09-APR-1998; 98AU-0002911.
 PR 23-APR-1998; 98AU-0003128.
 PR 05-MAY-1998; 98AU-0003338.
 PR 22-MAY-1998; 98AU-0003654.
 PR 29-JUL-1998; 98AU-0004917.
 XX (CSLC-) CSL LTD.
 PA Agius CT, Barr IG, Hocking DM, Margolis MB, Patterson MA;
 PI Ross BC, Rothel LJ, Webb EA;
 DR WPI: 1999-385613/32.
 DR N-PSDB; AAX91618.
 PT Antigenic Porphyromonas gingivalis peptides for preventing
 PT gingivitis
 PS Claim 1; Page 371; 588pp; English.
 XX AAX91536 to AAX91801 encode two hundred and sixty six antigenic
 CC Porphyromonas gingivalis (PG) polypeptide sequences given in AAY34318 to
 CC AAY34583. AAX91802 to AAX91989 represent PCR primers used in the
 CC isolation of the PG polypeptides. The PG polypeptides have antibacterial
 CC activity with a vaccine mechanism of action. The PG polypeptides can be
 CC used as vaccines especially against Porphyromonas gingivalis. Probes can
 CC be used to detect Porphyromonas gingivalis in standard hybridisation
 CC assays. Porphyromonas gingivalis is involved in periodontal disease
 CC especially gingivitis.
 XX Sequence 221 AA;
 SO Query Match 10.2%; Score 88.5; DB 20; Length 221;

Best Local Similarity 22.1%; Pred. No. 0.17;
 Matches 40; Conservative 35; Mismatches 65; Indels 41; Gaps 8;
 QY 8 LIALPAAA-LAEGASGFYVQADAAHAKASSLSIGAKFSPP-----ISAGYRINDL 59
 Db 68 IGVLRGAAAEAFALNDGFIAPGLAVTMGAKMESLSETTTRHLIQLIPVNAQMRRS-- 125
 QY 60 RFADYTRYKNNKAPSPDFELYSIGASAIYDPTQSPVRYLGLARLSLNRAVDLGSDS 119
 Db 126 -FA-----DNNALISLEAGPYFAYGVAGTIK---TKVAGVTAADAFDGDG 166
 QY 120 FSGTSGIGLVLTGVSAYVTPNVLDAGYRNYIGKVNTK-----NVRSGELSVGRVK 173
 Db 167 YNRFDLGLGLSALSY---DRIYVQIGYEH---GILNMLKADAPKTSIRNHDFFVGLGVR 220
 QY 174 F 174
 Db 221 F 221

RESULT 14
 AAW68202
 ID AAW68202 standard; Protein; 573 AA.
 AC AAW68202;
 DF 07-OCT-1998 (first entry)
 DE M. catarrhalis strain O35E UspA2 antigen.
 KM Moraxella catarrhalis; UspA1; UspA2; antigen; genetic vaccination;
 KM vaccine; otitis media; sinusitis; lower respiratory tract infection;
 KM immunity enhancer; immunoassay reagent.
 XX Moraxella catarrhalis.
 OS WO9828333-A2.
 PN 02-JUL-1998.
 PD 19-DEC-1997; 97WO-US23930.
 PR 20-DEC-1996; 96US-00033598.
 XX (TEXA) UNIT TEXAS SYSTEM.
 PA Aebi C, Cope LD, Fiske MJ, Friedenburt R, Hansen EJ;
 PI Maciver I;
 DR WPI: 1998-377595/32.
 DR N-PSDB; AAW41342.
 PT New peptide(s) containing the core epitope of Moraxella catarrhalis
 PT Usp proteins - useful in, e.g. vaccines to prevent or treat M.
 PT catarrhalis infection, and antibodies for passive immunisation
 PS Claim 24; Pages 138-140; 237pp; English.
 XX This represents a UspA2 antigen of Moraxella catarrhalis strain O35E.
 CC Nucleic acid sequences encoding the UspA1 and A2 antigens of
 CC M. catarrhalis isolates O35E, O46E, TR24 and TR237 can be used in
 CC genetic vaccination. An antigenic composition or vaccine containing
 CC antigenic peptides from UspA1 or UspA2 antigens are used to induce an
 CC immune response in mammals against M. catarrhalis and can be used to
 CC treat infections such as otitis media, sinusitis, lower respiratory
 CC tract infections. They can also be used as immunity enhancers for other
 CC bacterial, parasitic or viral antigens, to raise antibodies and as
 CC immunoassay reagents for detecting specific antibodies. The antibodies
 CC are useful for passive immunisation and as immunoassay reagents.
 CC Detection of the epitopic core sequence, by immunoassay or by PCR, is
 CC used to diagnose infection. The Usp antigens encoding nucleic acid
 CC sequences are also used to produce recombinant proteins and for screening
 CC for potential anti-M. catarrhalis agents, while their fragments are

CC useful as diagnostic probes or primers or to isolate variant sequences.
 XX Sequence 573 AA;

Query Match 10.2%; Score 88.5; DB 19; Length 573;
 Best Local Similarity 24.6%; Pred. No. 0.62;
 Matches 42; Conservative 29; Mismatches 59; Indels 41; Gaps 9;

QY 19 AEGASGEFYQADA-----AHAKASSLSGS-AKGFSPRISA-GYRINDLRPAVDYTR 67
 DB 429 ASADTKFAATADAITKNGNAITKNAKSTIDLGKVDGFGRVLTALDTRKVNAL----- 480
 OY 68 YKNKAPSTDKLXISGASAIYDFQSPV-----KPYLGARLSINRASVDLGSDSFSQ 123
 DB 481 --DTRKNAFDRITALDSKVENMAAQAALSGLFQPYSVGKFN--ATAALGGYGSKSAV 535
 QY 124 SIGIGVLTVGSYAVTPVNDLDAGRYRYTIGKNTVKNVRSGLSVGYRVKF 174
 DB 536 AIGAG-----YRVNPNLAFKAG-----AAINTSGN-KKGSYNTGVNVEF 573

RESULT 15

AAW68206
 ID AAW68206 standard; Protein: 610 AA.

XX AC AAW68206;

XX DT 07-OCT-1998 (first entry)

XX DE M. catarrhalis strain TTA24 Uspa2 antigen.

XX KW Moraxella catarrhalis; Uspa1; Uspa2; antigen; genetic vaccination;
 KW vaccine; otitis media; sinusitis; lower respiratory tract infection;
 KW immunity enhancer; Immunossay reagent.

XX OS Moraxella catarrhalis.

XX PN W09828333-A2.

XX PD 02-JUL-1998.

XX PF 19-DEC-1997; 97WO-US23930.

XX PR 20-DEC-1996; 96US-0033598.

XX PA (TEXA) UNIV TEXAS SYSTEM.

XX PI Aebi C, Cope ID, Fiske MJ, Fredenburg R, Hansen EJ;
 PI MacIver I;

XX DR WPI: 1998-377595/32.

XX DR N-PSDB: AAV41346.

XX PT New peptide(s) containing the core epitope of Moraxella catarrhalis
 PT Usp proteins - useful in, e.g. vaccines to prevent or treat M.
 PT catarrhalis infection, and antibodies for passive immunisation

XX PS Claim 32; Pages 157-159; 237pp; English.

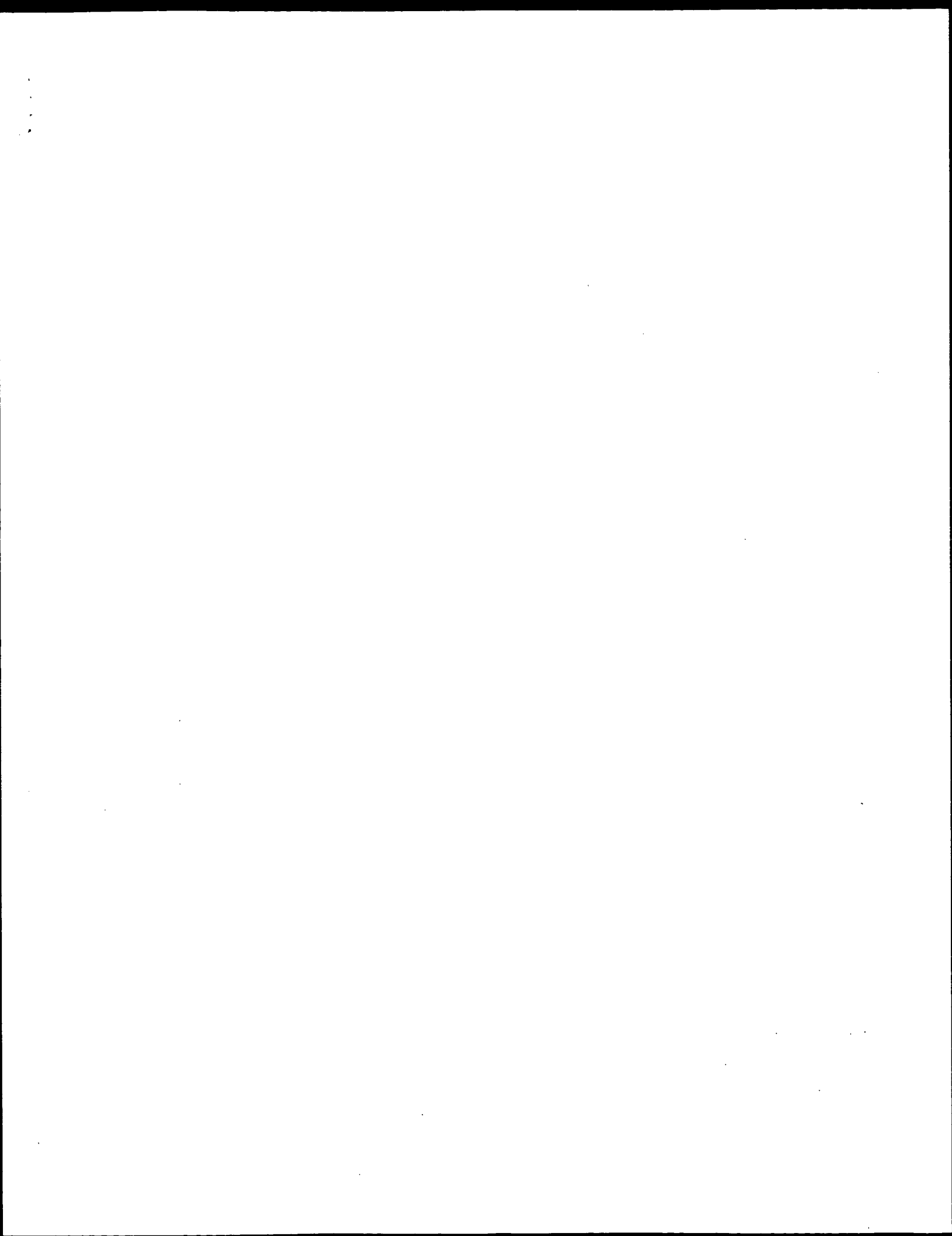
XX CC This represents a Uspa2 antigen of Moraxella catarrhalis strain TTA24.
 CC Nucleic acid sequences encoding the Uspa1 and A2 antigens of
 CC M. catarrhalis isolates 035E, 046E, TTA24 and TTA37 can be used in
 CC genetic vaccination. An antigenic composition or vaccine containing
 CC antigenic peptides from Uspa1 or Uspa2 antigens are used to induce an
 CC immune response in mammals against M. catarrhalis and can be used to
 CC treat infections such as otitis media, sinusitis, lower respiratory
 CC tract infections. They can also be used as immunity enhancers for other
 CC bacterial, parasitic or viral antigens, to raise antibodies and as
 CC immunossay reagents for detecting specific antibodies. The antibodies
 CC are useful for passive immunisation and as immunossay reagents.
 CC Detection of the epitopic core sequence, by immunossay or by PCR, is
 CC used to diagnose infection. The Usp antigens encoding nucleic acid
 CC sequences are also used to produce recombinant proteins and for screening

CC for potential anti-M. catarrhalis agents, while their fragments are
 CC useful as diagnostic probes or primers or to isolate variant sequences.
 XX Sequence 610 AA;

Query Match 10.1%; Score 88; DB 19; Length 610;
 Best Local Similarity 26.0%; Pred. No. 0.76;
 Matches 45; Conservative 22; Mismatches 54; Indels 52; Gaps 9;

QY 19 AEGASGEFYQADA-----AHAKASSLSGS-AKGFSPRISA-GYRIN--DLRPAVDY 65
 DB 473 ASADTKFAATADAITKNGNAITKNAKSTIDLGKVDGFGRVLTALDTRKVNALDGRIT 532
 QY 66 TRYKN-----YKAPSTDFKLXISGASAIYDFQSPVYPYLGARLSINRASVDLGSDSFS 121
 DB 533 SKVENGMAAQAALSGLFQPYSVGKFN-----NATAALGGYGSKSAV 570
 QY 122 QTSIGIGVLTVGSYAVTPVNDLDAGRYRYTIGKNTVKNVRSGLSVGYRVKF 174
 DB 571 AVALGAG-----YRVNPNLAFKAG-----AAINTSGN-KKGSYNTGVNVEF 610

Search completed: October 28, 2002, 16:00:36
 Job time : 26.7145 secs



GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 28, 2002, 15:58:54 ; Search time 9.48637 Seconds
(without alignments)
448.017 Million cell updates/sec

Title: US-09-684-883-2

Perfect score: 868
Sequence: 1 MKKALATLIALPAALAE.....VTVKVRSGELSYGVRYKF 174

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCTUS.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfilest1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	868	100.0	174	4	US-08-913-362-2
2	854	98.4	174	4	US-08-913-362-6
3	838.5	96.6	175	4	US-08-913-362-30
4	825	95.0	174	4	US-08-913-362-8
5	824.5	95.0	175	4	US-08-913-362-4
6	135	15.6	170	1	US-08-127-499A-20
7	135	15.6	170	1	US-08-482-847-20
8	133	15.3	25	4	US-08-913-362-26
9	88.5	10.2	573	4	US-09-336-447A-3
10	88	10.1	359	1	US-08-457-997B-2
11	88	10.1	359	3	US-08-467-722A-2
12	88	10.1	610	4	US-09-336-447A-11
13	88	10.1	624	4	US-09-336-447A-7
14	88	10.1	889	4	US-09-336-447A-15
15	87	10.0	16	4	US-08-913-362-15
16	85	9.8	568	5	PCT-US95-13749-5
17	82	9.4	433	2	US-08-883-515-2
18	81	9.3	15	4	US-08-913-362-23
19	79	9.1	15	4	US-08-913-362-18
20	78.5	9.0	286	1	US-08-382-184-3
21	78.5	9.0	286	2	US-08-641-356-3
22	78.5	9.0	286	4	US-09-132-528-4
23	78.5	9.0	286	4	US-08-875-494-3
24	78.5	9.0	286	4	US-09-599-366-4
25	78.5	9.0	325	1	US-08-382-184-2
26	78.5	9.0	325	2	US-08-641-356-2
27	78.5	9.0	325	4	US-09-132-528-2

28	78.5	9.0	325	4	US-09-132-528-3	Sequence 3, Appl1
29	78.5	9.0	325	4	US-08-875-494-2	Sequence 2, Appl1
30	78.5	9.0	325	4	US-09-599-366-2	Sequence 2, Appl1
31	78.5	9.0	325	4	US-09-599-366-3	Sequence 3, Appl1
32	78.5	9.0	332	4	US-08-818-112-53	Sequence 53, Appl1
33	78.5	9.0	332	4	US-08-818-111-53	Sequence 53, Appl1
34	78.5	9.0	332	4	US-09-056-556-53	Sequence 53, Appl1
35	78.5	9.0	802	4	US-09-056-556-214	Sequence 53, Appl1
36	78	9.0	15	4	US-08-913-362-14	Sequence 214, App
37	78	9.0	15	4	US-08-913-362-16	Sequence 14, Appl
38	77	8.9	15	4	US-08-913-362-11	Sequence 16, Appl
39	77	8.9	15	4	US-08-913-362-13	Sequence 11, Appl
40	77	8.9	2123	4	US-08-968-685A-10	Sequence 10, Appl
41	76	8.8	15	4	US-08-913-362-17	Sequence 17, Appl
42	76	8.8	15	4	US-08-913-362-22	Sequence 22, Appl
43	76	8.8	15	4	US-08-913-362-24	Sequence 24, Appl
44	76	8.8	207	2	US-08-381-881-6	Sequence 6, Appl1
45	76	8.8	207	4	US-09-281-221-6	Sequence 6, Appl1

ALIGNMENTS

RESULT 1
US-08-913-362-2
Sequence 2, Application US/08913362
Patent No. 6287574
GENERAL INFORMATION:
APPLICANT: Brodeur, Bernard R
APPLICANT: Martin, Denis
APPLICANT: Hamel, Josee
APPLICANT: Rioux, Clement
TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/001,983
FILING DATE: 04-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 047998/0128
TELEPHONE: (202)672-5300
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5399
TELEFAX: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-913-362-2
Query Match 100.0%, Score 868, DB 4, Length 174.

Best Local Similarity 100.0%; Pred. No. 3e-93;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
DB 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
QY 61 FAVDYTRYKNKAPSTDFKLYSIGASAIYDFDQSPVKPYLGARLSLNRAASVDLGSSDSF 120
DB 61 FAVDYTRYKNKAPSTDFKLYSIGASAIYDFDQSPVKPYLGARLSLNRAASVDLGSSDSF 120
QY 121 SQTSGIGLVLTGVSYAVTPNVDLDAGYRYNYIGKVTYKKNVRSGLSVGRVVF 174
DB 121 SQTSGIGLVLTGVSYAVTPNVDLDAGYRYNYIGKVTYKKNVRSGLSVGRVVF 174

RESULT 2

US-08-913-362-6
; Sequence 6, Application US/08913362
; Patent No. 6287574

GENERAL INFORMATION:

APPLICANT: Brodeur, Bernard R
APPLICANT: Martin, Denis
APPLICANT: Hamel, Josee
APPLICANT: Rioux, Clement
TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/001,983
FILING DATE: 04-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 04/998/0128
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-913-362-6

Query Match 98.4%; Score 854; DB 4; Length 174;
Best Local Similarity 98.3%; Pred. No. 1.3e-91;
Matches 171; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
DB 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

QY 61 FAVDYTRYKNKAPSTDFKLYSIGASAIYDFDQSPVKPYLGARLSLNRAASVDLGSSDSF 120
DB 61 FAVDYTRYKNKAPSTDFKLYSIGASAIYDFDQSPVKPYLGARLSLNRAASVDLGSSDSF 120

QY 121 SQTSGIGLVLTGVSYAVTPNVDLDAGYRYNYIGKVTYKKNVRSGLSVGRVVF 174
DB 121 SQTSGIGLVLTGVSYAVTPNVDLDAGYRYNYIGKVTYKKNVRSGLSVGRVVF 174

RESULT 3

US-08-913-362-30
; Sequence 30, Application US/08913362
; Patent No. 6287574

GENERAL INFORMATION:

APPLICANT: Brodeur, Bernard R
APPLICANT: Martin, Denis
APPLICANT: Hamel, Josee
APPLICANT: Rioux, Clement
TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/001,983
FILING DATE: 04-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 04/998/0128
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-913-362-30

Query Match 96.6%; Score 838.5; DB 4; Length 175;
Best Local Similarity 97.1%; Pred. No. 8.1e-90;
Matches 170; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
DB 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
QY 61 FAVDYTRYKNKAPSTDFKLYSIGASAIYDFDQSPVKPYLGARLSLNRAASVDLGSSDS 119
DB 61 FAVDYTRYKNKAPSTDFKLYSIGASAIYDFDQSPVKPYLGARLSLNRAASVDLGSSDS 120
QY 120 SQTSGIGLVLTGVSYAVTPNVDLDAGYRYNYIGKVTYKKNVRSGLSVGRVVF 174
DB 120 SQTSGIGLVLTGVSYAVTPNVDLDAGYRYNYIGKVTYKKNVRSGLSVGRVVF 174


```

Db      121  ESQTSXGLGVLAGVSYAVTPNVNDLAGYRNNIGKVTNTKNNRSGELSGAVRYKF 175

RESULT 4
US-08-913-362-8
; Sequence 8, Application US/08913362
; Patent No. 6287574
; GENERAL INFORMATION:
;   APPLICANT: Brodeur, Bernard R
;   APPLICANT: Martin, Denis
;   APPLICANT: Hamel, Josee
;   APPLICANT: Rioux, Clement
;   TITLE OF INVENTION: PROTEINASE R RESISTANT SURFACE PROTEIN
;   TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
;   NUMBER OF SEQUENCES: 30
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Foley & Lardner
;     STREET: 3000 K Street, N.W., Suite 500
;     CITY: Washington
;     STATE: D.C.
;     COUNTRY: USA
;     ZIP: 20007-5109
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/913,362
;     FILING DATE: 13-NOV-1997
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 08/406,362
;     FILING DATE: 17-MAR-1995
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 60/001,983
;     FILING DATE: 04-AUG-1995
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Bent, Stephen A.
;     REGISTRATION NUMBER: 29,768
;     REFERENCE/DOCKET NUMBER: 047998/0128
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE: (202)672-5300
;       TELEFAX: (202)672-5399
;     TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 8:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 174 amino acids
;       TYPE: amino acid
;       TOPOLOGY: linear
;     MOLECULE TYPE: protein
;   US-08-913-362-8

Query Match      95.0%; Score 825; DB 4; Length 174;
Best Local Similarity 94.3%; Pred. No. 3e-88;
Matches 164; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY      1  MKKALATLIALALPAAALAEAGSGTYQADAAHAHAASSLSGAKGFSRISAGYRINDR 60
      1  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1  MKKALATLIALALPAAALAEAGSGTYQADAAHAHAASSLSGAKGFSRISAGYRINDR 60
      1  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY      61  FAVDYTRKKNYKAPSTDEKLYSIGASATYDEPTQSPVKPYLDGARLSLNKASVDLGSDSF 120
      61  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      61  FAVDYTRKKNYKAPSTDEKLYSIGASATYDEPTQSPVKPYLDGARLSLNKASVDLGSDSF 120
      61  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY      121  SQTSGIGLVGVSYAVTPNVNDLDGGRYNTYKGYNTYKANNVSGELSGAVRYKF 174
      121  | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      121  SQTSGIGLVGVSYAVTPNVNDLDGGRYNTYKGYNTYKANNVSGELSGAVRYKF 174
      121  | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 5
US-08-913-362-4
; Sequence 4, Application US/08913362
; Patent No. 6287574

```

```

GENERAL INFORMATION:
APPLICANT: Brodeur, Bernard R
APPLICANT: Martin, Denis
APPLICANT: Hamel, Josee
APPLICANT: Rioux, Clement
TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
City: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/001,983
FILING DATE: 04-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 047998/0128
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-913-362-4

Query Match          95.0%; Score 824.5; DB 4; Length 175;
Best Local Similarity 95.4%; Pred. No. 3.5e-88;
Matches 167; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

OY 1 MKKALATLIALPAALALEGASGTYVQADAHAHAKASSLGSAGSPRISAGRIINDLR 60
    |||||
Db 1 MKKALATLIALPAALALEGASGTYVQADAHAHAKASSLGSAGSPRISAGRIINDLR 60
OY 61 FAVDYTRYKKYK-APSTDFKLSIGASATYDFDTPSPYKPYLGARLSLNASVDLGGSDS 119
    |||||
Db 61 FAVDYTRYKKYKQYPSTDEKLSIGASATYDFDTPSPYKPYLGARLSLNASVDFFMGSDS 120
OY 120 FSGTSLGLVLTGSYAVTPNVDLDAGYKRYNIGKRVNTVKNVRSGLSVGRVKE 174
    |||||
Db 121 FSGTSLGLVLTGSYAVTPNVDLDAGYKRYNIGKRVNTVKNVRSGLSVGRVKE 175

RESULT 6
US-08-127-499A-20
; Sequence 20, Application US/08127499A
; Patent No. 5510264
; GENERAL INFORMATION:
; APPLICANT: VAN ALSTYNE, Diane
; APPLICANT: SHARMA, Lawrence Rajendra
; TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
; TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
;

```

ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,499A
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/102/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-127-499A-20

Query Match 15.6%; Score 135; DB 1; Length 170;
Best Local Similarity 26.3%; Pred. No. 5.3e-08;
Matches 41; Conservative 20; Mismatches 47; Indels 48; Gaps 4;

QY 6 ATTALALPAAALAEAGSGFYVQADAH-----AKASSIGS-----AKG 45
::: : || : : ||||| : : : : :
DB 15 SSLFSSAAQAASEDRSPYVQADLVAERITHDYPQATGANNTSVSDYFNIRAH 74
QY 46 FSPRISAGYRINDREFADVTRYKNY-----KAPSTDEK 79
||: || ||: || ||: || : : : :
DB 75 IHPRVSVGDEFGWRVIAADYASYSKMNKYSVNTKELENKHNKKDKLTENQENGFHA 134
QY 80 IYSIGASAIYDFDQSPYKPYLGARSLN--RASVD 113
:|: ||||| : ||: ||||| : : : :
DB 135 ASSLSAISYDFKLGKFKPYIGARVAAGYHRHSID 170

RESULT 7
US-08-482-847-20
Sequence 20, Application US/08482847
Patent No. 5536757
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
NUMBER OF INVENTION: CNS CARRIER, ANTIBODIES THEREOF, AND USES THEREOF
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,847
FILING DATE: 07-JUN-1995

CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/104/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-482-847-20

Query Match 15.6%; Score 135; DB 1; Length 170;
Best Local Similarity 26.3%; Pred. No. 5.3e-08;
Matches 41; Conservative 20; Mismatches 47; Indels 48; Gaps 4;

QY 6 ATTALALPAAALAEAGSGFYVQADAH-----AKASSIGS-----AKG 45
::: : || : : ||||| : : : : :
DB 15 SSLFSSAAQAASEDRSPYVQADLVAERITHDYPQATGANNTSVSDYFNIRAH 74
QY 46 FSPRISAGYRINDREFADVTRYKNY-----KAPSTDEK 79
||: || ||: || ||: || : : : :
DB 75 IHPRVSVGDEFGWRVIAADYASYSKMNKYSVNTKELENKHNKKDKLTENQENGFHA 134
QY 80 IYSIGASAIYDFDQSPYKPYLGARSLN--RASVD 113
:|: ||||| : ||: ||||| : : : :
DB 135 ASSLSAISYDFKLGKFKPYIGARVAAGYHRHSID 170

RESULT 8
US-08-913-362-26
Sequence 26, Application US/08913362
Patent No. 6287574
GENERAL INFORMATION:
APPLICANT: Brodeur, Bernard R
APPLICANT: Martin, Denis
APPLICANT: Hamel, Josee
APPLICANT: Rioux, Clement
TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/001,983
FILING DATE: 04-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 047998/0128
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Neisseria meningitidis
STRAIN: 6088
US-08-913-362-26

Query Match 15.3%; Score 133; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.2e-09;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 FAVDYTRYKNYKAPSTDFKLYSIGA 85
1 FAVDYTRYKNYKAPSTDFKLYSIGA 25

RESULT 9
US-09-336-447A-3
Sequence 3, Application US/09336447A
Patent No. 6310190
GENERAL INFORMATION:
APPLICANT: HANSEN, ERIC J.
APPLICANT: AEBI, CHRISTOPH
APPLICANT: COPE, LESLIE D.
APPLICANT: MACIVER, ISOBEL
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FREDENBURG, ROSS A.
TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
FILE REFERENCE: AMCY:024
CURRENT APPLICATION NUMBER: US/09/336,447A
CURRENT FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 3
LENGTH: 573
TYPE: PRP
ORGANISM: Moraxella catarrhalis
US-09-336-447A-3

Query Match 10.2%; Score 88.5; DB 4; Length 573;
Best Local Similarity 24.6%; Pred. No. 0.084;
Matches 42; Conservative 29; Mismatches 59; Indels 41; Gaps 9;

QY 19 AEGASGFYQADA-----AHAKASSLSGS-AKGFSPRISA-GYRINDLRFVADYTR 67
1 AEGASGFYQADA-----AHAKASSLSGS-AKGFSPRISA-GYRINDLRFVADYTR 67
DB 429 ASADTFAATADAITKNGAIAITKNAKSTDLDTKYDFGGRVATLDTKYNAL----- 480
QY 68 YKNYKAPSTDFKLYSIGASAIYDFDQSPV---KPYLGARLSLNKASVDLGSDFSQGT 123
1 YKNYKAPSTDFKLYSIGASAIYDFDQSPV---KPYLGARLSLNKASVDLGSDFSQGT 123
DB 481 --DTKNAFDGRITLDSKVENGMMAQALSGLFQPSYSGKFN--ATRALGGYSGSKAV 535
1 --DTKNAFDGRITLDSKVENGMMAQALSGLFQPSYSGKFN--ATRALGGYSGSKAV 535
QY 124 SIGLGVLTGVSAVTPNVLDLGGYRNYGKYNVYKAVNAGSGELSGVRYKPF 174
1 SIGLGVLTGVSAVTPNVLDLGGYRNYGKYNVYKAVNAGSGELSGVRYKPF 174
DB 536 AIGAG-----YRVNPNLAFFKAG-----MAINTSGN-KKGSYNIGVNYEF 573
1 AIGAG-----YRVNPNLAFFKAG-----MAINTSGN-KKGSYNIGVNYEF 573

RESULT 10
US-08-457-997B-2
Sequence 2, Application US/08457997B
Patent No. 576608
GENERAL INFORMATION:
APPLICANT: Kolattukudy, P. E.
TITLE OF INVENTION: Otitis Media Vaccine
NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:
ADDRESSEE: Calfee, Halter and Griswold
STREET: Suite 1800 800 Superior Avenue
CITY: Cleveland
STATE: Ohio
COUNTRY: U.S.A.
ZIP: 44114-2688
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,997B
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Colrick, Mary E.
REGISTRATION NUMBER: 34,829
REFERENCE/DOCKET NUMBER: 22727/00102
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 622-8458
TELEFAX: (216) 241-0816
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-457-997B-2

Query Match 10.1%; Score 88; DB 1; Length 359;
Best Local Similarity 22.7%; Pred. No. 0.048;
Matches 52; Conservative 29; Mismatches 84; Indels 64; Gaps 11;

QY 1 MKKALATLIALALPAAALAEBA---SGFYQADA-----HAKSSSLSGAKGSPRISAG 53
1 MKKALATLIALALPAAALAEBA---SGFYQADA-----HAKSSSLSGAKGSPRISAG 53
DB 1 MKKALALVAGLAASVQAAPQENTFYAGYKAGGSGFHDGINNCAIKGLSSS-NG 59
QY 54 YRINDLRFVADYTRYKNYKAPSTDFKLYSIGASAIYDFD-----TQSPYKPYL----- 102
1 YRINDLRFVADYTRYKNYKAPSTDFKLYSIGASAIYDFD-----TQSPYKPYL----- 102
DB 60 YRRNTFTYGV---FGGYQLINOD---NGLAAELGYDDPGRAKLREAGKPRAKHTNNG 111
1 YRRNTFTYGV---FGGYQLINOD---NGLAAELGYDDPGRAKLREAGKPRAKHTNNG 111
QY 103 ARSLNRAVDLGGSDSEFSQTSIGL-----GVL-TGVAS 134
1 ARSLNRAVDLGGSDSEFSQTSIGL-----GVL-TGVAS 134
DB 112 AYLISLGSYEVLIDGYGKAGVALVRSQDYKFEEDANGTRDHHKGRHTARASGLFVNGAE 171
1 AYLISLGSYEVLIDGYGKAGVALVRSQDYKFEEDANGTRDHHKGRHTARASGLFVNGAE 171
QY 135 YAVTPNVLDLGGY-----RYNTIGKYNVYKAVRS--GELSGVRYKPF 174
1 YAVTPNVLDLGGY-----RYNTIGKYNVYKAVRS--GELSGVRYKPF 174
DB 172 YAVPELAVRLEYQMLTRVGKYPQDKPMTAINYNPMWIGCINAGISYRF 220
1 YAVPELAVRLEYQMLTRVGKYPQDKPMTAINYNPMWIGCINAGISYRF 220

RESULT 11
US-08-467-722A-2
Sequence 2, Application US/08467722A
Patent No. 6030626
GENERAL INFORMATION:
APPLICANT: Kolattukudy, P. E.
TITLE OF INVENTION: Otitis Media Vaccine
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calfee, Halter and Griswold
STREET: Suite 1800 800 Superior Avenue
CITY: Cleveland
STATE: Ohio
COUNTRY: U.S.A.
ZIP: 44114-2688
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

```

; APPLICATION NUMBER: US/08/467,722A
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Goltick, Mary E.
; REGISTRATION NUMBER: 34,829
; REFERENCE/DOCKET NUMBER: 22727/00102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (216) 622-8458
; TELEFAX: (216) 241-0816
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-467-722A-2

Query Match
Best Local Similarity 10.1%; Score 88; DB 3; Length 359;
Best Local Similarity 22.7%; Pred. No. 0.048;
Matches 52; Conservative 29; Mismatches 84; Indels 64; Gaps 11;

QY 1 MKKALATLIALPALAALAGA---SGFYQADAA---HAKASSLSGSKGSPRISAG 53
D 1 MKKTAIALVVAAGLAASVAADQENTFYAGVAKGCGFDGGINNKAIRKGLSSS-NYG 59
QY 54 YRINDLFAVDYTRKYNKAPSTDFKLYSGASAIYDFD-----TQSPKPYL-----G 102
D 60 YRRNTFTYGV---FGSYQILND---NFGLAELGYDDFGAKLRKAGKPKAKRTNNG 111
QY 103 ARLSLNRAVDLGSDSFSQTSIGL-----GVL-TGVS 134
D 112 AYLSLKGSEYELDGLDYAGAGVALVRSDYEDANGTRDHKKRHRTARASGLFAVGA 171
QY 135 YAVTPNDLDAGY-----RYNIGKVNTKKNVRS--GELSGVRYKF 174
D 172 YAVLPDLAHLRYQLWLTTRVGKTRPDKPNATNPNWIGCINAGISYRF 220

RESULT 12
US-09-336-447A-11
; Sequence 11, Application US/09336447A
; Patent No. 6310190
; GENERAL INFORMATION:
; APPLICANT: HANSEN, ERIC J.
; APPLICANT: AEBI, CHRISTOPH
; APPLICANT: COPE, LESLIE D.
; APPLICANT: MACIVER, ISOBEL
; APPLICANT: FISKE, MICHAEL J.
; APPLICANT: FREDENBURG, ROSS A.
; TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
; FILE REFERENCE: AMCY:024
; CURRENT APPLICATION NUMBER: US/09/336,447A
; CURRENT FILING DATE: 1999-06-21
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 610
; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
US-09-336-447A-11

Query Match
Best Local Similarity 10.1%; Score 88; DB 4; Length 610;
Best Local Similarity 26.0%; Pred. No. 0.11;
Matches 45; Conservative 22; Mismatches 54; Indels 52; Gaps 9;

QY 19 AEGASGTYVADA-----AHAKASSLSG--AKGFSPRISA-GYRIN--DLRFADV 65
D 473 ASADTRKFAATADAITKNGNAITKNAKSITDGLTKVDFGFRVATLDTKNAFEGRTALD 532
QY 66 TRYKN-----YKAPSTDFKLYSGASAIYDFDTPSPVKPLGARLSLNRAVDLGSDSFS 121
D 533 SKVENGMAAQAALSGLPFISYVKF-----NATAALGGYSGKS 570
```

```

QY 122 QTSIGLGYLVGVSAVTPNDLDAGRYNYIGKVTYKRVNSGELSGVRYKF 174
D 571 AVAIGAG-----YRVNPLAFKAG-----AAINTSGN-KKGSYINIGVNTFF 610

RESULT 13
US-09-336-447A-7
; Sequence 7, Application US/09336447A
; Patent No. 6310190
; GENERAL INFORMATION:
; APPLICANT: HANSEN, ERIC J.
; APPLICANT: AEBI, CHRISTOPH
; APPLICANT: COPE, LESLIE D.
; APPLICANT: MACIVER, ISOBEL
; APPLICANT: FISKE, MICHAEL J.
; APPLICANT: FREDENBURG, ROSS A.
; TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
; FILE REFERENCE: AMCY:024
; CURRENT APPLICATION NUMBER: US/09/336,447A
; CURRENT FILING DATE: 1999-06-21
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 624
; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
US-09-336-447A-7

Query Match
Best Local Similarity 10.1%; Score 88; DB 4; Length 624;
Best Local Similarity 26.0%; Pred. No. 0.11;
Matches 45; Conservative 22; Mismatches 54; Indels 52; Gaps 9;

QY 19 AEGASGTYVADA-----AHAKASSLSG--AKGFSPRISA-GYRIN--DLRFADV 65
D 487 ASADTRKFAATADAITKNGNAITKNAKSITDGLTKVDFGFRVATLDTKNAFEGRTALD 546
QY 66 TRYKN-----YKAPSTDFKLYSGASAIYDFDTPSPVKPLGARLSLNRAVDLGSDSFS 121
D 547 SKVENGMAAQAALSGLPFISYVKF-----NATAALGGYSGKS 584
D 585 AVAIGAG-----YRVNPLAFKAG-----AAINTSGN-KKGSYINIGVNTFF 624

RESULT 14
US-09-336-447A-15
; Sequence 15, Application US/09336447A
; Patent No. 6310190
; GENERAL INFORMATION:
; APPLICANT: HANSEN, ERIC J.
; APPLICANT: AEBI, CHRISTOPH
; APPLICANT: COPE, LESLIE D.
; APPLICANT: MACIVER, ISOBEL
; APPLICANT: FISKE, MICHAEL J.
; APPLICANT: FREDENBURG, ROSS A.
; TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
; FILE REFERENCE: AMCY:024
; CURRENT APPLICATION NUMBER: US/09/336,447A
; CURRENT FILING DATE: 1999-06-21
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 889
; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
US-09-336-447A-15

Query Match
Best Local Similarity 10.1%; Score 88; DB 4; Length 889;
Best Local Similarity 26.0%; Pred. No. 0.19;
Matches 45; Conservative 22; Mismatches 54; Indels 52; Gaps 9;
```


A:Molecule type: DNA
 A:Residues: 1-174 <P>
 A:Cross-references: GB:AL162754; GB:AL157959; NID:q7379424; PIDN:CAB84143.1; PID:q737957
 A:Experimental source: serogroup A, strain Z2491
 C:Genetics:
 A:Gene: nsps; NMA0862

Query Match 98.4%; Score 854; DB 2; Length 174;
 Best Local Similarity 98.3%; Pred. No. 1,1e-69;
 Matches 171; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKKALATLIALALPMAALAGAGSYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
 Db 1 MKKALATLIALALPMAALAGAGSYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
 QY 61 FAVDYTRYKKNYKAPSTDEKIXSTGASAIYDPQSPKPYLGLARLSINRASVLDGSDSF 120
 Db 61 FAVDYTRYKKNYKAPSTDEKIXSTGASAIYDPQSPKPYLGLARLSINRASVLDGSDSF 120
 QY 121 SQTSGIGLVLTGVSAYATPVNVDLAGRYNYIKGKNTKKNVRSGLSGVRYKVF 174
 Db 121 SQTSGIGLVLTGVSAYATPVNVDLAGRYNYIKGKNTKKNVRSGLSGVRYKVF 174

RESULT 3

Opacity protein opak precursor - Neisseria gonorrhoeae (strain MS11) (fragments)
 N:Alternate names: outer membrane protein opak
 C:Species: Neisseria gonorrhoeae
 A:Variety: strain MS11

C:Date: 13-Jan-1995 #sequence_revision 17-Oct-1997 #text_change 17-Oct-1997
 R:Bhat, K.S.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsch, M.O. Microbiol. 5, 1889-1901, 1991
 A:Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a fam1
 A:Reference number: S16610; MUID:92114767
 A:Accession: S16610
 A:Molecule type: DNA
 A:Residues: 1-261 <BHA>
 A:Cross-references: EMBL:X52364
 A:Experimental source: strain MS11, variant 4.8
 A:Note: the authors did not translate the sequence for the signal peptide
 A:Note: expression of opacity proteins is regulated by the number of translated repeat
 A:Note: repeats place the start codon in frame with the rest of the protein
 C:Genetics:
 A:Gene: opak
 C:Superfamily: opacity protein
 C:Keywords: cell surface component; transmembrane protein
 F:1-10,11-23/Domain: signal sequence (fragments) #status predicted <SIG>
 F:24-261/Product: opacity protein opak #status predicted <MAT>
 F:34-42/Domain: transmembrane #status predicted <TM1>
 F:43-75/Domain: extracellular #status predicted <EXT1>
 F:51-61/Region: semivariable region
 F:76-84/Domain: transmembrane #status predicted <TM2>
 F:89-95/Domain: transmembrane #status predicted <TM3>
 F:96-134/Domain: extracellular #status predicted <EXT2>
 F:102-129/Region: hypervariable region HV1
 F:135-149/Domain: transmembrane #status predicted <TM4>
 F:155-165/Domain: transmembrane #status predicted <TM5>
 F:166-212/Domain: extracellular #status predicted <EXT3>
 F:171-218/Region: hypervariable region HV2
 F:213-225/Domain: transmembrane #status predicted <TM6>
 F:229-237/Domain: transmembrane #status predicted <TM7>
 F:238-252/Domain: extracellular #status predicted <EXT4>
 F:253-261/Domain: transmembrane #status predicted <TM8>

Query Match 28.2%; Score 244.5; DB 2; Length 261;
 Best Local Similarity 29.9%; Pred. No. 1.3e-14;
 Matches 73; Conservative 26; Mismatches 58; Indels 87; Gaps 10;

QY 15 AALAAEG-ASGFYVQADAAHAKA-----SSLSGAKG-----FSPRI 50
 Db 21 AQAASBENGKGFYVQADAAHAKERTHDYPEPIGAKKGTITISVDFRNIRTHSHPRV 80

QY 51 SAGYRINDLRFAVDYTRYKNT-----KAPSTDEK-----LYS 82
 Db 81 SVGIDFGCMRIADYARKKNNKYSVSIKELLKNKGNNRTDLKAPENGTFHVVSS 140
 QY 83 IGASAIYDPDQSPVKPYLGLARLSLN--RASVD-----LGG-----116
 Db 141 LGLSAVYDFKLNDRKPYLGLARVAAGHRHSDTSKTEVTTLIHGGTTPPYPKNT 200
 QY 117 -----SDFSQTSIGLVLTGVSAYATPVNVDLAGRYNYIKGKNTKKNVRSGLSGV 170
 Db 201 QNAHRESDSIR--VGLGAVAGVGDITPNTLDAGRYHYHWGLENT-R-FKTHEASLGV 257
 QY 171 RYKF 174
 Db 258 RYRF 261

RESULT 4

Opacity protein opak precursor - Neisseria gonorrhoeae (strain MS11) (fragments)
 N:Alternate names: outer membrane protein opa58
 C:Species: Neisseria gonorrhoeae
 A:Variety: strain MS11

C:Date: 04-Jun-1997 #sequence_revision 17-Oct-1997 #text_change 26-Aug-1999
 R:Bhat, K.S.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsc M.O. Microbiol. 5, 1889-1901, 1991
 A:Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a f
 A:Reference number: S16610; MUID:92114767
 A:Accession: S16611
 A:Molecule type: DNA
 A:Residues: 1-260 <BHA>
 A:Cross-references: EMBL:X52371
 A:Experimental source: strain MS11, variant 4.8
 A:Note: the authors did not translate the sequence for the signal peptide
 A:Note: expression of opacity proteins is regulated by the number of translated repea
 A:Note: repeats place the start codon in frame with the rest of the protein
 R:Kupsch, E.M.; Knepper, B.; Kuroki, T.; Heuer, I.; Meyer, T.F.
 EMBL J. 12, 641-650, 1993

A:Title: Variable opacity (Opa) outer membrane proteins account for the cell tropisms
 A:Reference number: S36328; MUID:93178439
 A:Accession: S36345
 A:Molecule type: DNA
 A:Residues: 24-260 <KUP>
 A:Cross-references: EMBL:Z18937; NID:q49333; PIDN:CA79370.1; PID:q940799
 A:Experimental source: strain MS11, variant F3
 A:Note: expression of opacity proteins is regulated by the number of translated repea
 A:Note: repeats place the start codon in frame with the rest of the protein
 C:Genetics:
 A:Gene: opak
 C:Superfamily: opacity protein
 C:Keywords: cell surface component; transmembrane protein
 F:1-10,11-23/Domain: signal sequence (fragments) #status predicted <SIG>
 F:24-260/Product: opacity protein opak #status predicted <MAT>
 F:34-42/Domain: transmembrane #status predicted <TM1>
 F:43-74/Domain: extracellular #status predicted <EXT1>
 F:51-60/Region: semivariable region
 F:75-83/Domain: transmembrane #status predicted <TM2>
 F:88-94/Domain: transmembrane #status predicted <TM3>
 F:95-133/Domain: extracellular #status predicted <EXT2>
 F:101-128/Region: hypervariable region HV1
 F:134-148/Domain: transmembrane #status predicted <TM4>
 F:154-164/Domain: transmembrane #status predicted <TM5>
 F:165-211/Domain: extracellular #status predicted <EXT3>
 F:217-217/Region: hypervariable region HV2
 F:218-224/Domain: transmembrane #status predicted <TM6>
 F:225-236/Domain: transmembrane #status predicted <TM7>
 F:237-251/Domain: extracellular #status predicted <EXT4>
 F:252-260/Domain: transmembrane #status predicted <TM8>

Query Match 27.9%; Score 242; DB 2; Length 260;
 Best Local Similarity 29.5%; Pred. No. 2.1e-14;

Matches	76; Conservative	27; Mismatches	67; Indels	88; Gaps	10;
QY	2	KKALATLIALALPAAALAE	---ASGFYQADAAH	-----KASSLSGAKGS-	47
		: : : : : : : :	: : : : : : : :	: : : : : : :	
Db	6	KKPSLLFSSLFSSAAQAAG	EDHGGRGPRVQDIL	LAAYEHITDYPDGP	PSKGI
		: : : : : : : :	: : : : : : : :	: : : : : : :	: : : : : : :
QY	48	-----PRISAGYRINDL	FFAADYTRYKYN	-----KAPSTDFK	79
		: : : : : : : :	: : : : : : : :	: : : : : : :	: : : : : : :
Db	66	YFRNIRTHSIHPRVSG	YDFCGWRILAADY	YARKRMNNKYSVSI	KELLRNKVNCRDRK
		: : : : : : : :	: : : : : : : :	: : : : : : :	: : : : : : :
QY	80	-----LYSGASAIYD	PDTPQSVYKRYLAR	LSLN--RASVD	-----LG
		: : : : : : : :	: : : : : : : :	: : : : : : :	: : : : : : :
Db	126	TENQENGTFFHAVSS	UGSAVYDFKLNDEK	FYIGARRVAGHVR	SDISTKTEVTYLH
		: : : : : : : :	: : : : : : : :	: : : : : : :	: : : : : : :
QY	116	G-----SDSFSQTS	IGLVLTGVSYAAT	PVWDDLAGRYNY	IGKVN
		: : : : : : : :	: : : : : : : :	: : : : : : :	: : : : : : :
Db	186	GGPTTPYVYPGKNTQ	ADARESDSIR--	VGIGAAVAGV	IDITPMLTLADG
		: : : : : : : :	: : : : : : : :	: : : : : : :	: : : : : : :
QY	157	TVKNVRSGLSGVGR	VKFT	174	
		: : : : : : : :	: : : : : : : :	: : : : : : :	: : : : : : :
Db	244	NTR--FKTHIASL	GVARYR	260	

RESULT 5

opacity proteolipop precursor - *Neisseria gonorrhoeae* (strain MS11) (fragments)
 C:Species: *Neisseria gonorrhoeae*
 A:Variety: strain MS11
 C:Date: 04-Jun-1997 #sequence_revision 17-Oct-1997 #text_change 17-Oct-1997
 C:Accession: S16613
 R:Bhat, K.S.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehlig, F.; Stern, A.; Kupsch, Mol. Microbiol. 5, 1889-1901, 1991
 A:Title: The opacity proteins of *Neisseria gonorrhoeae* strain MS11 are encoded by a family of repeats
 A:Reference number: S16610; MUID:92114767
 A:Accession: S16613
 A:Molecule type: DNA
 A:Residues: 1-338 <BHA>
 A:Cross-references: EMBL:X52373
 A:Experimental source: strain MS11, variant 4.8
 A:Note: the authors did not translate the sequence for the signal peptide
 A:Note: expression of opacity proteins is regulated by the number of translated repeat elements
 C:Genetics: of repeats place the start codon in frame with the rest of the protein

C:Superfamily:	opacity protein			
C:Keywords:	cell surface component; transmembrane protein			
F:1.13.13.14-104/Domain:	signal sequence (fragments) #status predicted	<Sig>		
F:105-338/Product:	opacity protein opab #status predicted	<Mat>		
F:115-123/Domain:	transmembrane #status predicted	<TM1>		
F:124-155/Domain:	extracellular #status predicted	<EX1>		
F:132-141/Region:	semivariable region			
F:156-164/Domain:	transmembrane #status predicted	<TM2>		
F:169-175/Domain:	transmembrane #status predicted	<TM3>		
F:176-212/Domain:	extracellular #status predicted	<EX2>		
F:182-207/Region:	hypervariable region HV1			
F:213-227/Domain:	transmembrane #status predicted	<TM4>		
F:224-289/Domain:	extracellular #status predicted	<EX3>		
F:233-243/Domain:	transmembrane #status predicted	<TM5>		
F:249-295/Region:	hypervariable region HV2			
F:280-302/Domain:	transmembrane #status predicted	<TM6>		
F:306-314/Domain:	transmembrane #status predicted	<TM7>		
F:315-329/Domain:	extracellular #status predicted	<EX4>		
F:330-338/Domain:	transmembrane #status predicted	<TM8>		

Query Match	27.8%	Score 241.5	DB 2	Length 338
Best Local Similarly	30.0%	Pred. 3.3e-14		
Matches 73; Conservative	25	Mismatches 66	Indels 79	Gaps 9

```

OY      10 ALALPAAALAGC-ASGFVVDAAHA-----KASSSGS-----AKGF 46
          : : : : : : : : : : : : : : : : : : : : : : : :
Db      97 SLTFAARASGNGRGPPVQADLAYAALERTHODYPEPGAKDKKSYSDYFNIRITHSI 150
          : : : : : : : : : : : : : : : : : : : : : : : :
OY      47 SPRTSAGRIDLRFADVTRYK--NKKAPSTDEK-----L 80

```

Db	157	HPRVSVGDFEGGMRIADYARYRRMNANKYSVDIKELNNQNQRDLKTEQNGTFHAY	216
Qy	81	YSIASAATYDDPQSPVKPYTGARLSDLN--RASVD-----LGG-----	116
Db	217	SSLGLSNATDEKLMDFKRPYIGARVAAGVHNSIDSTKTKTKTFLTSYGGGLNPTVYTEEN	276
Qy	117	-----SDSFQTSIGLGLVLTGSVAATPNVDLDAGYRYNYIGKVNKYKNVRSGLSYGVR	171
Db	277	TQNAHQSNSSIRRVGLGIAGVGDIPKPLTLDGTYRHYWGRIENLR-FKTHASIGVR	355
Qy	172	VKF 174	
Db	336	YRF 338	

RESULT 6

opacity proteinopaef precursor - Neisseria gonorrhoeae (strains MS11) (fragments)
C:Species: Neisseria gonorrhoeae
A:Variety: strain MS11
C:Date: 04-Jun-1997 #sequence_revision 17-Oct-1997 #text_change 17-Oct-1997
C:Accession: S16612
R:Bat, K.S.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsc
Mol. Microbiol. 5, 1889-1901, 1991
A:Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a f
A:Reference number: S16610; MUID:92114767
A:Accession: S16612
A:Molecule type: DNA
A:Residues: 1-258 <BHA>
A:Cross-references: EMBL:X52369
A:Experimental source: strain MS11, variant 4.8
A:Note: the authors did not translate the sequence for the signal peptide
A:Note: expression of opacity proteins is regulated by the number of translated repea
of repeats place the start codon in frame with the rest of the protein

```

A:Gene: opae
C:Superfamily: opacity protein
C:Keywords: cell surface component: transmembrane protein
F:1-10,11-23/Domain: signal sequence (fragments) #status predicted <Sig>
F:24-258/Product: opacity protein opae #status predicted <Mat>
F:34-44/Domain: transmembrane #status predicted <TM1>
F:43-74/Domain: extracellular #status predicted <EXT1>
F:50-60/Region: semivariable region
F:75-83/Domain: transmembrane #status predicted <TM2>
F:88-94/Domain: transmembrane #status predicted <TM3>
F:95-131/Domain: extracellular #status predicted <EXT2>
F:101-125/Region: hypervariable region HV1
F:132-146/Domain: transmembrane #status predicted <TM4>
F:152-162/Domain: transmembrane #status predicted <TM5>
F:163-209/Domain: extracellular #status predicted <EXT3>
F:168-215/Region: hypervariable region HV2
F:210-222/Domain: transmembrane #status predicted <TM6>
F:226-234/Domain: transmembrane #status predicted <TM7>
F:235-249/Domain: extracellular #status predicted <EXT4>
F:250-258/Domain: transmembrane #status predicted <TM8>

```

Query Match	27.8%;	Score 241;	DB 2;	Length 256;
Best Local Similarity	29.7%;	Pred. No. 2.6e-14;		
Matches	76;	Conservative	26;	Mismatches 68;
			Indels	86;
			Gaps	10;

QY 2 KRALATLIALALPAAALAEG---ASGFVYQADANA-----KASSLSGSAK-----44
|| : || | | | || | | : |
Db 6 KKPSSLFSSLSFSSAAQAGEDHGRCPPVQADALAYAEHITHDYPPEPTGCTKKKIKISTVSD 65

```

QY 45 -----GSPRISAGYRIIDLREAVDYTRYK--NYKAPSTDER----- 79
      ||: || | | | | | | | |
Db 66 YFNRIRTHSIHPRVSYGDFGCGRIADYARYRKWMDNKSVDIELENNQNKRDLKTE 125

```

```

QY 80 -----LYSIGASAIYDFDTQSPKPYGLARSLN--RASVD-----LGG- 116
      : : : : : : : : : : : : : : : : : : : : : : : :
Db 126 NQENGTFHAAVSSLGLSAVYDFKLNDKFKPYIGARVAYGHVRSIDSTKKTTEVTTLIHGP 185

```

[illegible]

```

F:228-236/Domain: transmembrane #status predicted <TM7>
F:237-251/Domain: extracellular #status predicted <EXT4>
F:252-260/Domain: transmembrane #status predicted <TM8>

Query Match      27.8%; Score 241; DB 1; Length 260;
Best Local Similarity 28.8%; Pred. No. 2,6e+14;
Matches 72; Conservative 30; Mismatches 64; Indels 84; Gaps 9;

QY 6 ATLIALPALAALAGSAGFYQADPAHA-----KASSISGSAKKGS----- 47
   :: : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 14 SLPLSSAAQAASEGGCGGPYYQADLAAYAEHTIDPDKPPDSKGKISTVSDYFRNIRT 73
   :: : | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 48 ----PRISAGRYINDLRFADVDTX-----KNVKAPSTD-- 77
   |||::| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 74 HSHHRRVSVGDFGCGWRIRIADYARKRKMSDNKYSTIKMRYHKHNSRKNILKTENOENG 133
   |||::| | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 78 --FKLSIGASAIYDFTQSPVPKPYLAGRLSLN--RASVD-----LGG- 116
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 134 SEHVASSLGLAISLYDFQINDKFPIGARVAVGYHRHSIDAKTKITGLLTSTPGIMSGV 193
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 117 -----SDSEFSQTSLGVLGVSAVFPNVLDLDCGRNYTGKYNIVKANVSG 164
   ||| : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 194 YKVLFRTPEAHRESDSIRR--VELGIYAGVGFDPFKTLIDAGRYHNMGRLLENTR-FKTH 250
   ||| : | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 165 ELTVGVRVKE 174
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 251 EASLGVRVRE 260

RESULT 8
S36343
opacity protein opa57 - Neisseria gonorrhoeae (strain MS11) (fragment)
N.Alternate names: outer membrane protein opa57
C.Species: Neisseria gonorrhoeae
A.Variety: strain MS11
C.Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 26-Aug-1999
C.Accession: S36343; S28626
R.Kupsch, E.M.; Knepper, B.; Kurokl, T.; Heuer, I.; Meyer, T.F.
EMBO J. 12, 641-650, 1993
A.Title: Variable opacity (Opa) outer membrane proteins account for the cell tropisms
A.Reference number: S36328; MUID:93178439
A.Accession: S36343
A.Molecule type: DNA
A.Residues: 1-237 <KUP>
A.Cross-references: EMBL:Z18935; NID:g49331; PIDN:CAAT9368.1; PID:g940797
A.Experimental source: strain MS11, variant F3
A.Note: expression of opacity proteins is regulated by the number of translated repeats of repeats place the start codon in frame with the rest of the protein
C.Genetic:
A.Gene: opa57
C.Superfamily: opacity protein
C.Keywords: cell surface component; transmembrane protein
F.1-237/Product: opacity protein opa57 #status predicted <MAT>
F.11-19/Domain: transmembrane #status predicted <TM1>
F.20-51/Domain: extracellular #status predicted <EXT1>
F.28-37/Region: semivariable region
F.52-60/Domain: transmembrane #status predicted <TM2>
F.65-71/Domain: transmembrane #status predicted <TM3>
F.72-110/Domain: extracellular #status predicted <EXT2>
F.78-105/Region: hypervariable region HV1
F.11-135/Domain: transmembrane #status predicted <TM4>
F.131-141/Domain: transmembrane #status predicted <TM5>
F.147-188/Domain: extracellular #status predicted <EXT3>
F.147-144/Region: hypervariable region HV2
F.189-201/Domain: transmembrane #status predicted <TM6>
F.205-213/Domain: transmembrane #status predicted <TM7>
F.214-228/Domain: extracellular #status predicted <EXT4>
F.229-237/Domain: transmembrane #status predicted <TM8>

Query Match      27.7%; Score 240.5; DB 2; Length 237;
Best Local Similarity 29.6%; Pred. No. 2.6e+14;
Matches 71; Conservative 26; Mismatches 58; Indels 85; Gaps 9;

```

[illegible]

153 GKVNPTVKNVRSGELSGVRVKE 174

```

      |::      :      :: | {}::|| : |
Db 246 GRLENT-RKTHESLGVRRYR 266

```

RESULT 11

508514
 O:Subcellular localization: cytoplasm
 N:Alternate names: outer membrane protein class 5
 C:Species: *Neisseria meningitidis*
 A:Variety: strain C1938
 C:Date: 19-Mar-1997 #sequence_revision 17-Oct-1997 #text_change 20-Jun-2000
 C:Accession: S08514
 R:Stern, A.; Meyer, T.F.
 Mol. Microbiol. 1, 5-12, 1987
 A>Title: Common mechanism controlling phase and antigenic variation in pathogenic *neisseria*
 A:Reference number: S08513; MUID:88260884
 A:Accession: S08514
 A:Molecule type: DNA
 A:Residues: 1-258 <STB>
 A:Cross-references: EMBL:X06445; NTD:q44906; PID:q1333787
 A:Experimental source: strain C1938
 A>Note: expression of opacity proteins is regulated by the number of translated repeat e
 of repeats place the start codon in frame with the rest of the protein
 C:Genetics: 1
 C:OC: 1

```

A:Gene: Opm1
C:Superfamily: opacity protein
C:Keywords: cell surface component; transmembrane protein
F:1-13,14-21/Domain: signal sequence (fragments) #status predicted <SIG>
F:22-258/Product: opacity protein-related protein Opm1 #status predicted <MAT>
F:33-41/Domain: transmembrane #status predicted <TM1>
F:42-73/Domain: extracellular #status predicted <EX1>
F:50-59/Region: semivariable region
F:74-82/Domain: transmembrane #status predicted <TM2>
F:87-83/Domain: transmembrane #status predicted <TM3>
F:94-129/Domain: extracellular #status predicted <EXT2>
F:100-124/Region: hypervariable region HV1
F:130-144/Domain: transmembrane #status predicted <TM4>
F:150-160/Domain: transmembrane #status predicted <TM5>
F:161-209/Domain: extracellular #status predicted <EXT3>
F:166-215/Region: hypervariable region HV2
F:210-222/Domain: transmembrane #status predicted <TM6>
F:226-234/Domain: transmembrane #status predicted <TM7>
F:235-249/Domain: extracellular #status predicted <EXT4>
F:250-258/Domain: transmembrane #status predicted <TM8>

Query Match          27.4%;      Score 238;  DB 2;  Length 258;
Best Local Similarity 28.5%;      Pred. No. 4.9e-14;
Matches 70;  Conservative 29;  Mismatches 67;  Indels 80;  Gaps 7;

```

RESULT 12

S20043
opacity protein B precursor (clone pF10B1700) - *Neisseria meningitidis* (strain FAM18) (4

N:Alternate names: outer membrane protein class 5
C:Species: *Neisseria meningitidis*
A:Variety: strain FAM18
C:Date: 04-Jun-1997 #sequence-revision 04-Jun-1997 #text-change 17-Oct-1997
C:Accession: S20043
R:Alio, E.L.; Dempsey, J.A.; Hobbs, M.M.; Klapper, D.G.; Cannon, J.G.
Mol. Microbiol. 5, 1429-1437, 1991
A>Title: Characterization of the opa (class 5) gene family of *Neisseria meningitidis*.
A:Reference number: S16286; MUID:92157869
A:Accession: S20043
A:Molecule type: DNA
A:Residues: 1-254 <AHO>
A:Cross-references: EMBL:X63108
A:Experimental source: strain FAM18; clone pFLOH1700
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1991
A>Note: only a part of the translation is shown
A>Note: expression of opacity proteins is regulated by the number of translated repeats of repeats place the start codon in frame with the rest of the protein
C:Genetics:

```

A:Gene: opar
C:Superfamily: Opacity protein
Keywords: cell surface component; transmembrane protein
F:1-19/Domain: signal sequence (fragment) #status predicted <Sig>
F:20-254/Product: opacity protein opar #status predicted <Mat>
F:31-39/Domain: transmembrane #status predicted <Ext1>
F:40-69/Domain: extracellular #status predicted <Ext2>
F:48-55/Region: semivariable region
F:70-78/Domain: transmembrane #status predicted <TM2>
F:83-89/Domain: transmembrane #status predicted <TM3>
F:90-126/Domain: extracellular #status predicted <EXT2>
F:96-121/Region: hypervariable region HV1
F:127-141/Domain: transmembrane #status predicted <TM4>
F:147-157/Domain: transmembrane #status predicted <TM5>
F:158-205/Domain: extracellular #status predicted <EXT3>
F:163-211/Region: hypervariable region HV2
F:206-218/Domain: transmembrane #status predicted <TM6>
F:222-230/Domain: transmembrane #status predicted <TM7>
F:231-245/Domain: extracellular #status predicted <EXT4>
F:246-254/Domain: transmembrane #status predicted <TM8>

Query Match      27.3%;   Score 237;   DB 2;   Length 254;
Best Local Similarity 28.3%;   Pred. No. 5_9e-14;
Matches 69;   Conservative 31;   Mismatches 66;   Indels 78;   Gaps 7;

```

RESULT 13

504380
 opacit3 protein P.II precursor - Neisseria gonorrhoeae (strain F62-SF and others) (fr
 C:Species: Neisseria gonorrhoeae
 A:Variate: strain F62-SF
 C:Date: 30-Jun-1991 #sequence_revision 17-Oct-1997 #text_change 13-Nov-1998
 C:Accession: 504380; S16504
 R:Palmer, L.; Brooks, G.F.; Falkow, S.

Mol. Microbiol. 3, 663-671, 1989
A:Title: Expression of gonococcal protein II in *Escherichia coli* by translational fusion
A:Reference number: S04380; MUID:89343653
A:Accession: S04380
A:Molecule type: DNA
A:Residues: 1-270 <PAL>
A:Cross-references: EMBL:X15780
A:Experimental source: strain F62-SF, serogroup IB-3; clone F62-SFG1
A:Note: the authors did not translate the sequence of the signal peptide
A:Note: expression of opacity proteins is regulated by the number of translated repeat
of repeats place the start codon in frame with the rest of the protein
R:Tab, M.K.; So, M.; Seifert, H.S.; Bilyard, E.; Marchal, C.
EMBO J. 7, 4367-4378, 1988
A:Title: Pilin expression in *Neisseria gonorrhoeae* is under both positive and negative
A:Reference number: S02017; MUID:89210824
A:Accession: S16504
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 255-270 <TAH>
A:Cross-references: EMBL:X13965
A:Experimental source: strain MS11A
A:Note: expression of opacity proteins is regulated by the number of translated repeat
of repeats place the start codon in frame with the rest of the protein
C:Genetics:
A:Gene: opa1
C:Superfamily: opacity protein
C:Keywords: cell surface component; transmembrane protein
F:1-10,11-23/Domains: signal sequence (fragments) #status predicted <SIG>
F:24-270/Product: opacity protein opa #status predicted <MAT>
F:34-42/Domains: transmembrane #status predicted <TM1>
F:43-75/Domains: extracellular #status predicted <EXT1>
F:51-61/Region: semivariable region
F:76-84/Domains: transmembrane #status predicted <TM2>
F:89-95/Domains: transmembrane #status predicted <TM3>
F:96-141/Domains: extracellular #status predicted <EXT2>
F:102-136/Region: hypervariable region HV1
F:141-155/Domains: transmembrane #status predicted <TM4>
F:162-172/Domains: transmembrane #status predicted <TM5>
F:173-221/Domains: extracellular #status predicted <EXT3>
F:178-227/Region: hypervariable region HV2
F:228-234/Domains: transmembrane #status predicted <TM6>
F:238-246/Domains: transmembrane #status predicted <EXT4>
F:247-261/Domains: extracellular #status predicted <EXT5>
F:262-270/Domains: transmembrane #status predicted <TM8>
Query Match 27.3%; Score 237; DB 2; Length 270;
Best Local Similarity 27.1%; Pred. No. 6.3e-14;
Matches 72; Conservative 33; Mismatches 67; Indels 94; Gaps 8;
OY 2 KKALATLALPAAALAE---ASGFTYQADAAH-----AKASSLSGSAK 44
DB 6 KKPSSILFSSMAQAAGGNGRPPYQADLAAYEHITHDYPKPTGAKKGTISTVS 65
OY 45 GF-----SPRISAGYRINDLRFANDYTRYK----- 69
DB 66 DYFRIRTHSVHPRSVYDDEGGRRIADYARKMNNKKSYSIKELGRDNASAGVRC 125
OY 70 --NKAPSTDRK-----LVSIGASALYDDTOSPVKPYLGARLSL----- 107
DB 126 HLNIOQTQTEHQENGTFHAASLSLSTIYDFTGSRFPYIGARVAAGVHRHQRVSVEOE 185
OY 108 -----NRASVDGGS-----DSFSQTSIGLGVLTGVSAVTPNVLDAGYR 148
DB 186 TEIVTTTKEQNVASPPGAPTKKPAHHSRISISLGFAGVAVGIDITPNTLDAGYR 245
OY 149 YNYIGKVTYKRVNSGELSVGVRYKE 174
DB 246 YHNMGRLENTNRFKTHASLSGVRVRF 270
RESULT 14
KONH2C
opacity protein P.IIC precursor - *Neisseria gonorrhoeae* (strain J53) (fragments)

N:Alternate names: outer membrane protein P.IIC
C:Species: *Neisseria gonorrhoeae*
A:Variety: strain J53
C:Date: 31-Mar-1992 #sequence_revision 17-Oct-1997 #text_change 08-May-1998
C:Accession: S03095; S16360
R:van der Ley, P.
Mol. Microbiol. 2, 797-806, 1988
A:Title: Three copies of a single protein II-encoding sequence in the genome of *Neiss*
A:Reference number: S03095; MUID:89096501
A:Accession: S03095
A:Molecule type: DNA
A:Residues: 1-268 <VAN>
A:Cross-references: EMBL:X12625
A:Experimental source: strain J53
A:Note: 241-Val was also found
A:Note: expression of opacity proteins is regulated by the number of translated repea
of repeats place the start codon in frame with the rest of the protein
R:Barritt, D.S.; Schwalbe, R.S.; Klapper, D.G.; Cannon, J.G.
Infect. Immun. 55, 2026-2031, 1987
A:Title: Antigenic and structural differences among six proteins II expressed by a sl
A:Reference number: S16360; MUID:87306843
A:Accession: S16360
A:Status: preliminary
A:Molecule type: protein
A:Residues: 24-34 <BAR>
C:Genetics:
A:Gene: pilC
C:Superfamily: opacity protein
C:Keywords: cell surface component; transmembrane protein
F:1-10,11-23/Domains: signal sequence (fragments) #status predicted <SIG>
F:24-268/Product: opacity protein P.IIC #status experimental <MAT>
F:34-42/Domains: transmembrane #status predicted <TM1>
F:43-74/Domains: extracellular #status predicted <EXT1>
F:51-60/Region: semivariable region
F:75-83/Domains: transmembrane #status predicted <TM2>
F:88-94/Domains: transmembrane #status predicted <TM3>
F:95-140/Domains: extracellular #status predicted <EXT2>
F:101-135/Region: hypervariable region HV1
F:141-155/Domains: transmembrane #status predicted <TM4>
F:161-171/Domains: transmembrane #status predicted <TM5>
F:172-219/Domains: extracellular #status predicted <EXT3>
F:177-225/Region: hypervariable region HV2
F:220-232/Domains: transmembrane #status predicted <TM6>
F:236-244/Domains: transmembrane #status predicted <TM7>
F:245-259/Domains: extracellular #status predicted <EXT4>
F:260-268/Domains: transmembrane #status predicted <TM8>
Query Match 27.2%; Score 236.5; DB 1; Length 268;
Best Local Similarity 26.8%; Pred. No. 7e-14;
Matches 69; Conservative 32; Mismatches 67; Indels 89; Gaps 8;
OY 6 ATLIALALPAAALAEASGFTYQADAAHAKA-----SSLSGSAK 44
DB 13 SLLFSSMAAASSEDGGRPPYQADLAAYEHITHDYPKPTGKKNKISTVSDFRINRT 72
OY 45 -GSPRISAGYRINDLRFANDYTRYK-----NYKAPS 75
DB 73 HSHVPRSVYDDEGGRRIADYARKMNNKKSYSIKELGRDNASAGVRHLNIGYRK 132
OY 76 TDRK-----LVSIGASALYDDTOSPVKPYLGARLSL-----SYDL 114
DB 133 TEHQENGTFHAASLSLSTIYDFTGSRFPYIGMVAAGVHRHQRVSVEOEETIITYP 192
OY 115 -----GSDSPFSQ-----TSIGLGVLTGVSAVTPNVLDAGYRNYIGKVT 157
DB 193 SNGGKGVLSKMPKPSAHHSNIRKVLGVAAGVDFITPNTLDGVRHNMGRLEN 252
OY 158 VKNVRSGELSVGVRYKE 174
DB 253 TR-FKTHASLSGVRVRF 268
RESULT 15

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 28, 2002, 15:55:44 ; Search time 6.98996 Seconds

(without alignments)
963.840 Million cell updates/sec

Title: US-09-684-883-2

Perfect score: 866
Sequence: 1 MKKALATLIALPALAE.....VNTVKNVSGELSYGVKVF 174

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	240.5	27.7	237	1	OPAK_NEIGO
2	239	27.5	260	1	OPRL_NEIMC
3	236.5	27.2	270	1	OPMC_NEIGO
4	235	27.1	236	1	OPAC_NEIGO
5	232.5	26.8	234	1	OPAB_NEIGO
6	232.5	26.8	237	1	OPAL_NEIGO
7	232	26.7	234	1	OPAE_NEIGO
8	232	26.7	234	1	OPAF_NEIGO
9	231	26.6	233	1	OP67_NEIGO
10	226	26.0	234	1	OP28_NEIGO
11	226	26.0	234	1	OP65_NEIGO
12	226	26.0	238	1	OP66_NEIGO
13	226	26.0	238	1	OPAH_NEIGO
14	224.5	25.9	243	1	OPAD_NEIGO
15	224	25.8	244	1	OPAL_NEIGO
16	219	25.2	238	1	OP68_NEIGO
17	217	25.0	178	1	YES7_HAEN
18	215	24.8	239	1	OPAA_NEIGO
19	205.5	23.7	247	1	OPAG_NEIGO
20	180	20.7	121	1	OPA_HAEN
21	135	15.6	170	1	OPR3_NEIMC
22	126.5	14.6	70	1	Y414_HAEN
23	108	12.4	182	1	AIL_YERPS
24	100	11.5	213	1	OM25_BRUB
25	98.5	11.3	350	1	OMPA_SATRY
26	97.5	11.2	341	1	OMPU_VIBCH
27	94.5	10.9	349	1	OMPA_BUCOL
28	94	10.8	349	1	OMPA_BUCOL
29	94	10.8	353	1	OM51_HAEN
30	93	10.7	521	1	TSAS_RICIS
31	92	10.6	213	1	OM25_BRUSD
32	90.5	10.4	428	1	OM47_PASND
33	90	10.4	213	1	OM25_BRUME

34	90	10.4	353	1	OM52_HAEN	P38368 haemophilus
35	89	10.3	178	1	AIL_YEREN	P16454 yersinia en
36	88.5	10.2	346	1	OMPA_ECOLI	P02934 escherichia
37	88	10.1	359	1	OM53_HAEN	P45996 haemophilus
38	86	9.9	201	1	OM25_BRUV	P45335 brucella ov
39	86	9.9	213	1	OM25_BRUC	P45110 brucella ca
40	84.5	9.7	350	1	OMPA_ENTAE	P09146 enterobacte
41	84.5	9.7	995	1	Y1Q9_YEAST	P40442 saccharomyc
42	84	9.7	213	1	OM25_BRUNE	P45326 brucella ne
43	84	9.7	350	1	PORF_PSEAE	P13794 pseudomonas
44	82.5	9.5	350	1	PHOE_ENTCL	Q47490 enterobacte
45	82	9.4	433	1	FTSZ_ARATH	Q42545 arabidopsis

ALIGNMENTS

RESULT 1	OPAK_NEIGO	STANDARD	PRT	237 AA.
ID	OPAK_NEIGO			
AC	Q04880			
DT	01-OCT-1993 (Rel. 27, Created)			
DT	01-OCT-1993 (Rel. 27, Last sequence update)			
DT	01-NOV-1995 (Rel. 32, Last annotation update)			
DE	Opacity Protein OPA57 precursor (Fragment).			
GN	OPAK.			
OS	Neisseria gonorrhoeae.			
OC	Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.			
OX	NCBI_TaxID=485;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=MS11 / F3;			
RA	MEDLINE=93178439; PubMed=8440254;			
RX	Kusch E.-M., Kueper B., Kuroki T., Heuer I., Meyer T.F.;			
RT	"Variable opacity (Opa) outer membrane proteins account for the cell tropisms displayed by Neisseria gonorrhoeae for human leukocytes and epithelial cells."			
RT	EMBO J. 12:641-650(1993).			
RL	-1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA			
CC	PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE			
CC	VARIATION.			
CC	-1- SUBCELLULAR LOCATION: Outer membrane.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL: Z18935; CAA79368.1; -			
DR	PIR: S28626; S28626.			
DR	InterPro: IPR003394; Opacity.			
DR	Pfam: PF02462; Opacity; 1.			
KW	Outer membrane; Multigene family; signal.			
FT	NON_TER	1		
FT	SIGNAL	<1	1	POTENTIAL.
FT	CHAIN	2	>237	OPACITY PROTEIN OPA57.
FT	NON_TER	237		
SO	SEQUENCE	237 AA; 26703 MW; F8B1A0FB5C7BECAD CRC64;		
Query Match	27.7%; Score 240.5; DB 1; Length 237;			
Best Local Similarity	29.6%; Pred. No. 4.4e-15;			
Matches	71; Conservative 26; Mismatches 58; Indels 85; Gaps 9;			
OY	17 ALAAGAGFYQADAAHA-----KASSLSG-----ANGFSPRISAGY 54			
DB	1 ASEDGGRPYQADLAYAYEITHDYEPAPNNKISTVSDYRNITRISVHPVSVG 60			
OY	55 RINDRFADVDTTRYKNY-----KASTDFK-----LYSGAS 86			
DB	61 DFGWRITADYARFKRNWNNKYSVSIKELLRNKNGCNTDLKENQNGTFPFAVSLG 120			

```

QY 87 AYDFDQSPVKKYLGARLSLN--RASVD-----LGG-----116
DB 121 AYDEKLNDRKPKYIGANVAAGVHRHSIDSKTKTEVTTLHGCTTPPYPKNTODAH 180
QY 117 --SDSFQTSIGLGVNLSAATVPNDLDAGRYNYIKGVNYSRSGELSGVGRVKE 174
DB 181 RESDSIRK--VGLGAVAGVGIDITPNLTLADGYRHYWGRLENTR-PKTHEASIGVGRV 237

RESULT 2
OPRL_NEIMC STANDARD; PRT; 260 AA.
AC P10170;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Opacity-related protein POPML.
GN OPR.
OS Neisseria meningitidis (serogroup C).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=135720;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C1938 / SEROGROUP C;
RX MEDLINE=8826084; PubMed=2455211;
RA Stern A., Meyer T.F.;
RT "Common mechanism controlling phase and antigenic variation in
  pathogenic neisseriae."
RL Mol. Microbiol. 1:5-12(1987).
CC -1- SUBCELLULAR LOCATION: Outer membrane.
CC -1- SIMILARITY: STRONG TO THE OPACITY-RELATED PROTEIN POPM3 AND
  REGIONS OF HOMOLOGY WITH N.GONORRHOEA (STRAIN MS11) OPA GENE
  PRODUCTS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL, X06445; CA29748.1; ALT-SEQ.
DR PIR: S08514; S08514.
DR InterPro: IPR003394; Opacity.
DR Pfam: PF02462; Opacity; 1.
KW Outer membrane.
SQ SEQUENCE 260 AA; 28936 MW; EB47A2843B3F037B CRC64;

Query Match 27.5%; Score 239; DB 1; Length 260;
Best Local Similarity 27.6%; Pred. No. 6.8e-15;
Matches 71; Conservative 34; Mismatches 66; Indels 86; Gaps 8;

```

```

RESULT 3
OMPC_NEIGO STANDARD; PRT; 270 AA.
AC P09888;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE Outer membrane protein P.IIC precursor (Protein IIC).
GN P.IIC.
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=485;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=J53;
RX MEDLINE=89096501; PubMed=3145386;
RA van der Ley P.;
RT "Three copies of a single protein II-encoding sequence in the genome
  of Neisseria gonorrhoeae J53: evidence for gene conversion and gene
  duplication."
RL Mol. Microbiol. 2:797-806(1988).
CC -1- FUNCTION: THIS PROTEIN SERVES AS A PORIN.
CC -1- SUBUNIT: HOMOTRIMER.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL, X12625; CA31144.1; -.
DR PIR: S03095; KONR2C.
DR InterPro: IPR003394; Opacity.
DR Pfam: PF02462; Opacity; 1.
KW Outer membrane; Porin; Transmembrane; Antigen; Signal.
FT SIGNAL 1 25
FT CHAIN 26 270
FT TRANSMEM 36 44 OUTER MEMBRANE PROTEIN P. IIC.
FT TRANSMEM 77 85
FT TRANSMEM 90 96 POTENTIAL.
FT TRANSMEM 143 157 POTENTIAL.
FT TRANSMEM 163 173 POTENTIAL.
FT TRANSMEM 222 234 POTENTIAL.
FT TRANSMEM 238 246 POTENTIAL.
FT TRANSMEM 262 270 POTENTIAL.
SQ SEQUENCE 270 AA; 30269 MW; FB448373830A50D CRC64;

Query Match 27.2%; Score 236.5; DB 1; Length 270;
Best Local Similarity 26.8%; Pred. No. 1.2e-14;
Matches 69; Conservative 32; Mismatches 67; Indels 89; Gaps 8;

```


DB 255 TR-FTHESLGMRYRF 270

RESULT 4

OPAC_NEIGO STANDARD; PRT; 236 AA.

AC P11296;

DT 01-JUL-1989 (Rel. 11, Created)

DT 01-JUL-1989 (Rel. 11, Last sequence update)

DT 01-NOV-1995 (Rel. 32, Last annotation update)

DE Opa50 protein OPA50 precursor (OPA50) (VO) (Fragment).

GN OPAC.

OS Neisseria gonorrhoeae.

OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.

OX NCBI_TaxID=485;

RN [1]

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RC STRAIN-MS11 / V0;

RX MEDLINE=87002493; PubMed=3093085;

RA Stern A., Brown M., Nickel P., Meyer T.F.;

RT "Opacity genes in Neisseria gonorrhoeae: control of phase and antigenic variation."

RL Cell 47:61-71(1986).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-MS11 / F3;

RX MEDLINE=93178439; PubMed=8440254;

RA Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;

RT "Variable opacity (Opa) outer membrane proteins account for the cell tropisms displayed by Neisseria gonorrhoeae for human leukocytes and epithelial cells."

RL EMO J. 12:641-650(1993).

CC -1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE VARIATION.

CC -1- SUBCELLULAR LOCATION: Outer membrane.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC EMBL: M14746; NOT_ANNOTATED_CDS.

DR EMBL: Z18927; CAA79360.1; -.

DR PIR: A24429; KONHO.

DR PIR: S28621; S28621.

DR PIR: S36328; S36328.

DR InterPro: IPR003394; Opacity.

DR Pfam: PF02462; Opacity.1.

KW Outer membrane; Multigene family; Signal.

FT SIGNAL 1 1

FT NON_TER 1 1

FT CHAIN 2 >236 POTENTIAL.

FT NON_TER 236 236 OPACITY PROTEIN OPA50.

SQ SEQUENCE 236 AA; 26685 MW; 68DC237692183398 CRC64;

Query Match 27.1%; Score 235; DB 1; Length 236;

Best Local Similarity 29.3%; Pred. No. 1,4e-14;

Matches 70; Conservative 26; Mismatches 59; Indels 84; Gaps 9;

DB 17 ALAAGAGGYVQADAAHA-----KASSSLGSAKGF-----PRISAGY 54

DB 1 ASDSDGGRGYVQADLAAYAEHTHDYPRKPTDPSKAKISTVSDYFNRIRTHSHPRVSAY 60

DB 55 RINDLRFAYDYTRY-----KNYAPSTD-----FKYISIGAS 86

DB 61 DFGGMRIADYARYRRKWDNKKYSVSIKNRVRHNSNRNLKTENQENGFHAVSSIGLS 120

DB 87 AAYDFTQSGPVKRYLGRSLN--RASVD-----LGG----- 116

DB 121 AYDFOJNDFKRYIGARVAGVHRHSIDSTKRTIGLLTSTEGINSGYKYLRTPGAHR 180

DB 117 SDSFSOTSIGLVLTGVSAAVTPNVLDAGRYNYTGNVTKNVSGLSVGRVF 174

DB 181 ESDSIR--VGLGIYAGVGFDITPKLTLDGCRYRHNMGRLENTR-FKTHASLGRYRF 236

RESULT 5

OPAB_NEIGO STANDARD; PRT; 234 AA.

AC 004874;

DT 01-OCT-1993 (Rel. 27, Created)

DT 01-OCT-1993 (Rel. 27, Last sequence update)

DT 01-NOV-1995 (Rel. 32, Last annotation update)

DE Opa51 protein OPA51 precursor (Fragment).

GN OPAB.

OS Neisseria gonorrhoeae.

OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.

OX NCBI_TaxID=485;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-MS11 / F3;

RX MEDLINE=93178439; PubMed=8440254;

RA Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;

RT "Variable opacity (Opa) outer membrane proteins account for the cell tropisms displayed by Neisseria gonorrhoeae for human leukocytes and epithelial cells."

RL EMO J. 12:641-650(1993).

CC -1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE VARIATION.

CC -1- SUBCELLULAR LOCATION: Outer membrane.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC EMBL: Z18928; CAA79361.1; -.

DR PIR: S28628; S28628.

DR PIR: S36329; S36329.

DR InterPro: IPR003394; Opacity.

DR Pfam: PF02462; Opacity.1.

KW Outer membrane; Multigene family; Signal.

FT SIGNAL 1 1

FT NON_TER 1 1

FT CHAIN 2 >234 POTENTIAL.

FT NON_TER 234 234 OPACITY PROTEIN OPA51.

SQ SEQUENCE 234 AA; 26772 MW; 9FEB5B5DABBA96CA CRC64;

Query Match 26.8%; Score 232.5; DB 1; Length 234;

Best Local Similarity 29.3%; Pred. No. 2,4e-14;

Matches 69; Conservative 25; Mismatches 61; Indels 79; Gaps 9;

DB 19 AEG-ASGPPYVQADAAHA-----KASSSLGSAK-----GFSPRISAGY 55

DB 2 SEGNGRGYVQADLAAYAEHTHDYPRDGTGKKKISTVSDYFNRIRTHSHPRVSAY 61

DB 56 INDLRFAYDYTRY--KNYAPSTD-----LYSTGASAY 89

DB 62 FGMRIADYARYRRKWDNKKYSVDIKELKNQKRDLTENQENGFHAVSSIGLSAY 121

DB 90 DEDDQSPKRYPLGRSLN--RASVD-----LGG-----SDSF 120

DB 122 DFKLNGKRPYIGARVAGVHRHSIDSTKRTKFLTSYGLNPFVTEBNTONAHQSN 181

DB 121 SOTSIGLVLTGVSAAVTPNVLDAGRYNYTGNVTKNVSGLSVGRVF 174

DB 182 SIRRGVGLVAGVGFDITPKLTLDTGCRYRHNMGRLENTR-FKTHASLGRYRF 234

RESULT 6
OPAE_NEIGO
ID OPAE_NEIGO STANDARD; PRT; 237 AA.
AC 004878;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Opacity protein OPA58 precursor (Fragment).
GN OPAE.
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
NCBI_TaxID=485;
RX STRAIN=MS11 / F3;
MEDLINE=93178439; PubMed=8440254;
RA Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
RT "Variable opacity (Opa) outer membrane proteins account for the cell tropisms displayed by Neisseria gonorrhoeae for human leukocytes and epithelial cells."
RT EMO J. 12:641-650(1993).
RL
CC -1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
CC VARIATION.
CC -1- SUBCELLULAR LOCATION: Outer membrane.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: Z18937; CAA79370.1; -
CC PIR: S28624; S28624.
CC InterPro: IPR003394; Opacity.
CC Pfam: PF02462; Opacity; 1.
CC Outer membrane; Multigene family; Signal.
CC
CC FT SIGNAL 1 1
CC FT NON_TER <1 1 POTENTIAL.
CC FT CHAIN 2 >237 OPACITY PROTEIN OPA58.
CC FT NON_TER 237 237
CC SEQUENCE 237 AA; 26855 MW; B165033B2CHD6A53 CRC64;
Query Match 26.8%; Score 232.5; DB 1; Length 237;
Best Local Similarity 29.6%; Pred. No. 2.4e-14;
Matches 69; Conservative 25; Mismatches 54; Indels 85; Gaps 9;
QY 24 GFYVQADAAHA-----KASSSLGSAKGS-----PRISAGYRINDLR 61
DB 8 GPHYQADLAAYAEHITHDYPEQTPSKGKISTYSDYFRNIRTHSHPRVSGVDFGGMRI 67
QY 62 AVDYTRKRYK-----KAPSTDFK-----LYSIGASAIYDFDT 93
DB 68 AADYARRKNNNNKYSVSIKELRNKVNGRNTRKTENQNGTFHVAVSSIGLSAVYDFDK 127
QY 94 QSPKPYLGARLSLN--RASVD-----LGG-----SDSS 121
DB 128 NDKFYTGARVAAGVHSHSIDSTKTKTEVTTILHGGCTTPVYPKKNQDAHRESDSIR 187
QY 122 QTSIGLGVLSVAVYPPNDLAGYRYNYIGKVNTPKVNRSGLSVGYVKF 174
DB 188 R--VGLGAVAGVGIDITPRLTDLAGRYHYWGLNEMR-FKTHIASLGYRYR 237
RESULT 7
OPAE_NEIGO
ID OPAE_NEIGO STANDARD; PRT; 234 AA.
AC 004878;
DT 01-OCT-1993 (Rel. 27, Created)

DT 01-OCT-1993 (Rel. 27, Last sequence update)
DE 01-NOV-1995 (Rel. 32, Last annotation update)
DE Opacity protein OPA55 precursor (Fragment).
GN OPAE.
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
NCBI_TaxID=485;
RX STRAIN=MS11 / F3;
MEDLINE=93178439; PubMed=8440254;
RA Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
RT "Variable opacity (Opa) outer membrane proteins account for the cell tropisms displayed by Neisseria gonorrhoeae for human leukocytes and epithelial cells."
RT EMO J. 12:641-650(1993).
RL
CC -1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
CC VARIATION.
CC -1- SUBCELLULAR LOCATION: Outer membrane.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: Z18933; CAA79366.1; -
CC PIR: S28632; S28632.
CC InterPro: IPR003394; Opacity.
CC Pfam: PF02462; Opacity; 1.
CC Outer membrane; Multigene family; Signal.
CC
CC FT SIGNAL 1 1
CC FT NON_TER <1 1 POTENTIAL.
CC FT CHAIN 2 >234 OPACITY PROTEIN OPA55.
CC FT NON_TER 234 234
CC SEQUENCE 234 AA; 26881 MW; 8EBB30B3A774C766 CRC64;
Query Match 26.7%; Score 232; DB 1; Length 234;
Best Local Similarity 29.4%; Pred. No. 2.6e-14;
Matches 67; Conservative 24; Mismatches 59; Indels 78; Gaps 8;
QY 24 GFYVQADAAHA-----KASSSLGSAK-----GPSRISAGYRINDLR 61
DB 8 GPHYQADLAAYAEHITHDYPEQTPSKGKISTYSDYFRNIRTHSHPRVSGVDFGGMRI 67
QY 62 AVDYTRKRYK-----KAPSTDFK-----LYSIGASAIYDFDT 95
DB 68 AADYARRKNNNNKYSVSIKELRNKVNGRNTRKTENQNGTFHVAVSSIGLSAVYDFDK 127
QY 96 PYKPYLGARLSLN--RASVD-----LGG-----SDSSQSIG 126
DB 128 KFKPYTGARVAAGVHSHSIDSTKTKTKFLLSSGGLNPTVTEENTONAHQNSIRRVG 187
QY 127 LGVLTGVSAAVYPPNDLAGYRYNYIGKVNTPKVNRSGLSVGYVKF 174
DB 188 LGVIAGVGEDITPKLTDGTGRYHYWGLNEMR-FKTHIASLGYRYR 234
RESULT 8
OPAE_NEIGO
ID OPAE_NEIGO STANDARD; PRT; 234 AA.
AC 004879;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Opacity protein OPA56 precursor (Fragment).
GN OPAE.
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
NCBI_TaxID=485;

```

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MS11 / F3; PubMed=8440254;
RA MEDLINE-93178439; PubMed=8440254;
RX Kuepich E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
RT "Variable opacity (Opa) outer membrane proteins account for the cell
epithelial cells";
RL EMBL J. 12:641-650(1993).
CC -1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
CC VARIATION.
CC -1- SUBCELLULAR LOCATION: Outer membrane.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: 218934; CAA79367.1; -.
DR PIR: S28620; S28620.
DR InterPro: IPR003394; Opacity.
DR Pfam: PF02462; Opacity.1.
KW Outer membrane; Multigene family; signal.
FT SIGNAL 1 1
FT NON_TER <1 1 POTENTIAL.
FT CHAIN 2 >234 OPACITY PROTEIN OPA56.
FT NON_TER 234 234
SQ SEQUENCE 234 AA; 26868 MW; 5175C606839EFFB CRC64;

Query Match 26.7%; Score 232; DB 1; Length 234;
Best Local Similarity 28.9%; Pred. No. 2.6e-14;
Matches 66; Conservative 25; Mismatches 59; Indels 78; Gaps 8;

QY 24 GRYVQADAAHA-----KASSLSGSAK-----GPSRISAGYRINDLR 61
DB 8 GRYVQADLAAYAEHTHDYPEQTGTRKDKISTVDFRNVRTHSIHPRVSVGDEGGR 67
QY 62 AVDYPRYKRYKAP--STDPK-----LXSGASAIYPTQOS 95
DB 68 AADYATRYKRWNDKYSDVLEKLENNQNKRDIKTENQNGTFHAASISLGSAYVDFK 127
QY 96 PVKPYLGARLSLN--RASVD-----LGG-----SDPSQTSISG 126
DB 128 KFKPYIGAVAVAGVHRHSIDSTKTKTFLTSYGLNPTVYTEENTQNAHHQSNISIR 187
QY 127 LGVINGVSAVTPNVDLDAGYRYNYIGKYNVKNVRSGLSVGRVKE 174
DB 188 LGVINGVGFDTIPKLLDITGRYHYWGRLENTR-FKTHEASLGVYRFE 234

RESULT 9
OP67_NEIGO STANDARD; PRT; 233 AA.
AC Q05034;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Opacity protein OPA67 precursor (Fragment).
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_Taxid=485;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-VPI;
RA MEDLINE-93178439; PubMed=8440254;
RX Kuepich E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
RT "Variable opacity (Opa) outer membrane proteins account for the cell
epithelial cells";

```

```

RL EMBL J. 12:641-650(1993).
CC -1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
CC VARIATION.
CC -1- SUBCELLULAR LOCATION: Outer membrane.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: 218942; CAA79375.1; -.
DR PIR: S28625; S28625.
DR InterPro: IPR003394; Opacity.
DR Pfam: PF02462; Opacity.1.
KW Outer membrane; Multigene family; signal.
FT SIGNAL 1 1
FT NON_TER <1 1 POTENTIAL.
FT CHAIN 2 >233 OPACITY PROTEIN OPA67.
FT NON_TER 233 233
SQ SEQUENCE 233 AA; 26039 MW; 6C13A46A163C67F CRC64;

Query Match 26.6%; Score 231; DB 1; Length 233;
Best Local Similarity 27.5%; Pred. No. 3.2e-14;
Matches 64; Conservative 31; Mismatches 60; Indels 78; Gaps 7;

QY 19 AEG-ASGRYVQADAAHA-----KASSLSGSAKGF-----SPRISAGY 54
DB 2 SEGNGRGYPVQADLAAYAEHTHDYPEATQAKKGTITVSDYFRNIRTHSVPRVSVG 61
QY 55 RINDPRVAVDYTRKYN-----KAPSTDEKLYSIGSAIYD 92
DB 62 DFGGWRIAADYARARKNNNSKYSYIKKIONOYKKTENQNGTFHAASISLGSAYVDF 121
QY 93 TQSPVKRYLGARLSLN--RASVDL-----GSDSPS 121
DB 122 LNDKFKPYIGARVAVAGVHRHSIDSTKTKTFLTTAGARGAAPVSSPYKTTQADH 181
QY 122 QTSIGLGVLSAVTPNVDLDAGYRYNYIGKYNVKNVRSGLSVGRVKE 174
DB 182 IRRVGLGIVAGVGFDTIPNLTLDAGRYHNMGRLENTR-FKTHEASLGVYRFE 233

RESULT 10
OP28_NEIGO STANDARD; PRT; 234 AA.
AC P11297;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Opacity protein V28 precursor (Fragment).
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_Taxid=485;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-87002493; PubMed=3093085;
RX Stern A., Brown M., Nickel P., Meyer T.F.;
RT "Opacity genes in Neisseria gonorrhoeae: control of phase and
antigenic variation";
RL Cell 47:61-71(1986).
CC -1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
CC VARIATION.
CC -1- SUBCELLULAR LOCATION: Outer membrane.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way

```

modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC -----

DR EMBL; M14747; -; NOT_ANNOTATED_CDS.

DR PIR; B24429; KONH8.

DR InterPro; IPR003394; Opacity.

DR Pfam; PF02462; Opacity; 1.

KW Outer membrane; Multigene family; Signal.

FT NON_TER 1

FT SIGNAL <1 1 POTENTIAL.

FT CHAIN 2 >234 OPACITY PROTEIN V28.

FT NON_TER 234 234

SO SEQUENCE 234 AA; 26770 MW; 339AEB09C2FE75E4 CRC64;

Query Match

Best Local Similarity 26.0%; Score 226; DB 1; Length 234;

Matches 67; Conservative 24; Mismatches 59; Indels 78; Gaps 8;

QY 24 GPHYVADAAHA-----KASSSLGSAR-----GFSPRISAGYRINDLF 61

DB 8 GPHYVADAAHAERHTHDYPTGAKKOLSTVDYFNIRTHSIHPRVSGYDFGWMRI 67

QY 62 AVDYTRYK--NYKAPSTDFK-----LYSIGASAIYDEDTQS 95

DB 68 AADYARYRKWKSSNSIKKVTEDIKNTKYTEHOENGTFHVASSLGLSTYDFQISDK 127

QY 96 PVKPYIGARLSLN--RASVD-----LGS-----SDSPSQTSIG 126

DB 128 KFKPIGRVAVGHVHRSIDSTKTKTKFLSSYGLNPTTYTEENTONAHQSNISIRVG 187

QY 127 LGVLGVSTAVTPNVDLDAGRYNYIGKVTYKRVSGELSVGRVKE 174

DB 188 LGVLGVSTAVTPNVDLDAGRYNYIGKVTYKRVSGELSVGRVKE 234

RESULT 11

OP65_NEIGO STANDARD; PRT; 234 AA.

AC 004885;

DT 01-OCT-1993 (Rel. 27, Created)

DT 01-OCT-1993 (Rel. 27, Last sequence update)

DT 01-NOV-1995 (Rel. 32, Last annotation update)

DE Opacity protein OPA65 precursor (Fragment).

OS Neisseria gonorrhoeae.

CC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.

OX NCBI_TaxID=485;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=VPI;

RX MEDLINE=93178439; PubMed=8440254;

RA Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;

RT "Variable opacity (Opa) outer membrane proteins account for the cell tropisms displayed by Neisseria gonorrhoeae for human leukocytes and epithelial cells."

RL EMO J. 12:641-650(1993).

CC -1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA

CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE

CC VARIATION.

CC -1- SUBCELLULAR LOCATION: Outer membrane.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC EMBL; Z18940; CAA79373.1; -

DR PIR; S28617; S28619.

DR InterPro; IPR003394; Opacity.

DR Pfam; PF02462; Opacity; 1.

KW Outer membrane; Multigene family; Signal.

FT NON_TER 1

FT SIGNAL <1 1 POTENTIAL.

FT CHAIN 2 >238 OPACITY PROTEIN OPA66.

FT NON_TER 238 238

SO SEQUENCE 238 AA; 26888 MW; B6E38AF1585263AA CRC64;

Query Match

Best Local Similarity 26.0%; Score 226; DB 1; Length 238;

Matches 64; Conservative 28; Mismatches 58; Indels 78; Gaps 8;

KW Outer membrane; Multigene family; Signal.

FT NON_TER 1

FT SIGNAL <1 1 POTENTIAL.

FT CHAIN 2 >234 OPACITY PROTEIN OPA65.

FT NON_TER 234 234

SO SEQUENCE 234 AA; 26242 MW; D66A0BAA842AC2F1 CRC64;

Query Match

Best Local Similarity 26.0%; Score 226; DB 1; Length 234;

Matches 64; Conservative 28; Mismatches 58; Indels 78; Gaps 8;

QY 24 GPHYVADAAHA-----KASSSLGS-----AKGSPRISAGYRINDLF 61

DB 8 GPHYVADAAHAERHTHDYPTGAKKOLSTVDYFNIRTHSIHPRVSGYDFGWMRI 67

QY 62 AVDYTRYK--NYKAPSTDFK-----LYSIGASAIYDEDTQS 96

DB 68 AADYARYRKWKSSNSIKKVTEDIKNTKYTEHOENGTFHVASSLGLSTYDFQISDK 127

QY 97 VPKYIGARLSLN--RASVD-----LGS-----SDSPSQTSIG 126

DB 128 KFKPIGRVAVGHVHRSIDSTKTKTKFLSSYGLNPTTYTEENTONAHQSNISIRVG 187

QY 127 LGVLGVSTAVTPNVDLDAGRYNYIGKVTYKRVSGELSVGRVKE 174

DB 188 LGVLGVSTAVTPNVDLDAGRYNYIGKVTYKRVSGELSVGRVKE 234

RESULT 12

OP66_NEIGO STANDARD; PRT; 238 AA.

AC 005033;

DT 01-OCT-1993 (Rel. 27, Created)

DT 01-OCT-1993 (Rel. 27, Last sequence update)

DT 01-NOV-1995 (Rel. 32, Last annotation update)

DE Opacity protein OPA66 precursor (Fragment).

OS Neisseria gonorrhoeae.

CC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.

OX NCBI_TaxID=485;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=VPI;

RX MEDLINE=93178439; PubMed=8440254;

RA Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;

RT "Variable opacity (Opa) outer membrane proteins account for the cell tropisms displayed by Neisseria gonorrhoeae for human leukocytes and epithelial cells."

RL EMO J. 12:641-650(1993).

CC -1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA

CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE

CC VARIATION.

CC -1- SUBCELLULAR LOCATION: Outer membrane.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC EMBL; Z18941; CAA79374.1; -

DR PIR; S28619; S28619.

DR InterPro; IPR003394; Opacity.

DR Pfam; PF02462; Opacity; 1.

KW Outer membrane; Multigene family; Signal.

FT NON_TER 1

FT SIGNAL <1 1 POTENTIAL.

FT CHAIN 2 >238 OPACITY PROTEIN OPA66.

FT NON_TER 238 238

SO SEQUENCE 238 AA; 26888 MW; B6E38AF1585263AA CRC64;

Query Match

Best Local Similarity 26.0%; Score 226; DB 1; Length 238;

Best Local Similarity 28.4%; Pred. No. 9.5e-14;
Matches 66; Conservative 27; Mismatches 57; Indels 82; Gaps 8;

QY 24 GPVQADAAH-----KASSSLGSAKF-----SPRISAGYRINDLR 61
D 8 GPVQADAAHAYEHITHDYPRKPTDPSKGLSTVSDYFRNIRTHSHRVSVDGDFGMR 67
QY 62 AVDTTRK--NYKAPSDER-----LYSIGASAIYDFDT 93
D 68 AADTARTKMKNDKSYVSIKLNCRRTSGNCRDRKTEQNGSFHVAVSSIGLSAVYDFKL 127
QY 94 QSPKPYLGARLSLN--RASVD-----LGSD-----SFSQ 122
D 128 NDKKPYLGARVAVGHVHSHIDSKTTEFLITAGARGITPYVSSPKTKQDAHESNST 187
QY 123 TSGIGLVTVSAVTPNVLDAGYRNYIGKVTYKNNVSGELSGVRYKF 174
D 188 RRGGLAVIAGVGFDTPLTLIDAGYRHYHNGMLENTR-FKTHASLGVRVF 238

RESULT 13

OPAD_NEIGO STANDARD; PRT; 238 AA.
AC 004884;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Opacity protein OP460 precursor (Fragment).
GN OPAH.
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=485;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MS11 / F3;
RX MEDLINE=93178439; PubMed=8440254;
RA Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
RT "Variable opacity (Opa) outer membrane proteins account for the cell
epithelial cells";
RL EMBO J. 12:641-650(1993).
RN [2]

RP SEQUENCE FROM N.A.
RC STRAIN=MS11 / V18;
RX MEDLINE=92114767; PubMed=1815562;
RA Bhat K.S., Gibbs C.P., Barrera O., Morrison S.G., Jaehnig F.,
RT Stern A., Kupsch E.-M., Meyer T.F., Swanson J.;
RT "The opacity proteins of Neisseria gonorrhoeae strain MS11 are
encoded by a family of 11 complete genes";
RL Mol. Microbiol. 5:1889-1901(1991).
RN [3]
RP ERRATUM.
RX MEDLINE=92261323; PubMed=1584024;
RA Bhat K.S., Gibbs C.P., Barrera O., Morrison S.G., Jaehnig F.,
RT Stern S., Kupsch E.-M., Meyer T.F., Swanson J.;
RL Mol. Microbiol. 6:1073-1076(1992).

-1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
VARIATION.
-1- SUBCELLULAR LOCATION: Outer membrane.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC EMBL; Z18939; CAA79372.1; -;
DR EMBL; X60711; CAA43121.1; -;
DR PIR; S28631; S28631.
DR InterPro; IPR003394; Opacity.

DR Pfam; PF02462; Opacity; 1.
KW Outer membrane; Multigene family; Signal.

FT SIGNAL 1 1
FT CHAIN 2 2
FT VARIANTS 2 238
FT VARIANTS 234 234
FT NON_TER 238 238
SQ SEQUENCE 238 AA; 27073 MW; 883A3560C2DF1B9F CRC64;

Query Match 26.0%; Score 226; DB 1; Length 238;
Best Local Similarity 27.6%; Pred. No. 9.5e-14;
Matches 66; Conservative 26; Mismatches 65; Indels 82; Gaps 6;

QY 17 ALAEGASGFYQADAAH-----KASSSLG-----AKSPRISAGY 54
D 1 ASEDGGRGVQADAAHAYEHITHDYPRTPAPKKNKISTVSDYFRNIRTHSHRVSVDG 60
QY 55 RINDRFADVYRKYNY-----KAPDFKLYSIGAS 86
D 61 DFGWRIRADYARVYKNNKNSVNIENVRIKENGITIDKTEQNGTFHVAVSSIGLS 120
QY 87 AYPDPTQSPKPYLGARLSLN--RASVD-----LG 115
D 121 AYPDPTQSPKPYLGARVAVGHVHSHIDSKTTEFLITAGARGITPYVSSPKTKQDAH 180
QY 116 GSDSFSQTSIGLVTVSAVTPNVLDAGYRNYIGKVTYKNNVSGELSGVRYKF 174
D 181 DYQNSIRVGLVAGVGFDTPLTLIDAGYRHYHNGMLENTR-FKTHASLGVRVF 238

RESULT 14

OPAD_NEIGO STANDARD; PRT; 243 AA.
AC 004883;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Opacity protein OPA59 precursor (Fragment).
GN OPAD.
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=485;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=MS11 / F3;
RX MEDLINE=93178439; PubMed=8440254;
RA Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
RT "Variable opacity (Opa) outer membrane proteins account for the cell
epithelial cells";
RL EMBO J. 12:641-650(1993).
RN [2]

-1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
VARIATION.
-1- SUBCELLULAR LOCATION: Outer membrane.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC EMBL; Z18938; CAA79371.1; -;
DR PIR; S28629; S28629.
DR InterPro; IPR003394; Opacity.
DR Pfam; PF02462; Opacity; 1.
KW Outer membrane; Multigene family; Signal.
FT NON_TER 1 1
FT SIGNAL 1 1
FT CHAIN 2 243
POTENTIAL.
OPACITY PROTEIN OPA59.

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 28, 2002, 15:56:04 ; Search time 19.9713 Seconds
(without alignments)
1507.218 Million cell updates/sec

Title: US-09-684-883-2
Perfect score: 1 MKKALTLTLLALPAAALAE.....VNTKVRSGELSGVRKAF 174
Sequence: 868

Scoring table: BLUSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mhc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*
15: SP rivirus:*
16: SP bacteriophage:*
17: SP archaeop:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	868	100.0	174	2	P96943
2	864	99.5	174	16	Q9RP17
3	857	98.7	174	2	Q9R2R1
4	854	98.4	174	16	P95372
5	852	98.2	174	2	Q9RP16
6	846	97.5	174	2	Q9RP18
7	825	95.0	174	2	P95343
8	824.5	95.0	175	2	P95371
9	247	28.5	256	2	051124
10	246.5	28.4	186	16	Q9CML9
11	244	28.1	234	2	Q9R719
12	244	28.1	234	2	Q9R718
13	243	28.0	234	2	Q9R718
14	241.5	27.8	232	2	Q9K4T9
15	241.5	27.8	241	2	Q9A8E0
16	240.5	27.7	230	2	Q9R9A7

17	240	27.6	241	2	Q9K4T4
18	240	27.6	256	2	Q51126
19	240	27.6	259	2	Q51125
20	239.5	27.6	232	2	Q9R3P5
21	238.5	27.5	257	2	Q50929
22	238	27.4	234	2	Q07287
23	238	27.4	237	2	Q31176
24	237	27.3	262	2	Q33388
25	236.5	27.2	232	2	Q9K4T3
26	236	27.2	270	2	Q9R0V4
27	236	27.2	283	2	Q50943
28	234.5	27.0	241	2	Q07274
29	234	27.0	240	2	Q07925
30	234	27.0	272	2	Q51013
31	233.5	26.9	241	2	Q07912
32	233.5	26.9	253	2	Q51303
33	233	26.8	233	2	Q9K4T5
34	233	26.8	235	2	Q30753
35	232.5	26.8	232	2	Q9R9A9
36	232.5	26.8	232	2	Q9R9A8
37	232	26.7	237	2	Q9K4T6
38	231	26.6	235	2	Q30752
39	229.5	26.4	232	2	Q9K4T7
40	228.5	26.3	241	2	Q07273
41	228	26.3	242	2	Q9K4T8
42	227.5	26.2	238	2	Q31172
43	227.5	26.2	243	2	Q07278
44	227	26.2	260	2	Q33389
45	226.5	26.1	242	2	Q07279

ALIGNMENTS

RESULT 1
P96943 PRELIMINARY; PRT; 174 AA.
AC P96943;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE OUTER MEMBRANE PROTEIN PRECURSOR.
GN NSP.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=608B;
RX MEDLINE=97149429; PubMed=8996237;
RA Martin D., Cadieux N., Hamel J., Brodeur B.R.;
RT "Costimulation of T cell activation by Integrin-associated protein (CD47) is an adhesion-dependent, CD28-independent signaling pathway.";
RL J. Exp. Med. 185:1-11(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NGP165, M986, AND NG6/88;
RA Moe G.R., Tan S., Granoff D.M.;
RT "Differences in Surface Expression of Neisserial Surface Protein A among Neisseria meningitidis Group B strains.";
RL Infect. Immun. 0:0-0(1999).
DR EMBL; U52066; AAC36000.1; -;
DR EMBL; AF175683; AAD53286.1; -;
DR EMBL; AF175680; AAD53283.1; -;
DR EMBL; AF175682; AAD53285.1; -;
DR InterPro: IPR003394; Opacity.
DR Pfam: PF02462; Opacity; 1.
FT Signal.
FT SIGNAL.
SQ SSQUNCE 174 AA; 18425 MW; EBB02767DDCFE19 CRC64;
Query Match 100.0%; Score 868; DB 2; Length 174;
Best Local Similarity 100.0%; Pred. No. 2.7e-64;

Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MKKALATLIALPALPAALAEAGSGFYVQADAAHAKASSLSGSKGSPRISAGYRINDLR 60
   |||
Db 1 MKKALATLIALPALPAALAEAGSGFYVQADAAHAKASSLSGSKGSPRISAGYRINDLR 60
QY 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDQSPVKPYLGARLSLNRAVDLGSDSF 120
   |||
Db 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDQSPVKPYLGARLSLNRAVDLGSDSF 120
QY 121 SQTSTIGLVLTGVSVAATPNDVLDAGRYNRYIGKNTVKNVNSGELSGVGRKF 174
   |||
Db 121 SQTSTIGLVLTGVSVAATPNDVLDAGRYNRYIGKNTVKNVNSGELSGVGRKF 174

```

RESULT 2

Q9RP17 PRELIMINARY; PRT; 174 AA.

```

AC 09RP17;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE SURFACE PROTEIN A (OUTER MEMBRANE PROTEIN NSGA).
GN NSPA OR NME0663.
OS Neisseria meningitidis, and
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_Taxid=487, 491;
RN 1]
RP SEQUENCE FROM N.A.
RC STRAIN=CU385;
RA Moe G.R., Tan S., Granoff D.M.;
RT "Differences in Surface Expression of Neisserial Surface Protein A
   among Neisseria meningitidis Group B strains.";
RL Infect. Immun. 0:0-0(1999).
RN 12]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / SEROGROUP B;
RX MEDLINE=2017575; PubMed=10710307;
RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
RA Nelson W.C., Gwin M.L., Deboy R., Peterson J.D., Hickey E.K.,
RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
RA Mason T., Clecko A., Parksey D.S., Blair E., Clifton H., Clark E.B.,
RA Cotton M.D., Ulterback T.R., Knouri H., Qin H., Vamathevan J.,
RA Gill J., Scariato V., Maignani V., Pizzo M., Grandi G., Sun L.,
RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
   MC58.";
RL Science 287:1809-1815(2000).
DR EMBL; AF175678; AAD53281.1; -;
DR EMBL; AE002420; AAF41081.1; -;
DR TIGR; NME0663; -;
DR InterPro; IPR003394; Opacity.
DR Pfam; PF02462; Opacity; 1.
KM Complete proteome.
SQ SEQUENCE 174 AA; 18397 MM; E8B02767DDC6E109 CRC64;

```

Query Match 99.5%; Score 864; DB 16; Length 174;

Best Local Similarity 99.4%; Pred. No. 5,7e-64;

Matches 173; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 MKKALATLIALPALPAALAEAGSGFYVQADAAHAKASSLSGSKGSPRISAGYRINDLR 60
   |||
Db 1 MKKALATLIALPALPAALAEAGSGFYVQADAAHAKASSLSGSKGSPRISAGYRINDLR 60
QY 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDQSPVKPYLGARLSLNRAVDLGSDSF 120
   |||
Db 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDQSPVKPYLGARLSLNRAVDLGSDSF 120
QY 121 SQTSTIGLVLTGVSVAATPNDVLDAGRYNRYIGKNTVKNVNSGELSGVGRKF 174
   |||
Db 121 SQTSTIGLVLTGVSVAATPNDVLDAGRYNRYIGKNTVKNVNSGELSGVGRKF 174

```

RESULT 3

Q9R2R1 PRELIMINARY; PRT; 174 AA.

```

AC 09R2R1;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE SURFACE PROTEIN A.
GN NSPA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_Taxid=487;
RN 1]
RP SEQUENCE FROM N.A.
RC STRAIN=M136, AND B232;
RA Moe G.R., Tan S., Granoff D.M.;
RT "Differences in Surface Expression of Neisserial Surface Protein A
   among Neisseria meningitidis Group B strains.";
RL Infect. Immun. 0:0-0(1999).
DR EMBL; AF175679; AAD53280.1; -;
DR InterPro; IPR003394; Opacity.
DR Pfam; PF02462; Opacity; 1.
SQ SEQUENCE 174 AA; 18385 MM; ECF6F39A9286910E CRC64;

```

Query Match 98.7%; Score 857; DB 2; Length 174;

Best Local Similarity 98.3%; Pred. No. 2.2e-63;

Matches 171; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

QY 1 MKKALATLIALPALPAALAEAGSGFYVQADAAHAKASSLSGSKGSPRISAGYRINDLR 60
   |||
Db 1 MKKALATLIALPALPAALAEAGSGFYVQADAAHAKASSLSGSKGSPRISAGYRINDLR 60
QY 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDQSPVKPYLGARLSLNRAVDLGSDSF 120
   |||
Db 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDQSPVKPYLGARLSLNRAVDLGSDSF 120
QY 121 SQTSTIGLVLTGVSVAATPNDVLDAGRYNRYIGKNTVKNVNSGELSGVGRKF 174
   |||
Db 121 SQTSTIGLVLTGVSVAATPNDVLDAGRYNRYIGKNTVKNVNSGELSGVGRKF 174

```

RESULT 4

P95372 PRELIMINARY; PRT; 174 AA.

```

AC P95372;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE OUTER MEMBRANE PROTEIN PRECURSOR.
GN NSPA OR NMA0862.
OS Neisseria meningitidis, and
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_Taxid=487, 65699;
RN 1]
RP SEQUENCE FROM N.A.
RC STRAIN=24063;
RA Martin D., Cadieux N., Hamel J., Rioux C., Brodeur B.R.;
RT submitted (MAR-1996) to the EMBL/Genbank/DBJ databases.
RL [2]
RX MEDLINE=20222556; PubMed=10761919;

```

```

RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Feltham T., Hamlin N., Holtroyd S.,
RA Jørgensen K., Leather S., Moule S., Mungall K., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrall B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria

```


RT meningitidis 22491."
 RL Nature 404:502-506(2000).
 DR EMBL; U52068; AAB41580.1; -
 DR EMBL; AL162754; CAB84143.1; -
 DR InterPro; IPR003394; Opacity.
 DR Pfam; PF02462; Opacity: 1.
 DR Signal; Complete proteome.
 KW SIGNAL
 FT SIGNAL
 SQ SEQUENCE 174 AA; 18355 MW; E8A4A1AD4F6F009 CRC64;

Query Match 98.4%; Score 854; DB 16; Length 174;
 Best Local Similarity 98.3%; Pred. No. 3.8e-63;
 Matches 171; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKKALATLIALALPAAALABGASGFYQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 DB 1 MKKALATLIALALPAAALABGASGFYQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 QY 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDQSPVKPYLGARLSLNRAVDLGSSDSF 120
 DB 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDQSPVKPYLGARLSLNRAVDLGSSDSF 120
 QY 121 SQTSTGLGVLGVSAYAVTPNVDLDAGRYNYIGKNTYKVRSGELSGYRVKF 174
 DB 121 SQTSTGLGVLGVSAYAVTPNVDLDAGRYNYIGKNTYKVRSGELSGYRVKF 174

RESULT 5

Q9RP16 PRELIMINARY; PRT; 174 AA.

DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE SURFACE PROTEIN A.
 GN NSPA.
 OS Neisseria meningitidis.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_TaxID=487;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-NG3/88;
 RA Moe G.R., Tan S., Granoff D.M.;
 RT "Differences in Surface Expression of Neisserial Surface Protein A
 among Neisseria meningitidis Group B strains.";
 RL Infect. Immun. 0:0-0(1999).
 DR EMBL; AF175681; AAD53284.1; -
 DR InterPro; IPR003394; Opacity.
 DR Pfam; PF02462; Opacity: 1.
 SQ SEQUENCE 174 AA; 18355 MW; ECF6F3B9286800E CRC64;

Query Match 98.2%; Score 852; DB 2; Length 174;
 Best Local Similarity 97.7%; Pred. No. 5.6e-63;
 Matches 170; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKKALATLIALALPAAALABGASGFYQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 DB 1 MKKALATLIALALPAAALABGASGFYQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 QY 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDQSPVKPYLGARLSLNRAVDLGSSDSF 120
 DB 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDQSPVKPYLGARLSLNRAVDLGSSDSF 120
 QY 121 SQTSTGLGVLGVSAYAVTPNVDLDAGRYNYIGKNTYKVRSGELSGYRVKF 174
 DB 121 SQTSTGLGVLGVSAYAVTPNVDLDAGRYNYIGKNTYKVRSGELSGYRVKF 174

RESULT 6
 Q9RP18 PRELIMINARY; PRT; 174 AA.
 AC Q9RP18;
 DT 01-MAY-2000 (Tremblrel. 13, Created)

DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE SURFACE PROTEIN A.
 GN NSPA.
 OS Neisseria meningitidis.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_TaxID=487;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-8047;
 RA Moe G.R., Tan S., Granoff D.M.;
 RT "Differences in Surface Expression of Neisserial Surface Protein A
 among Neisseria meningitidis Group B strains.";
 RL Infect. Immun. 0:0-0(1999).
 DR EMBL; AF175676; AAD53279.1; -
 DR InterPro; IPR003394; Opacity.
 DR Pfam; PF02462; Opacity: 1.
 SQ SEQUENCE 174 AA; 18357 MW; 0205A1DA1B7F005 CRC64;

Query Match 97.5%; Score 846; DB 2; Length 174;
 Best Local Similarity 97.1%; Pred. No. 1.7e-62;
 Matches 169; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MKKALATLIALALPAAALABGASGFYQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 DB 1 MKKALATLIALALPAAALABGASGFYQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 QY 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDQSPVKPYLGARLSLNRAVDLGSSDSF 120
 DB 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDQSPVKPYLGARLSLNRAVDLGSSDSF 120
 QY 121 SQTSTGLGVLGVSAYAVTPNVDLDAGRYNYIGKNTYKVRSGELSGYRVKF 174
 DB 121 SQTSTGLGVLGVSAYAVTPNVDLDAGRYNYIGKNTYKVRSGELSGYRVKF 174

RESULT 7

P95343 PRELIMINARY; PRT; 174 AA.

DT 01-MAY-1997 (Tremblrel. 03, Created)
 DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE OUTER MEMBRANE PROTEIN PRECURSOR.
 OS Neisseria gonorrhoeae.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_TaxID=485;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-B2;
 RX MEDLINE=99270944; PubMed=10338491;
 RA Plante M., Cadieux N., Rioux C.R., Hamel J., Brodeur B.R., Martin D.;
 RT "Antigenic and molecular conservation of the gonococcal NSPA
 protein.";
 RL Infect. Immun. 67:2855-2861(1999).
 DR EMBL; U52069; AAB41581.1; -
 DR InterPro; IPR003394; Opacity.
 DR Pfam; PF02462; Opacity: 1.
 KW SIGNAL
 FT SIGNAL
 SQ SEQUENCE 174 AA; 18337 MW; 1B558ECBA040841A CRC64;

Query Match 95.0%; Score 825; DB 2; Length 174;
 Best Local Similarity 94.3%; Pred. No. 9.5e-61;
 Matches 164; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 MKKALATLIALALPAAALABGASGFYQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 DB 1 MKKALATLIALALPAAALABGASGFYQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 QY 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDQSPVKPYLGARLSLNRAVDLGSSDSF 120
 DB 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDQSPVKPYLGARLSLNRAVDLGSSDSF 120

OY 121 SOTSIGLVLTGVSVAATPVNDLDAGRYRNYIGKVTNKNVRSGLSVGRVKE 174
 DB 121 SKTSAGLVLAGVSVAATPVNDLDAGIRINVTGKNTVKNVRSGLSVGRVKE 174

RESULT 8

P95371 PRELIMINARY; PRT; 175 AA.
 AC P95371;
 DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE OUTER MEMBRANE PROTEIN PRECURSOR.
 OS Neisseria meningitidis.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 ON NCBI_TaxId=487;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MCH 88;
 RX MEDLINE=9386904; PubMed=10456958;
 RA Cadiereux N., Plante M., Rioux C.R., Brodeur B.R., Martin D.;
 RT "Bactericidal and cross-protective activities of a monoclonal antibody
 directed against Neisseria meningitidis Nspa outer membrane protein.";
 RL Infect. Immun. 67:4955-4959(1999).
 DR EMBL: U52067; AAB41579.1; -;
 DR InterPro: IPR003394; Opacity.
 DR Pfam: PF02462; Opacity; 1.
 KM Signal.
 FT SIGNAL 1 19 POTENTIAL.
 SQ SEQUENCE 175 AA; 18572 MW; 18582F2F5CC2FEA CRC64;

Query Match 95.0%; Score 824.5; DB 2; Length 175;
 Best Local Similarity 95.4%; Pred. No. 1.1e-60;
 Matches 167; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

OY 1 MKKALATLIALALPAALAEAGSGFYVQADAAHAKASSSGSAGSPRISAGYRINDLR 60
 DB 1 MKKALATLIALALPAALAEAGSGFYVQADAAHAKASSSGSAGSPRISAGYRINDLR 60
 OY 61 FAVDYTRYKNKK-APSTDFKLYSGASAIYDFQSPVKRYLGLARLSLNASVDLGSSDS 119
 DB 61 FAVDYTRYKNKKQVPSDFKLYSGASAIYDFQSPVKRYLGLARLSLNASVDLGSSDS 120
 OY 120 FSGTSGIGLVLTGVSVAATPVNDLDAGRYRNYIGKVTNKNVRSGLSVGRVKE 174
 DB 121 FSGTSGIGLVLTGVSVAATPVNDLDAGRYRNYIGKVTNKNVRSGLSVGRVKE 175

RESULT 9

O51124 PRELIMINARY; PRT; 256 AA.
 ID O51124;
 AC O51124;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
 DE OPA
 GN OPA.
 OS Neisseria meningitidis.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 ON NCBI_TaxId=487;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=24197;
 RX MEDLINE=98129089; PubMed=9467908;
 RA Hobbs J.E., Cannon J.G., Achtman M.;
 RT "Recombinational reassortment among opa genes from ET-37 complex
 Neisseria meningitidis isolates of diverse geographical origins.";
 RL Microbiology 144:157-166(1998).
 DR EMBL: U37255; AAC46101.1; -;
 DR InterPro: IPR003394; Opacity.
 DR Pfam: PF02462; Opacity; 1.

FT NON_TER 1 1
 SQ SEQUENCE 256 AA; 28335 MW; 9D41C6079C6DD13F CRC64;

Query Match 28.5%; Score 247; DB 2; Length 256;
 Best Local Similarity 32.3%; Pred. No. 8.3e-13;
 Matches 69; Conservative 32; Mismatches 64; Indels 78; Gaps 7;

OY 8 LIALALPAALAEAGSGFYVQADAAHAKASSSGSAGSPRISAGYRINDLR 108
 DB 14 LESSAQAASDESGHGPIYVQADLAALAEIRTHDYPKATGANNSTSDYFRNIRASHIH 73
 OY 48 PRISAGYRINDLRPAVDYTRYK-----NYKAPSDFK-----LYS 82
 DB 74 PVSAGYDFGGWRILADYASRYKMKESNSYKVTEDIANDKETKTEHOGNSFHAASS 133
 OY 83 IGASAIYDFQSPVKRYLGLARLSLN-----ASVDLG-----116
 DB 134 LGLSAIYDFKLNDRKPRIGARVAAGHYKQVHSYERKTTVTSKPATSPQGGPIIQT 193
 OY 117 -----SDSFGTSGIGLVLTGVSVAATPVNDLDAGRYRNYIGKVTNKNVRSGLSVG 170
 DB 194 PCKPYHSHSISISGLGVLAGVGFDPKLTLDGYRYHNMGRLENTFR-FKTHEVSLGM 252
 OY 171 RYKF 174
 DB 253 RYKF 256

RESULT 10

O9CM19 PRELIMINARY; PRT; 186 AA.
 ID O9CM19;
 AC O9CM19;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE OPA.
 GN OPA OR PM1025.
 OS Pasteurella multocida.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 ON NCBI_TaxId=747;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PM70;
 RX MEDLINE=21145866; PubMed=11248100;
 RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
 RT "Complete genomic sequence of Pasteurella multocida PM70.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
 DR EMBL: AE06143; AAK03109.1; -;
 DR InterPro: IPR003394; Opacity.
 DR Pfam: PF02462; Opacity; 1.
 KM Complete proteome.
 SQ SEQUENCE 186 AA; 20512 MW; 1B17F0A4AFC0157 CRC64;

Query Match 28.4%; Score 246.5; DB 16; Length 186;
 Best Local Similarity 32.3%; Pred. No. 6.2e-13;
 Matches 61; Conservative 32; Mismatches 77; Indels 19; Gaps 5;

OY 1 MKKALATLIALALPAALAEAGSGFYVQADAAHAKASSSGSAGSPRISAGYRIN 57
 DB 2 MKK---SLVLAIAGALCSLTASANFYOGDLGVAKTSSSYEMNKTINVPVSVGYDLG 58
 OY 58 DLRFVDYTRYKNKAP-----TDFKLYSGASAIYDFQSPVKRYLGLARLSLN 108
 DB 59 AMRLADYTHYGFSGTSTFGVNOKEHSTKIYGLSLAFDFNINSVLKPYVGRRLASN 118
 OY 109 RASVDLGSSDSF-----SOTSIGLVLTGVSVAATPVNDLDAGRYRNYIGKVTNKNVRSGE 165
 DB 119 IPIETKSGSNFRPSEKTKTLGIGTLAGAGYGLMTNLFVNGGLEIYRRLGRFSDF-SVNGYG 177
 OY 166 LSVGRVKE 174
 DB 178 AKVGLRYDF 186

```

RESULT 11
Q9R719 PRELIMINARY; PRT; 234 AA.
AC 09R719;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE OPACITY PROTEIN (FRAGMENT).
GN OPA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID:487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=23906;
RX MEDLINE=98010345; PubMed=9350862;
RA Morelli G., Malorny B., Mueller K., Seller A., Wang J., del Valle J.,
RA Achtman M.;
RT "Clonal descent and microevolution of Neisseria meningitidis during 30
RT years of epidemic spread.";
RL Mol. Microbiol. 25:1047-1064(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=3926;
RA Zhu P., van der Ende A., Falush D., Brieske N., Morelli G., Linz B.,
RA Popovic T., Schutman I.G.A., Adegoke R.A., Zurth K., Gagneux S.,
RA Platonov A.E., Rion J.Y., Gaugant D.A., Nicolas P., Achtman M.;
RT "Genotypes and escape variants of subgroup III Neisseria
RT meningitidis during three pandemics of epidemic meningitis.";
RL EMBL: AF001194; AAC32715.1; -
DR EMBL: AJ292235; CAC36358.1; -
DR InterPro: IPR003394; Opacity.
DR Pfam: PF02462; Opacity; 1.
FT NON_TER 1
SQ SEQUENCE 234 AA; 26161 MW; F97142F463136EC1 CRC64;

Query Match 28.1%; Score 244; DB 2; Length 234;
Best Local Similarity 28.9%; Pred. No. 1.3e-12;
Matches 67; Conservative 32; Mismatches 59; Indels 74; Gaps 8;

QY 16 AALAEGA-SGEYVQADAAH-----AKSSSLGS-----AKGSPRISAGY 54
DB 4 AASEDGSRSPPYVQADLAAERITHDYPOATGANNSTVSDYFNRNIRASHIPRVSVGY 63
QY 55 RINDLRFAVDYTRYK-----NYKAPSTDFK-----LYSIGASAI 88
DB 64 DFGDMRIADYASYRKKEESNYSKYTEFKHONGKQEDKTEHOGNGSFHATSSLGLSAI 123
QY 89 YPDFDQSPYKPYIGARLSINR-----ASVDLGC-----SDSFQ 122
DB 124 YDFKLSDFKPYIGARLSINR-----ASVDLGC-----SDSFQ 122
QY 123 TSIGLGLTVGSYAVTPNVDAGRYNYIGKRVNKNVRSGLSVGYRKE 174
DB 184 SSVGLGVIAVGCFDITPKLTLDGTGRYHNMGRLENTR-FKTHVSLGKRYHF 234

RESULT 12
007280 PRELIMINARY; PRT; 234 AA.
AC 007280;
DT 01-JUL-1997 (TREMblrel. 04, Created)
DT 01-JUL-1997 (TREMblrel. 04, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE OPACITY PROTEIN (FRAGMENT).
GN OPA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID:487;
RN [1]

```

```

RP SEQUENCE FROM N.A.
RC STRAIN=23524;
RX MEDLINE=98010345; PubMed=9350862;
RA Morelli G., Malorny B., Muller K., Seller A., Wang J.F., del Valle J.,
RA Achtman M.;
RT "Clonal descent and microevolution of Neisseria meningitidis during 30
RT years of epidemic spread.";
RL Mol. Microbiol. 25:1047-1064(1997).
DR EMBL: AF001195; AAC32716.1; -
DR InterPro: IPR003394; Opacity.
DR Pfam: PF02462; Opacity; 1.
FT NON_TER 1
SQ SEQUENCE 234 AA; 26134 MW; 005AD356E93BC50 CRC64;

Query Match 28.1%; Score 244; DB 2; Length 234;
Best Local Similarity 28.9%; Pred. No. 1.3e-12;
Matches 67; Conservative 32; Mismatches 59; Indels 74; Gaps 8;

QY 16 AALAEGA-SGEYVQADAAH-----AKSSSLGS-----AKGSPRISAGY 54
DB 4 AASEDGSRSPPYVQADLAAERITHDYPOATGANNSTVSDYFNRNIRASHIPRVSVGY 63
QY 55 RINDLRFAVDYTRYK-----NYKAPSTDFK-----LYSIGASAI 88
DB 64 DFGDMRIADYASYRKKEESNYSKYTEFKHONGKQEDKTEHOGNGSFHATSSLGLSAI 123
QY 89 YPDFDQSPYKPYIGARLSINR-----ASVDLGC-----SDSFQ 122
DB 124 YDFKLSDFKPYIGARLSINR-----ASVDLGC-----SDSFQ 122
QY 123 TSIGLGLTVGSYAVTPNVDAGRYNYIGKRVNKNVRSGLSVGYRKE 174
DB 184 SSVGLGVIAVGCFDITPKLTLDGTGRYHNMGRLENTR-FKTHVSLGKRYHF 234

RESULT 13
Q9R718 PRELIMINARY; PRT; 234 AA.
AC 09R718;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE OPACITY PROTEIN (FRAGMENT).
GN OPA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID:487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BI;
RX MEDLINE=98010345; PubMed=9350862;
RA Morelli G., Malorny B., Muller K., Seller A., Wang J.F., del Valle J.,
RA Achtman M.;
RT "Clonal descent and microevolution of Neisseria meningitidis during 30
RT years of epidemic spread.";
RL Mol. Microbiol. 25:1047-1064(1997).
DR EMBL: AF001196; AAC32717.1; -
DR InterPro: IPR003394; Opacity.
DR Pfam: PF02462; Opacity; 1.
FT NON_TER 1
SQ SEQUENCE 234 AA; 26191 MW; F01D3B9163066171 CRC64;

Query Match 28.0%; Score 243; DB 2; Length 234;
Best Local Similarity 28.9%; Pred. No. 1.6e-12;
Matches 67; Conservative 31; Mismatches 60; Indels 74; Gaps 8;

QY 16 AALAEGA-SGEYVQADAAH-----AKSSSLGSAG-----FSPRISAGY 54
DB 4 AASEDGSRSPPYVQADLAAERITHDYPOATGANNSTVSDYFNRNIRASHIPRVSVGY 63
QY 55 RINDLRFAVDYTRYK-----NYKAPSTDFK-----LYSIGASAI 88
DB 64 DFGDMRIADYASYRKKEESNYSKYTEFKHONGKQEDKTEHOGNGSFHATSSLGLSAI 123

```

```

RP SEQUENCE FROM N.A.
RC STRAIN=29620;
RC MEDLINE=21221108; PubMed=11287631;
RA Zhu P., van der Ende A., Falush D., Brieske N., Morelli G., Bodo L.,
RA Popovic T., Schuurman I.G.A., Adegbola R.A., Zurch K., Gagneux S.,
RA Platonov A.E., Khou J.Y., Caugant D.A., Nicolas P., Achtman M.,
RT "fit genotypes and escape variants of subgroup III Neisseria
RT meningitidis during three pandemics of epidemic meningitis.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:5234-5239(2001).
DR EMBL: AJ292238; CAC36361.1;
DR InterPro: IPR003394; Opacity.
DR Pfam: PF02462; Opacity; 1.
FT NON_TER 1
SQ SEQUENCE 241 AA; 26923 MW; 4923ACF9484BF183 CRC64;

Query Match 27.8%; Score 241.5; DB 2; Length 241;
Best Local Similarity 28.9%; Pred. No. 2.2e-12;
Matches 69; Conservative 33; Mismatches 56; Indels 81; Gaps

QY 16 AALAEGA-SGEYVQADAAHA-----KASSISLG-----AKGSPRISAGY 54
DB 4 AASBDGSRSPYYQADLATAERITHDYPKASGANNTSVSDYFRNIRAHSHPRVSVGY 63
QY 55 RINDLRPAVDYTRYKNY-----KAPSTDFKIYISIGAS 86
DB 64 DFGDMRIADYASYRKMDNKKYSVNTKNYQVKNKSGNRQDLKTENQENGTFHAAVSLGLS 123
QY 87 AIYDFDTQSPVKRYLGLARSLN--RASVDL-----GGS----- 117
DB 124 AYVDFENGSRFPKYAGVRAVYAGVHSHSIDSTKKTNTNVLTPFTNIPDGGPTIYNQGSTODA 183
QY 118 --DSFSQTSIGLGLTVGSAVATPNVNDLDAGRYNYIGKVNTRYKNVRSGLSVGRYKF 174
DB 184 YHESHSTRKLGLGVAGVGEFDITPKLTLDTGYRINMGRLENTFR-FKHHEVSLGVRYRF 241

Search completed: October 28, 2002, 16:02:38
Job time : 22.9713 secs

```


DR WPI: 1996-443187/44.
 DR N-PSDB: AAT39040.
 XX
 PT Neisseria meningitidis antigen, highly conserved between different
 PT strains - useful for prodn. of antibodies for immunisation against,
 PT or diagnosis of, N. meningitidis infection
 XX
 PS Claim 7: Fig 8; 117pp; English.
 XX
 CC A protease K resistant surface protein has been isolated
 CC from 4 strains of N. meningitidis (AAT39039 to AAT39042). The isolated
 CC 22 kd antigen, antigenic fragments of antibodies can be used
 CC in a vaccine for the prevention of infection by N. meningitidis or
 CC by N. gonorrhoeae in humans. The antibodies may also be used
 CC diagnostically to detect N. meningitidis infection. The antigen
 CC may also be used to detect antibodies specific to N. meningitidis
 CC antigen.
 CC DNA sequences encoding the antigen, or their fragments, can be used
 CC as probes for the detection of pathogenic Neisseria bacteria.
 CC
 XX
 SQ Sequence 175 AA;
 Query Match 100.0%; Score 874; DB 17; Length 175;
 Best Local Similarity 100.0%; Pred. No. 2e-85;
 Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 MKKALALIALALPAALAEAGSGFYVQADAAHAKASSISGAKGSPRISAGYRINDLR 60
 DB 1 MKKALALIALALPAALAEAGSGFYVQADAAHAKASSISGAKGSPRISAGYRINDLR 60
 OY 61 FAVDYTRYKKNYKQVSTDFEFLYSIGASAIYDPTQSPVKPYLGARLSLNRAVDENGSDS 120
 DB 61 FAVDYTRYKKNYKQVSTDFEFLYSIGASAIYDPTQSPVKPYLGARLSLNRAVDENGSDS 120
 OY 121 FSGTSTGLGVLGAGSYAVTPNVDLDAGYRNYIGKVTYKKNVRSGLSAGYRVKF 175
 DB 121 FSGTSTGLGVLGAGSYAVTPNVDLDAGYRNYIGKVTYKKNVRSGLSAGYRVKF 175

RESULT 2
 AAM04893
 ID AAM04893 standard; Protein; 174 AA.
 XX
 AC AAM04893;
 XX
 DT 22-DEC-1996 (first entry)
 XX
 DE Proteinase K resistant N. meningitidis 22 kd surface protein.
 XX
 KW Proteinase K resistant; Neisseria meningitidis;
 KW Neisseria gonorrhoeae; antibody; detection; probe; surface protein.
 XX
 OS Neisseria meningitidis strain 24063.
 XX
 FH Key Location/Qualifiers
 FH Peptide 1..19
 FT /label= sig_peptide
 FT Protein 20..174
 FT /label= mat_protein
 XX
 PN WO9629412-A1.
 XX
 PD 26-SEP-1996.
 XX
 PF 15-MAR-1996; 96WO-CA00157.
 XX
 PR 04-AUG-1995; 95US-0001983.
 PR 17-MAR-1995; 95US-0406362.
 XX
 PA (IAFB-) IAF BIO VAC INC.
 XX
 PI Brodeur BR, Hamel J, Martin D, Rioux C;
 XX

DR WPI: 1996-443187/44.
 DR N-PSDB: AAT39041.
 XX
 PT Neisseria meningitidis antigen, highly conserved between different
 PT strains - useful for prodn. of antibodies for immunisation against,
 PT or diagnosis of, N. meningitidis infection
 XX
 PS Claim 7: Fig 9; 117pp; English.
 XX
 CC A protease K resistant surface protein has been isolated
 CC from 4 strains of N. meningitidis (AAT39039 to AAT39042). The isolated
 CC 22 kd antigen, antigenic fragments of antibodies can be used
 CC in a vaccine for the prevention of infection by N. meningitidis or
 CC by N. gonorrhoeae in humans. The antibodies may also be used
 CC diagnostically to detect N. meningitidis infection. The antigen
 CC may also be used to detect antibodies specific to N. meningitidis
 CC antigen.
 CC DNA sequences encoding the antigen, or their fragments, can be used
 CC as probes for the detection of pathogenic Neisseria bacteria.
 CC
 XX
 SQ Sequence 174 AA;
 Query Match 95.9%; Score 838.5; DB 17; Length 174;
 Best Local Similarity 97.1%; Pred. No. 1.2e-81;
 Matches 170; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
 OY 1 MKKALALIALALPAALAEAGSGFYVQADAAHAKASSISGAKGSPRISAGYRINDLR 60
 DB 1 MKKALATIALALPAALAEAGSGFYVQADAAHAKASSISGAKGSPRISAGYRINDLR 60
 OY 61 FAVDYTRYKKNYKQVSTDFEFLYSIGASAIYDPTQSPVKPYLGARLSLNRAVDENGSDS 120
 DB 61 FAVDYTRYKKNYKQVSTDFEFLYSIGASAIYDPTQSPVKPYLGARLSLNRAVDENGSDS 119
 OY 121 FSGTSTGLGVLGAGSYAVTPNVDLDAGYRNYIGKVTYKKNVRSGLSAGYRVKF 175
 DB 120 FSGTSTGLGVLGAGSYAVTPNVDLDAGYRNYIGKVTYKKNVRSGLSAGYRVKF 174

RESULT 3
 AAM04891
 ID AAM04891 standard; Protein; 174 AA.
 XX
 AC AAM04891;
 XX
 DT 22-DEC-1996 (first entry)
 XX
 DE Proteinase K resistant N. meningitidis 22 kd surface protein.
 XX
 KW Proteinase K resistant; Neisseria meningitidis;
 KW Neisseria gonorrhoeae; antibody; detection; probe; surface protein.
 XX
 OS Neisseria meningitidis strain 608B.
 XX
 FH Key Location/Qualifiers
 FH Peptide 1..19
 FT /label= sig_peptide
 FT Protein 20..174
 FT /label= mat_protein
 XX
 PN WO9629412-A1.
 XX
 PD 26-SEP-1996.
 XX
 PF 15-MAR-1996; 96WO-CA00157.
 XX
 PR 04-AUG-1995; 95US-0001983.
 PR 17-MAR-1995; 95US-0406362.
 XX
 PA (IAFB-) IAF BIO VAC INC.
 XX
 PI Brodeur BR, Hamel J, Martin D, Rioux C;
 XX

DR WPI: 1996-443187/44.
 DR N-PSDB: AAT39039.
 XX Neisseria meningitidis antigen, highly conserved between different
 PT strains - useful for prodn. of antibodies for immunisation against,
 PT or diagnosis of, N. meningitidis infection
 XX
 PS Claim 7; Fig 1; 117pp: English.
 XX
 CC A proteinase K resistant surface protein has been isolated
 CC from 4 strains of N. meningitidis (AAT39039 to AAT39042). The isolated
 CC 22 kD antigen, antigenic fragments of antibodies can be used
 CC in a vaccine for the prevention of infection by N. meningitidis or
 CC by N. gonorrhoeae in humans. The antibodies may also be used
 CC diagnostically to detect N. meningitidis infection. The antigen
 CC may also be used to detect antibodies specific to N. meningitidis
 CC antigen.
 CC DNA sequences encoding the antigen, or their fragments, can be used
 CC as probes for the detection of pathogenic Neisseria bacteria.
 CC
 SQ Sequence 174 AA;

Query Match 94.3%; Score 824.5; DB 17; Length 174;
 Best Local Similarity 95.4%; Pred. No. 3.9e-80;
 Matches 167; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

OY 1 MKKALALIALALPAALAEAGSGFYVOADAHAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 DB 1 MKKALALIALALPAALAEAGSGFYVOADAHAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 OY 61 FAVDYTRYKNKYQVPSIDFKLYSIGASAIYDFDTQSPVKPYFGARLSLNRASVDLFGSDS 120
 DB 61 FAVDYTRYKNKYK-APSTDFKLYSIGASAIYDFDTQSPVKPYFGARLSLNRASVDLFGSDS 119
 OY 121 FSQSTGLGVLAGSVYATPVNDLADAGRYNYIGKVTYKVRSGELSGAYRVKF 175
 DB 120 FSQSTGLGVLAGSVYATPVNDLADAGRYNYIGKVTYKVRSGELSGAYRVKF 174

RESULT 4
 AAM04894

ID AAM04894 standard; Protein; 174 AA.

AC AAM04894;

DT 22-DEC-1996 (first entry)

DE Proteinase K resistant N. meningitidis 22 kD surface protein.

KM Proteinase K resistant; Neisseria meningitidis;

KM Neisseria gonorrhoeae; antibody; detection; probe; surface protein.

OS Neisseria meningitidis strain b2.

XX Key Location/Qualifiers

FT Peptide 1..19

FT Protein /label= sig_peptide

FT /label= mat_protein

PN W09629412-A1.

PD 26-SEP-1996.

PF 15-MAR-1996; 96WO-CA00157.

PR 04-AUG-1995; 95US-0001983.

PR 17-MAR-1995; 95US-0406362.

PA (IAPB-) IAF BIO VAC INC.

PI Brodeur BR, Hamel J, Martin D, Rioux C;

DR WPI: 1996-443187/44.
 DR N-PSDB: AAT39042.
 XX Neisseria meningitidis antigen, highly conserved between different
 PT strains - useful for prodn. of antibodies for immunisation against,
 PT or diagnosis of, N. meningitidis infection
 XX
 PS Claim 7; Fig 10; 117pp: English.
 XX
 CC A proteinase K resistant surface protein has been isolated
 CC from 4 strains of N. meningitidis (AAT39039 to AAT39042). The isolated
 CC 22 kD antigen, antigenic fragments of antibodies can be used
 CC in a vaccine for the prevention of infection by N. meningitidis or
 CC by N. gonorrhoeae in humans. The antibodies may also be used
 CC diagnostically to detect N. meningitidis infection. The antigen
 CC may also be used to detect antibodies specific to N. meningitidis
 CC antigen.
 CC DNA sequences encoding the antigen, or their fragments, can be used
 CC as probes for the detection of pathogenic Neisseria bacteria.
 CC
 SQ Sequence 174 AA;

Query Match 93.1%; Score 813.5; DB 17; Length 174;
 Best Local Similarity 93.7%; Pred. No. 5.9e-79;
 Matches 164; Conservative 2; Mismatches 8; Indels 1; Gaps 1;

OY 1 MKKALALIALALPAALAEAGSGFYVOADAHAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 DB 1 MKKALALIALALPAALAEAGSGFYVOADAHAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 OY 61 FAVDYTRYKNKYQVPSIDFKLYSIGASAIYDFDTQSPVKPYFGARLSLNRASVDLFGSDS 120
 DB 61 FAVDYTRYKNKYK-APSTDFKLYSIGASAIYDFDTQSPVKPYFGARLSLNRASVDLFGSDS 119
 OY 121 FSQSTGLGVLAGSVYATPVNDLADAGRYNYIGKVTYKVRSGELSGAYRVKF 175
 DB 120 FSQSTGLGVLAGSVYATPVNDLADAGRYNYIGKVTYKVRSGELSGAYRVKF 174

RESULT 5
 AAB19895

ID AAB19895 standard; Protein; 155 AA.

AC AAB19895;

DT 19-MAR-2001 (first entry)

DE Neisseria meningitidis NspA protein.

KM NspA; infection; diagnosis; therapy; vaccine; meningococcal B.

OS Neisseria meningitidis.

XX Key Location/Qualifiers

FT Region 6..17 "transmembrane beta-strand"

FT Region 18..26 "surface-exposed connecting loop"

FT Region 27..37 "transmembrane beta-strand"

FT Region 40..50 "transmembrane beta-strand"

FT Region 51..62 "transmembrane beta-strand"

FT Region 63..74 "surface-exposed connecting loop"

FT Region 78..88 "transmembrane beta-strand"

FT Region 89..104 "transmembrane beta-strand"

FT Region 105..114 "surface-exposed connecting loop"

FT Region 118..130 "transmembrane beta-strand"

```

FT  /note="transmembrane beta-strand"
FT  131..145
FT  /note="surface-exposed connecting loop"
FT  146..155
FT  Region
FT  /note="transmembrane beta-strand"
XX  WO200071725-A2.
XX  30-NOV-2000.
XX  19-MAY-2000; 2000WO-IB00828.
XX  19-MAY-1999; 99GB-0011692.
XX  19-AUG-1999; 99GB-0019705.
XX  09-MAR-2000; 2000GB-0005730.
XX  (CHIR-) CHIRON SPA.
XX  Giuliani M, Pizzi M, Rappuoli R;
XX  WPI: 2001-025167/03.
XX  Novel composition comprising first and second biological molecules from
XX  a Neisseria bacterium, useful as vaccines or immunogenic compositions
XX  for treating Neisserial infections
XX  Example 12; Fig 32; 126pp; English.
XX  The present sequence is that of the Neisseria meningitidis NspA
XX  protein, which contains 8 transmembrane beta-strands and 4
XX  surface-exposed connected loops. Recombinant NspA is being
XX  developed as a vaccine for the prevention of meningococcal
XX  disease caused by all serotypes. The invention provides
XX  combination compositions comprising: (i) 2 or more Neisserial
XX  proteins, (ii) 2 or more different Neisserial nucleic acids; or
XX  (iii) mixtures of 1 or more Neisserial protein and 1 or more
XX  Neisserial nucleic acid. The proteins and nucleic acids are
XX  preferably from different Neisseria spp., especially Neisseria
XX  meningitidis and Neisseria gonorrhoeae, but may be from the same
XX  species. A claimed composition includes the NspA protein,
XX  preferably in mature form. The compositions are used e.g. as
XX  immunogenic compositions, vaccines or diagnostic reagents. They
XX  are used to treat or prevent Neisserial infection, to detect the
XX  presence of Neisserial bacteria or of antibodies raised against
XX  Neisserial bacteria, and/or as reagents which can raise antibodies
XX  against Neisserial bacteria.
XX  Sequence 155 AA:
SQ
Query Match 85.4%; Score 746.5; DB 22; Length 155;
Best Local Similarity 95.5%; Pred. No. 7.3e-72;
Matches 149; Conservative 0; Mismatches 6; Indels 1; Gaps 1;
OY 20 EGASGFYQADAAHAKKASSLSGSAKGFSPRISAGYRINDLRFADVTRYKNKQVPSNDF 79
DB 1 EGASGFYQADAAHAKKASSLSGSAKGFSPRISAGYRINDLRFADVTRYKNK APTDF 59
OY 80 KLYSIGASAIYDEPTQSPVRYKPYLGARLSLNRAVDENGSDSFQSTGLGVLAGVSYAVT 139
DB 60 KLYSIGASAIYDEPTQSPVRYKPYLGARLSLNRAVDENGSDSFQSTGLGVLAGVSYAVT 119
OY 140 PNVDLDAGYRYNYIGKVTYKNNVRSGLSAGVRYKF 175
DB 120 PNVDLDAGYRYNYIGKVTYKNNVRSGLSAGVRYKF 155
XX  RESULT 6
XX  AAR73911
XX  ID AAR73911 standard; protein: 170 AA.
XX  AC AAR73911;
XX  DT 05-DEC-1995 (first entry)

```

```

XX  Neisseria meningitidis opacity related protein POPM3.
DE  Neisseria meningitidis; opacity related protein POPM3; vaccine;
XX  Neisseria meningitidis related homologous antigenic sequence; MRHNS; RV-1;
XX  immunosassay; diagnosis; treatment; prophylactic; bacterial;
XX  viral.
XX  Neisseria meningitidis.
XX  WO9509232-A.
XX  06-APR-1995.
XX  28-SEP-1994; 94WO-CA00516.
XX  28-SEP-1993; 93US-0127499.
XX  (SHAR/) SHARMA L R.
XX  (VALS/) VAN ALSTYNE D.
XX  Sharma LR, Van Alstyne D;
XX  WPI: 1995-147431/19.
XX  New peptide(s) and corresp. antibodies for the treatment of
XX  meningitis - the peptide(s) corresp. to homologous antigenic
XX  sites on bacterial and viral agents and on chemokine(s), used for
XX  detecting and preventing meningitis
XX  Claim 47; Fig 5/10; 98pp; English.
XX  AAR73911 is the Neisseria meningitidis opacity related protein POPM3.
XX  It contains the meningitis related antigenic sequences (MRHNS)
XX  claimed in AAR73889 and AAR73901, which are recognised by a monoclonal
XX  antibody from the hybridoma Rubella virus (RV-1). The claimed MRHNS
XX  peptides may be used in immunoassays to diagnose the presence of
XX  bacterial and/or viral meningitis agents in a sample, or in
XX  prophylactic and therapeutic meningitis treatments. The peptides may
XX  also be used as vaccines against meningitis.
XX  NB: Identified by matching corresponding MRHNS peptides.
XX  Sequence 170 AA:
SQ
Query Match 15.8%; Score 138.5; DB 16; Length 170;
Best Local Similarity 26.9%; Pred. No. 8.5e-07;
Matches 42; Conservative 19; Mismatches 48; Indels 47; Gaps 4;
OY 6 AALIALPALPAALAEAGSGFYQADAAH-----AKASSLSG-----AKG 45
DB 15 SSILFSSMAQAASEDRSPYQADLVAERITHDYPQATGANNSTVSDYFRNIRAH 74
OY 46 FSPRISAGYRINDLRFADVTRYKNY-----KQVSTDFK 80
DB 75 IHPRVSGYDFGSGWRIAADYASRYKNNKNNKYSVNTKELENKNNKDKLTEQNGCTFHA 134
OY 81 LYSIGASAIYDEPTQSPVRYKPYLGARLSLN--RASVD 114
DB 135 ASSISGASAIYDEFTLKGKFKPYIGARVAYGVHSHSD 170
XX  RESULT 7
XX  AAW04912
XX  ID AAW04912 standard; protein: 25 AA.
XX  AC AAW04912;
XX  DT 22-DEC-1996 (first entry)
XX  N. meningitidis 608B peptide CS-857.
XX  Proteinase K resistant; Neisseria meningitidis; epitope; mapping;
XX  Neisseria gonorrhoeae; antibody; detection; probe; surface protein.

```


XX Synthetic.
 OS
 XX
 PN WO9629412-A1.
 XX
 XX
 PD 26-SEP-1996.
 XX
 PF 15-MAR-1996; 96WO-CA00157.
 XX
 PR 04-AUG-1995; 95US-0001983.
 PR 17-MAR-1995; 95US-0406362.
 XX
 PA (IAFB-) IAF BIO VAC INC.
 PI Brodeur BR, Hamel J, Martin D, Rioux C;
 DR WPI, 1996-443187/44.
 XX
 XX Neisseria meningitidis antigen, highly conserved between different
 PT strains - useful for prodn. of antibodies for immunisation against,
 PT or diagnosis of, N. meningitidis infection
 PS Claim 24; Page 84; 117pp; English.
 XX
 CC Example 9 describes the epitope mapping of the 22 kD
 CC N. meningitidis protein. Identification was accomplished
 CC using 18 overlapping synthetic peptides (AAW04895 to AAW04912).
 CC
 SQ Sequence 25 AA;
 Query Match 13.6%; Score 118.5; DB 17; Length 25;
 Best Local Similarity 92.3%; Pred. No. 8.7e-06;
 Matches 24; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
 QY 61 FAVDYTRYKNYKQVSTDFKLYSICA 86
 ID 1 FAVDYTRYKNYK-APSTDFKLYSICA 25
 DB
 RESULT 8
 AAU38252
 ID AAU38252 standard; Protein; 257 AA.
 XX
 AC AAU38252;
 XX
 DT 14-FEB-2002 (first entry)
 DE Salmonella typhi cellular proliferation protein #143.
 XX
 KW Antisense; prokaryotic cellular proliferation protein;
 KW antibiotic; antibacterial; drug design.
 XX
 OS Salmonella typhi.
 XX
 PN WO200170955-A2.
 PD 27-SEP-2001.
 XX
 PF 21-MAR-2001; 2001WO-US09180.
 XX
 PR 21-MAR-2000; 2000US-191078P.
 PR 23-MAY-2000; 2000US-206848P.
 PR 26-MAY-2000; 2000US-207727P.
 PR 23-OCT-2000; 2000US-242578P.
 PR 27-NOV-2000; 2000US-253625P.
 PR 22-DEC-2000; 2000US-257931P.
 PR 16-FEB-2001; 2001US-269308P.
 XX
 PA (ELITR-) ELITRA PHARM INC.
 PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
 PI Yamamoto RT, Xu HH;
 XX

DR WPI, 2001-611495/70.
 DR N-PSDB; AAS56111.
 XX
 PT New polynucleotides for the identification and development of
 PT antibiotics, comprise sequences of antisense nucleic acids -
 XX
 PS Example 3; Seq ID No 13845; 511pp; English.
 XX
 CC The invention relates to antisense inhibitors of genes essential to
 CC prokaryotic cellular proliferation, their use in identifying the
 CC genes, their use in the discovery of novel antibiotics, the essential
 CC genes themselves and the encoded proteins. The prokaryotes used are
 CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
 CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
 CC invention is also useful for the identification of potential new targets
 CC for antibiotic development. The antisense nucleic acids can also be used
 CC to identify proteins used in proliferation, to express these proteins,
 CC and to obtain antibodies capable of binding to the expressed proteins.
 CC The proteins can be used to screen compounds in rational drug discovery
 CC programmes. The antisense nucleic acid sequence is also useful to screen
 CC for homologous nucleic acids which are required for cell proliferation in
 CC a wide variety of organisms. The present sequence represents an
 CC essential prokaryotic cellular proliferation protein.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 CC
 SQ Sequence 257 AA;
 Query Match 11.4%; Score 99.5; DB 22; Length 257;
 Best Local Similarity 25.2%; Pred. No. 0.022;
 Matches 55; Conservative 29; Mismatches 81; Indels 53; Gaps 12;
 QY 1 MKKLAALIALA--LPAALAEAGSGFYQADAAHAK-----ASSSIGSAKGFSPRSAGY 54
 ID 27 MKKTTVALALITLSSGSAFAHEAGFEFMRAGPYVAPTEGAGCTGLHNGFD--VSNNMT 84
 DB 55 RINDLRPAVDYTRYKNYKQVSTDFKLYSICASAIYDF-----DPQSP 97
 QY 85 QLG-LFTFYMATDNIGVELLAAPFER-HKVGATGATGDIATVHLPLPLMAQWFGSSSK 142
 DB 98 VKPYLGARLSINRASV---DPNG-----SDSEFQSTGSLGVLGVSIAVTPN----- 141
 QY 143 VRPYVG--VGWVYTFEPDNDFNNGKKTGLSLDFKDSKGAQGVGYDLINRDMIGAS 200
 DB 142 ---VDLDAGYRYNYIGKVTYKNVRSGE---LSAGVR 172
 QY 201 VWYMDIDITANYK-MGQVQOHDSVRLDPWVFMSAGXR 237
 DB
 RESULT 9
 AAU34556
 ID AAU34556 standard; Protein; 212 AA.
 XX
 AC AAU34556;
 XX
 DT 14-FEB-2002 (first entry)
 DE E. coli cellular proliferation protein #137.
 XX
 KW Antisense; prokaryotic cellular proliferation protein;
 KW antibiotic; antibacterial; drug design.
 XX
 OS Escherichia coli.
 XX
 PN WO200170955-A2.
 PD 27-SEP-2001.
 XX
 PF 21-MAR-2001; 2001WO-US09180.
 PR 21-MAR-2000; 2000US-191078P.
 XX

PR 23-MAY-2000; 2000US-206848P.
 PR 26-MAY-2000; 2000US-207272P.
 PR 23-OCT-2000; 2000US-242578P.
 PR 27-NOV-2000; 2000US-253625P.
 PR 22-DEC-2000; 2000US-257931P.
 PR 16-FEB-2001; 2001US-269308P.
 XX (ELIT-) ELITRA PHARM INC.
 PA Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ,
 PI Yamamoto RT, Xu HH;
 XX WPI: 2001-611495/70.
 DR N-PSDB; AAS52415.
 XX
 FT New polynucleotides for the identification and development of
 PT antibiotics, comprise sequences of antisense nucleic acids -
 PS
 XX Example 3; Seq ID No 10149; 511pp; English.
 CC The invention relates to antisense inhibitors of genes essential to
 CC prokaryotic cellular proliferation, their use in identifying the
 CC genes, their use in the discovery of novel antibiotics, the essential
 CC genes themselves and the encoded proteins. The prokaryotes used are
 CC *Escherichia coli*, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella*
 CC *pneumoniae*, *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The
 CC invention is also useful for the identification of potential new targets
 CC for antibiotic development. The antisense nucleic acids can also be used
 CC to identify proteins used in proliferation, to express these proteins,
 CC and to obtain antibodies capable of binding to the expressed proteins.
 CC The proteins can be used to screen compounds in rational drug discovery
 CC programmes. The antisense nucleic acid sequence is also useful to screen
 CC for homologous nucleic acids which are required for cell proliferation in
 CC a wide variety of organisms. The present sequence represents an
 CC essential prokaryotic cellular proliferation protein.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 212 AA;
 Query Match 10.9%; Score 95.5; DB 22; Length 212;
 Best Local Similarity 24.8%; Pred. No. 0.045;
 Matches 54; Conservative 29; Mismatches 82; Indels 53; Gaps 11;
 QY 1 MKKALALIALA--LPAALAEAGSGFYQADAAHAK-----ASSSLGAKGSPRISAGY 54
 DB 1 MKKLTVALLAVTTLLSGSAFAHEAGFEFFMRGSAFTVRPTBGAGGTLGSGFS--VTNNT 58
 QY 55 RINDLREAVDYTRYKNKYQVSTDFKLYSIGASAIYDF-----DTOSP 97
 DB 59 QLG-LTFYMAVDNIGVELLAATPFR-HKIGTRATGDIATVHMLPTLMQWTFEGDASSK 116
 QY 98 VKPTIGATLSINRASVDPNF-----SDSFQSTSTGIGVLAGSYAVTPN----- 141
 DB 117 FRPYVGA--GINTYTFEDNGFNDGKEAGSLDSLKDSWGAAQGVGYDYLINRWMLVMS 174
 QY 142 ---VDLAGYRYNTYKNTVKNRSGE---LSAGVR 172
 DB 175 VWMYMDITITANYK-LGGAQCHDSVRLDPRWPMFSAGTR 211
 RESULT 10
 AAR6294
 ID AAR6294 standard; Protein; 359 AA.
 AC AAR6294;
 XX
 DT 09-AUG-1995 (first entry)
 XX
 DE Non-typable Haemophilus influenza (NTHI) fimbria protein.

KW Fimbria protein; vaccine; otitis media.
 XX
 OS Haemophilus influenza strain 1128.
 XX
 FH Key Location/Qualifiers
 FT Region 22..33
 FT Peptide 234..249
 FT /Label= amino terminus
 FT /Label= internal CNBR fragment
 XX
 PN WO9426304-A.
 XX
 PD 24-NOV-1994.
 XX
 PF 12-MAY-1994; 94WO-US05477.
 XX
 PR 18-MAY-1993; 93US-0065442.
 XX
 PA (OHIO-) OHIO STATE RES FOUND.
 XX
 PI Bakaletz LO, Kolatukudy PE, Sirakova T;
 XX
 DR WPI: 1995-006359/01.
 DR N-PSDB; AAQ78916.
 XX
 PT Vaccine comprising non-typable Haemophilus influenza fimbria
 PT protein - useful in studying, preventing or reducing the
 PT severity of otitis media, also fimbria protein and DNA.
 PS Disclosure; Fig 5; 45pp; English.
 XX
 CC The fimbria proteins from 15 randomly selected type b and non-
 CC typable clinical isolates of Haemophilus influenza share common
 CC epitopes. Thus fimbria isolated from non-typable Haemophilus
 CC influenzae 1128 strain is a particularly suitable immunogen to
 CC protect against the different non-typable H₂ influenzae that cause
 CC otitis media. Fimbria protein is produced by culturing a transformed
 CC microbial host, pref. *E. coli*, *Sporoptera frugiperda* or a mucosal
 CC pathogen. Fimbria protein (FP) produced by this process is claimed.
 CC The FP protein migrates in polyacrylamide gels to a posn. equiv. to
 CC a mol. wt. of 25.5 kD or 37.5 kD.
 XX
 SQ Sequence 359 AA;
 Query Match 10.9%; Score 95.5; DB 16; Length 359;
 Best Local Similarity 22.7%; Pred. No. 0.092;
 Matches 51; Conservative 30; Mismatches 89; Indels 55; Gaps 9;
 QY 1 MKKALALIALA--LPAALAEAG--SGFYQADAA-----HAKASSLSGAKGSPRISAG 53
 DB 1 MKKTAIALVAVAGLAAASVAQAPOENTFYAGVAGAGSGFHDGINNNGAIIKGLSS--NYG 59
 QY 54 YRINDLREAVDYTRYKNKYQVSTDFKLYSIGASAIYDFDTOSP 107
 DB 60 YRNTFTTGYV---FEGYIILMDNFGLAELGYHDFGAKLREKRAKHAHTNHGAIL 115
 QY 108 LNRASVDPNFSDSFQSTSTGL-----GVLA-GVSYAVT 139
 DB 116 LKGSYVLDLGLDLYVAGAVALVRSDFKFEYDANGTRDHRKKGHTARASGLFVAGAEVAVL 175
 QY 140 PNVLDLAGY-----RYNTYKNTVKNRSGE---GELSGAVRVP 175
 DB 176 PELAVRLLEYQWLTWVGKYPQDKPMTAINYNPIMGICINAGISYRF 220
 RESULT 11
 AAR6210
 ID AAR6210 standard; Protein; 568 AA.
 AC AAR6210;
 XX
 DT 24-AUG-1996 (first entry)

QY 57 NDL-----RFAVDYTRYKNY---KÖVPSTDFKLYSIGASAIYDFEDTOSPPVKPYLGARLSL 108
::|||::|::|::|::|

Dd 60 ----FLTDDVELALSYGEIHDVRCIYETGNKKVHGNTSL--DAIYHFGTGGVGLRPYVS 113

DB 114 AGLA-HQNTITNNSDSQGRQOMTMANIGAGLYTFTEFPKASLDQY-----GLEKR 166
 QY 160 KNVRSGLSAGVRYKF 175
 DB 167 DNGHGGEMMAGLGVGF 182

RESULT 13

AAB59179 standard; protein: 350 AA.

AAB59179;

22-MAR-2001 (first entry)

protein associated with C.coli and C.jejuni Cadf.

Fibronectin binding protein; Cadf; vaccine; diagnostic assay.

Pseudomonas aeruginosa.

US6156546-A.

05-DEC-2000.

15-MAY-1998; 98US-0080025.

16-MAY-1997; 97US-0046763.

(UNIV) UNIV WASHINGTON STATE RES FOUND.

Garvis SG, Konkel ME;

WPI; 2001-079546/09.

Novel isolated polynucleotide useful for producing fibronectin binding proteins which are useful in production of vaccine, in diagnostic assays and for prophylactic and therapeutic purposes

Disclosure: Column 37-40; 29pp; English.

The present invention relates to a Campylobacter jejuni or Campylobacter coli fibronectin binding protein (Cadf). A recombinant expression vector with cadf is useful in an assay for determining the presence of C. jejuni or C. coli in a test sample or for determining whether a test isolate of Campylobacter is a strain of C. coli. cadf is useful in the construction of DNA probes for identifying and quantifying the level of expression of Cadf in a cell. The gene can also be used in a vaccine.

Sequence 350 AA;

Query Match 10.7%; Score 93.5; DB 22; Length 350;
 Best Local Similarity 23.5%; Pred. No. 0.15;
 Matches 46; Conservative 31; Mismatches 82; Indels 37; Gaps 9;

QY 1 MKKALALALALPAAAL--AAGAGGFVVOA-----DAAHKASSLSGAKGSPR 49
 DB 3 LKNTLVVIGSLVAAAMAFAGGONSVEIEAFGRKRYFDSVRNMKNADLYGSGISGY--- 59
 QY 50 ISAGYRINDLRFADVTRYKNYKQVPSDFK-----LVSIGASATVDFDTQS-PVKPYIG 103
 DB 60 ----FLTDVELALSGEYHDVKGVTETGNKKVHGNLTSL--DAIYHFGTPEGVGLRPYVS 113
 QY 104 ARLSLRASVDENGSDSFQSTGTGLAGVLAQVSTAVTPN-----VDLDAGRYRYTKVNTV 159
 DB 114 AGLA-HQNTITNNSDSQGRQOMTMANIGAGLYTFTEFPKASLDQY-----GLEKR 166
 QY 160 KNVRSGLSAGVRYKF 175
 DB 167 DNGHGGEMMAGLGVGF 182

RESULT 14

AAB47447 standard; protein: 353 AA.

AAB47447;

31-OCT-2001 (first entry)

MOMP P5.

surface exposed loop; major outer membrane protein p5; MOMP P5; non-typeable H. influenzae; nH1; LB1(f) peptide; B cell epitope; otitis media; sinusitis; conjunctivitis; lower respiratory tract infection.

Haemophilus influenzae.

Key Location/Qualifiers

FT Domain /label= Loop 1

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 2

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 3

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 4

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 1

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 2

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 3

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 4

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 1

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 2

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 3

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 4

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 1

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 2

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 3

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 4

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 1

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 2

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 3

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 4

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 1

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 2

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 3

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 4

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 1

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 2

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 3

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 4

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 1

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 2

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 3

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 4

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 1

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 2

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 3

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 4

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 1

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 2

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 3

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 4

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 1

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 2

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 3

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 4

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 1

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 2

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 3

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 4

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 1

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 2

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 3

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 4

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 1

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 2

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 3

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 4

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 1

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 2

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 3

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 4

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 1

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 2

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 3

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 4

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 1

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 2

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 3

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 4

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 1

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 2

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 3

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 4

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 1

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 2

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 3

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 4

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 1

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 2

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 3

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 4

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 1

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 2

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 3

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 4

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 1

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 2

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 3

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 4

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 1

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 2

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 3

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 4

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 1

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 2

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 3

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 4

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 1

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 2

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 3

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 4

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 1

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 2

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 3

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 4

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 1

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 2

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 3

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 4

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 1

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 2

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 3

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 4

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 1

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 2

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 3

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 4

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 1

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 2

FT Domain /note= "Extracellular domain"

FT Domain /label= Loop 3

FT Domain /note= "Extracellular domain"</

QY 1 MKKALALIALPAAALAEGA---SGFYQADAAHAKASSSIGS-----AKGFS 47
 DB 1 MKKATLALVAGLAASVAGAPQEMTFEYAGVAKGQASPHDGLRALAREYKGYHNSFT 60
 QY 48 PRISAGYRI---NDLREAV-----DYTRYKNYKQVPSTDFKLYSIGASAIYDF-----DT 94
 DB 61 YGVEGGYQIILNQNNGIAVBLGYDDGGRAGK-REKRTYVKKHINHSTHLSLKGSTYVLEG 119
 QY 98 VKPYLGLARLSLNRASVDENGSDFSGTSTGLG-----VLGVSYAVTPNVDLDAG 147
 DB 120 LDVYGRAGVALVRS--DYKLYNENSSTLKKLGHHRRARASGLFVAGAEYAVLPBELAVRL 177
 QY 148 Y-----RNYIGKYNVTKNRS--GELSAQYRYKF 175
 DB 178 YQMLTRVGKTRPQDKPNTALNTPWIGSINAGISYRF 214

RESULT 15

AAB44589
 ID AAB44589 standard: Protein; 369 AA.

AC AAB44589;

DT 08-FEB-2001 (first entry)

DE Virulence gene protein #69.

KW Virulence gene: antibacterial; vaccine; bacterial infection;

KW septicaemia; bronchopneumonia; rhinitis; wound infection.

OS Actinobacillus pleuropneumoniae.

PN W0200061724-A2.

PD 19-OCT-2000.

PF 06-APR-2000; 2000WO-US09218.

PR 09-APR-1999; 99US-0128689.

PR 10-SEP-1999; 99US-0153453.

PA (PHNA) PHARMACIA & UPJOHN INC.

PI Lowery DE, Fuller TE, Kennedy MJ;

PI WPI: 2000-647422/62.

DR N-PSDB; AAC79664.

PT Attenuated Pasteurellaceae bacteria comprising mutations in virulence genes, useful as a live attenuated vaccine against bacterial infections

PS Claim 39; Pages 308-309; 322pp; English.

CC The family Pasteurellaceae encompasses several pathogens that infect a wide variety of animals. The present invention relates to virulence genes from Pasteurellaceae. The present sequence is a protein encoded by one such virulence gene. The virulence genes of the present invention may be mutated in order to produce an inactive gene. The inactive virulence gene may in turn be used to produce a vaccine, which is useful for treating bacterial infections such as septicaemias, bronchopneumonias, rhinitis and wound infections.

CC Sequence 369 AA;

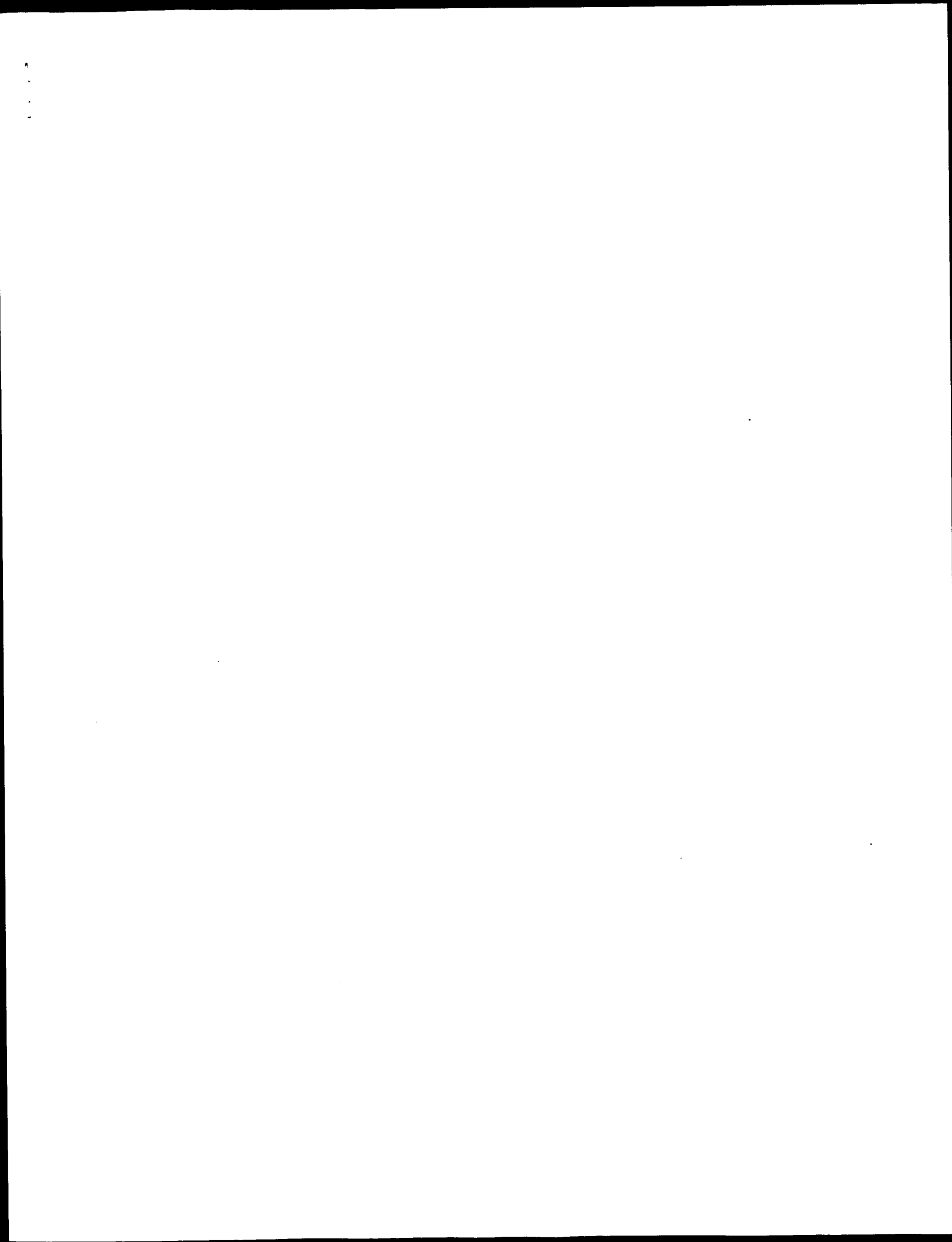
Query Match 10.7%; Score 93.5; DB 21; Length 369;

Best Local Similarity 23.2%; Pred. No. 0.16; Mismatches 78; Indels 67; Gaps 12;

QY 1 MKKALALIALPAAALAEGA---SGFYQADAAHAKASSSIGSAGSPRI---SAG 53
 DB 1 MKKSLVALAVYS--AAAVYQAAPQONTFYAGAKYQSSFFHHGVNQLKSGHDDRYNDKTRK 58

QY 54 YRINDLREAVDYTRYKNYKQVPSTDFKLYSIGASAIYDF-----DT 94
 DB 59 YGIN--RNSVTYGVVGGYQIILNQN---GLAELGTDYGRVGNNDDEFTYKHAHGL 113
 QY 95 OSPVKEP-----YLGARLSLNRASVDENGSDFSGTSTGLGVL-----AGVSYA 137
 DB 114 NLALKPSYEVLPLDLVYGRVGIADVVRNDYKKYGAEENTVESTTKFHKLKASTIILGAGYEYA 173
 QY 138 VTPNVDLDAGYRYNYIGKYNVTKN--VRSQ-----ELSAQYRYKF 175
 DB 174 ILP--ELARVEYQYTLNKAQNLKALVRSQYQVDYFQYAPDIHSVTAGLSYRF 224

Search completed: October 28, 2002, 16:00:38
 Job time : 26.8565 secs



GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 28, 2002, 15:58:54 ; Search time 9.54089 Seconds
(without alignments)
448.017 Million cell updates/sec

Title: US-09-684-883-4

Perfect score: 874
Sequence: 1 MKKALALALALPALALAE.....VNTVKNVSGELSGAVRVK 175

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCrus.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/Backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	874	100.0	175	4	US-08-913-362-4
2	843	96.5	175	4	US-08-913-362-30
3	838.5	95.9	174	4	US-08-913-362-6
4	824.5	94.3	174	4	US-08-913-362-2
5	813.5	93.1	174	4	US-08-913-362-8
6	138.5	15.8	170	1	US-08-127-489A-20
7	138.5	15.8	170	1	US-08-482-847-20
8	118.5	13.6	25	4	US-08-913-362-26
9	95.5	10.9	568	5	PCR-US95-13749-5
10	93.5	10.7	359	1	US-08-457-997B-2
11	93.5	10.7	359	3	US-08-467-722A-2
12	86	9.8	282	4	US-08-953-326-6
13	86	9.8	282	4	US-08-953-326-6
14	86	9.8	286	1	US-08-382-184-3
15	86	9.8	286	2	US-08-641-356-3
16	86	9.8	286	4	US-09-132-528-4
17	86	9.8	286	4	US-08-875-494-3
18	86	9.8	286	4	US-09-599-366-4
19	86	9.8	325	1	US-08-582-184-2
20	86	9.8	325	2	US-08-641-356-2
21	86	9.8	325	4	US-09-132-528-2
22	86	9.8	325	4	US-09-132-528-3
23	86	9.8	325	4	US-08-875-494-2
24	86	9.8	325	4	US-09-599-366-2
25	86	9.8	332	4	US-09-599-366-3
26	86	9.8	332	4	US-08-818-112-53
27	86	9.8	332	4	US-08-818-111-53

28	86	9.8	332	4	US-09-056-556-53	Sequence 53, Appl
29	86	9.8	802	4	US-09-056-556-214	Sequence 214, App
30	81.5	9.3	2123	4	US-08-968-685A-10	Sequence 10, Appl
31	81	9.3	15	4	US-08-913-362-23	Sequence 23, Appl
32	79.5	9.1	433	2	US-08-883-515-2	Sequence 2, Appl
33	79	9.0	15	4	US-08-913-362-18	Sequence 18, Appl
34	78.5	9.0	884	1	US-08-066-167-2	Sequence 2, Appl
35	78.5	9.0	908	1	US-08-487-890A-94	Sequence 94, Appl
36	78.5	9.0	908	2	US-08-478-435-94	Sequence 94, Appl
37	78.5	9.0	908	2	US-08-337-483-94	Sequence 94, Appl
38	78.5	9.0	908	2	US-08-478-373-94	Sequence 94, Appl
39	78.5	9.0	908	3	US-08-474-671-94	Sequence 94, Appl
40	78.5	9.0	908	3	US-08-483-577A-94	Sequence 94, Appl
41	78.5	9.0	908	3	US-08-448-194-4	Sequence 94, Appl
42	78.5	9.0	908	3	US-08-613-009A-16	Sequence 16, Appl
43	78.5	9.0	908	4	US-08-897-438-94	Sequence 94, Appl
44	78.5	9.0	908	4	US-08-867-921-4	Sequence 94, Appl
45	78.5	9.0	908	4	US-08-637-654-94	Sequence 94, Appl

ALIGNMENTS

RESULT 1
US-08-913-362-4
; Sequence 4, Application US/08913362
; Patent No. 6287574
; GENERAL INFORMATION:
; APPLICANT: Brodeur, Bernard R
; APPLICANT: Martin, Denis
; APPLICANT: Hamel, Josee
; APPLICANT: Rioux, Clement
; TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
; TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/913,362
; FILING DATE: 13-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406,362
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/001,983
; FILING DATE: 04-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-913-362-4
Query Match 100.0%; Score 874; DB 4; Length 175;

Best Local Similarity 100.0%; Pred. No. 4e-92;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKALALIALALPAALAEAGSGFYVQADAAHAKASSLSGAGSPRISAGYRINDLR 60
DB 1 MKKALALIALALPAALAEAGSGFYVQADAAHAKASSLSGAGSPRISAGYRINDLR 60
QY 61 FAVDYTRYKNKQVSPDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRAVDLGSDDS 120
DB 61 FAVDYTRYKNKQVSPDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRAVDLGSDDS 120

QY 121 FSQSTGLGVLGAGSYAVTPNVLDAGRYNYIGKVTYVKNVSGELSGAVRYKF 175
DB 121 FSQSTGLGVLGAGSYAVTPNVLDAGRYNYIGKVTYVKNVSGELSGAVRYKF 175

RESULT 2

US-08-913-362-30
Sequence 30, Application US/08913362
Patent No. 6287574

GENERAL INFORMATION:

APPLICANT: Brodeur, Bernard R
APPLICANT: Martin, Denis
APPLICANT: Hamel, Josee
APPLICANT: Rioux, Clement
TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/913,362

FILING DATE: 13-NOV-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/406,362

FILING DATE: 17-MAR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/001,983

FILING DATE: 04-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: Bent, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 047998/0128

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 30:

SEQUENCE CHARACTERISTICS:

LENGTH: 175 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-913-362-30

Query Match 96.5%; Score 843; DB 4; Length 175;

Best Local Similarity 96.6%; Pred. No. 1.4e-88;

Matches 169; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MKKALALIALALPAALAEAGSGFYVQADAAHAKASSLSGAGSPRISAGYRINDLR 60
DB 1 MKKALALIALALPAALAEAGSGFYVQADAAHAKASSLSGAGSPRISAGYRINDLR 60

QY 61 FAVDYTRYKNKQVSPDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRAVDLGSDDS 120

DB 61 FAVDYTRYKNKQVSPDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRAVDLGSDDS 120

QY 121 FSQSTGLGVLGAGSYAVTPNVLDAGRYNYIGKVTYVKNVSGELSGAVRYKF 175

DB 121 FSQSTGLGVLGAGSYAVTPNVLDAGRYNYIGKVTYVKNVSGELSGAVRYKF 175

RESULT 3

US-08-913-362-6
Sequence 6, Application US/08913362
Patent No. 6287574

GENERAL INFORMATION:

APPLICANT: Brodeur, Bernard R
APPLICANT: Martin, Denis
APPLICANT: Hamel, Josee
APPLICANT: Rioux, Clement
TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/913,362

FILING DATE: 13-NOV-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/406,362

FILING DATE: 17-MAR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/001,983

FILING DATE: 04-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: Bent, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 047998/0128

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 174 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-913-362-6

Query Match 95.9%; Score 838.5; DB 4; Length 174;

Best Local Similarity 97.1%; Pred. No. 4.5e-88;

Matches 170; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 MKKALALIALALPAALAEAGSGFYVQADAAHAKASSLSGAGSPRISAGYRINDLR 60
DB 1 MKKALALIALALPAALAEAGSGFYVQADAAHAKASSLSGAGSPRISAGYRINDLR 60

QY 61 FAVDYTRYKNKQVSPDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRAVDLGSDDS 120
DB 61 FAVDYTRYKNKQVSPDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRAVDLGSDDS 120

QY 121 FSQSTGLGVLGAGSYAVTPNVLDAGRYNYIGKVTYVKNVSGELSGAVRYKF 175
DB 121 FSQSTGLGVLGAGSYAVTPNVLDAGRYNYIGKVTYVKNVSGELSGAVRYKF 175

DB 120 FSQSTGLGVLAGVSYAVTPNVDLDAGRYRNYTKVNTVKNVSGELSGAVRYKF 174

RESULT 4
US-08-913-362-2
; Sequence 2, Application US/08913362
; Patent No. 6287574
; GENERAL INFORMATION:
; APPLICANT: Brodeur, Bernard R
; APPLICANT: Martin, Denis
; APPLICANT: Hamel, Josee
; APPLICANT: Rioux, Clement
; TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
; TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/913,362
; FILING DATE: 13-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406,362
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/001,983
; FILING DATE: 04-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 047998/0128
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 174 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-913-362-2

Query Match 94.3%; Score 824.5; DB 4; Length 174;
Best Local Similarity 95.4%; Pred. No. 1.8e-86;
Matches 167; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 1 MKKALALIALALPAAALAGAGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
DB 1 MKKALALIALALPAAALAGAGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

QY 61 FAVDYTRYKNYKQVSTDFKLYSIGASAIYDPTQSPVKPYLGARLSLNRAVDENGSDS 120
DB 61 FAVDYTRYKNYK-ARSTDFKLYSIGASAIYDPTQSPVKPYLGARLSLNRAVDENGSDS 119

QY 121 FSQSTGLGVLAGVSYAVTPNVDLDAGRYRNYTKVNTVKNVSGELSGAVRYKF 175
DB 120 FSQSTGLGVLAGVSYAVTPNVDLDAGRYRNYTKVNTVKNVSGELSGAVRYKF 174

RESULT 5
US-08-913-362-8
; Sequence 8, Application US/08913362
; Patent No. 6287574

; GENERAL INFORMATION:
; APPLICANT: Brodeur, Bernard R
; APPLICANT: Martin, Denis
; APPLICANT: Hamel, Josee
; APPLICANT: Rioux, Clement
; TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
; TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/913,362
; FILING DATE: 13-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406,362
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/001,983
; FILING DATE: 04-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 047998/0128
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 174 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-913-362-8

Query Match 93.1%; Score 813.5; DB 4; Length 174;
Best Local Similarity 93.7%; Pred. No. 3.2e-85;
Matches 164; Conservative 2; Mismatches 8; Indels 1; Gaps 1;

QY 1 MKKALALIALALPAAALAGAGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
DB 1 MKKALALIALALPAAALAGAGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

QY 61 FAVDYTRYKNYKQVSTDFKLYSIGASAIYDPTQSPVKPYLGARLSLNRAVDENGSDS 120
DB 61 FAVDYTRYKNYK-ARSTDFKLYSIGASAIYDPTQSPVKPYLGARLSLNRAVDENGSDS 119

QY 121 FSQSTGLGVLAGVSYAVTPNVDLDAGRYRNYTKVNTVKNVSGELSGAVRYKF 175
DB 120 FSQSTGLGVLAGVSYAVTPNVDLDAGRYRNYTKVNTVKNVSGELSGAVRYKF 174

RESULT 6
US-08-127-499A-20
; Sequence 20, Application US/08127499A
; Patent No. 5510264
; GENERAL INFORMATION:
; APPLICANT: VAN ALSTYNE, Diane
; APPLICANT: SHARMA, Lawrence Rajendra
; TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
; TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:

REFERENCE/DOCKET NUMBER: 047998/0128
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Neisseria meningitidis
STRAIN: 608B
US-08-913-362-26

Query Match 13.6%; Score 118.5; DB 4; Length 25;
Best Local Similarity 92.3%; Pred. No. 4.2e-07;
Matches 24; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

OY 61 FAVDYTRYKRYKQVPSDFKLYSIGA 86
DB 1 FAVDYTRYKRYK-APSTDFKLYSIGA 25

RESULT 9
PCT-US95-13749-5
Sequence 5, Application PC/TUS9513749
GENERAL INFORMATION:
APPLICANT: Amgen Inc.
TITLE OF INVENTION: COMPOSITIONS FOR INCREASED
TITLE OF INVENTION: BIOAVAILABILITY OF ORALLY DELIVERED THERAPEUTIC AGENTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Delavilla Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13749
FILING DATE:
CLASSIFICATION:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 568 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
PCT-US95-13749-5

Query Match 10.9%; Score 95.5; DB 5; Length 568;
Best Local Similarity 26.6%; Pred. No. 0.019;
Matches 49; Conservative 29; Mismatches 71; Indels 35; Gaps 9;

OY 12 ALPAALAGASGFYQADAAHAKASSLSIGA-----KGFSPRISAGYRI 56
DB 396 SVGRSGISGRASVNY---AASESSISIGYASQSHKENGTYLDDPKGFN--LRYREL 450

OY 57 NDL-----KFAVDYTRYKRYK---KQVPSDFKLYSIGASAIYDFDQSPVKEPYLGARLSL 108
DB 451 DDMMGVYGSFAFYHOGYDFEYGSNKGHDVDYSGVTMGSPFRINDEYSLYGLGAAGK 510

OY 109 NRASVDFNGSDSFQSTGLGLAGSYAVTPPNDLDAGYRNYTGKRYTVKYNVANSGLS 168
DB 511 VASV-FDESISASKTSMAIG--AGVQNPDPLEFVIDASYS---KIDSIK-VGTWMLG 563

OY 169 AGVR 172
DB 564 AGTR 567

RESULT 10
US-08-457-997B-2
Sequence 2, Application US/08457997B
Patent No. 576608
GENERAL INFORMATION:
APPLICANT: Kolattukudy, P. E.
TITLE OF INVENTION: Otitis Media Vaccine
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calfee, Walter and Griswold
STREET: Suite 1800 800 Superior Avenue
CITY: Cleveland
STATE: Ohio
COUNTRY: U.S.A.
ZIP: 44114-2688
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,997B
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Goldrick, Mary E.
REGISTRATION NUMBER: 34,829
REFERENCE/DOCKET NUMBER: 22727/00102
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 622-8458
TELEFAX: (216) 241-0816
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-457-997B-2

Query Match 10.7%; Score 93.5; DB 1; Length 359;
Best Local Similarity 23.5%; Pred. No. 0.017;
Matches 54; Conservative 29; Mismatches 82; Indels 65; Gaps 11;

OY 1 MKKALALIALALPAALAEGA---SGFYQADAA---HAKASSLSIGSAKGFSPRISAG 53
DB 1 MKTAIALVYAGLAASVAAQAPQENTFYAGVKAGQSPFHGINNCAIKGLSSS-NYG 59

OY 54 YRINDLFAVDYTRYKRYKQVPSDFKLYSIGASAIYDFD-----TQSPVKEPYL----- 102
DB 60 YRNTFTTYGV---FGGQILINDNF-----GLAAELGYDFGRAKLREAGKPRAKHTNH 110

OY 103 GARLSLNRAVDNFNGSDSFQSTGL-----GYLA-GV 134
DB 111 GAVLSLKSQSYEVLDGLDYKAGVALYRSDKFEEDANGTRDKKGGHTTARAAGLRAVGA 170

OY 135 SYAVTPPNDLDAGY-----RYNYTGKRYTVKYNVRS--GELSGAVRYK 175
DB 171 EYALPPELAVLEQYQWLTWVGKYPQDKPNTALINYPMICINAGISYRF 220

RESULT 11
US-08-467-722A-2
Sequence 2, Application US/08467722A
Patent No. 6030626
GENERAL INFORMATION:
APPLICANT: Kolattukudy, P. E.
TITLE OF INVENTION: Otitis Media Vaccine

```

NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSER: Calfee, Halter and Griswold
STREET: Suite 1800 800 Superior Avenue
CITY: Cleveland
STATE: Ohio
COUNTRY: U.S.A>
ZIP: 44114-2688
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,722A
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Golrick, Mary E.
REGISTRATION NUMBER: 34,829
REFERENCE/DOCKET NUMBER: 22727/00102
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 622-8458
TELEFAX: (216) 241-0816
INFORMATION FOR SEQ. ID NO.: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-467-722A-2

```

```

Query Match      10.7% Score 93.5; DB 3; Length 359;
Best Local Similarity 23.5%; Pred. No. 0.017;
Matches 54; Conservative 29; Mismatches 82; Indels 65; Gaps 11

OY    1 MKKALMALIALAPAAALEGA---SGEYVQADA--HAKASSUSGAKGPSPRISAG 53
       ||| | : : : : : ||| : : : : : ||| : : : : :
DB    1 MKKTALAVLAGLAASVAQAAPQEETFEFYGAKAQGSFHDIINNKKIKGLSSS-NYG 59
OY    54 YRIDLRFADVIRRYKNKYOVSTDEKLXLSASAITYPD-----TQSVPKPPL---- 102
       ||| : : : : : ||| : : : : : ||| : : : : :
DB    60 YRRRTFTFGV---FGGYQLNODNN---GLAELGIIDDFGRAKLRAGKPKPAKITNH 110
OY    103 GARSLNRASVDENGSDPSFSQSITGL-----GVIA-GV 134
       ||||| : : : : : ||| : : : : : ||| : : : : :
DB    111 GAYISLNGSEVLGDLDVYGGKAGVALVRSDYKFEDANGTRDHKKGRHTARASGLFAVGA 170
OY    135 SYAVTPNVDDIAGT-----RNTYGNKYNYKNVS--GELSAGVRYKEF 175
       ||| : : : : : ||| : : : : : ||| : : : : :
DB    171 EYAVLPVELAVLEFYOMLTRVGKRPODKPENTAIINYPWIGICINGISYRF 220

RESULT 12
US-08-733-230-6
; Sequence 6, Application US/08733230
; Patent NO. 6025338
; GENERAL INFORMATION:
; APPLICANT: Barbet, Anthony F.
; APPLICANT: Ganta, Roman Reddy
; APPLICANT: McGuire, Travis C.
; APPLICANT: BurrIDGE, Michael J.
; APPLICANT: Nyika, Aceme
; APPLICANT: Rurangirwa, Fred R.
; APPLICANT: Mahan, Sunan M.
TITLE OF INVENTION: Nucleic Acid Vaccines Against
NUMBER OF SEQUENCES: 6
TITLE OF INVENTION: Ricketsial Diseases and Methods of Use
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL

```

```

/ COUNTRY: USA
/ ZIP: 32606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentln Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/733,230
/ FILING DATE:
/ CLASSIFICATION: 514
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Whitlock, Ted W.
/ REGISTRATION NUMBER: 36,965
/ REFERENCE/DOCKET NUMBER: UF-167
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 352-375-8100
/ TELEFAX: 352-372-5800
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 282 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-733-230-6

Query Match 9.8%, Score 86; DB 3; Length 282;
Best Local Similarity 26.6%; Pred. NO. 0.083;
Matches 49; Conservative 17; Mismatches 58; Indels 60; Gaps 11;

QY 20 EGAGFEYVOADAHAKASSLSGASGFSRISAGYRINDLRFVAV---DYTR----- 67
   10 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 111 DDAVGY-----SLGAR---VELEASR---RATLADQOYAKSGAESLAA 150
   68 -----YKNKYQVPSDFKLYSIGASAIYD-FPTQSPVKYLYLARSLNRSAYDFNGS 118
   111 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 151 ITRDANITETNFYFKIDEITNTSTMLNCXYVHLHTDLPVSRYVCA--GIGASFVDIS-- 206
   119 DSFQSTSTGLGV--LAGSVAYTPVWVDLAG-----YRNYIGKVNTVKNVSGELS 168
   111 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 207 ---KQVTKLAVRGVGVISQFTPELSLVAGSFYHGLPDESIXDIPAHNSV--FSGEAK 261
   169 AGVR 172
   111 |||
Db 262 ASVK 265

RESULT 13
US-08-953-326-6
/ Sequence 6, Application US/08953326
/ Patent No. 6251872
/ GENERAL INFORMATION:
/ APPLICANT: Barbett, Anthony F.
/ APPLICANT: Ganta, Roman R.
/ APPLICANT: McGUIRE, Travis C.
/ APPLICANT: Burridge, Michael J.
/ APPLICANT: Nyika, Aceme
/ APPLICANT: Rurangirwa, Fred R.
/ APPLICANT: Mahan, Susan M.
/ TITLE OF INVENTION: Nucleic Acid Vaccines Against Rickettsial Diseases of
/ TITLE OF INVENTION: Animals and Humans
/ FILE REFERENCE: UF-167C1
/ CURRENT APPLICATION NUMBER: US/08/953,326
/ CURRENT FILING DATE: 1997-10-17
/ EARLIER APPLICATION NUMBER: 08/953,326
/ EARLIER FILING DATE: 1997-10-17
/ EARLIER APPLICATION NUMBER: 08/733,230
/ EARLIER FILING DATE: 1996-10-17
/ NUMBER OF SEQ ID NOS: 24
/ SOFTWARE: Patentln Ver. 2.0
/ SEQ ID NO 6
/ LENGTH: 282
/ TYPE: PRT

```

ORGANISM: Anaplasma marginale
US-08-953-326-6

Query Match 9.8%; Score 86; DB 4; Length 282;
Best Local Similarity 26.6%; Pred. No. 0.083;
Matches 49; Conservative 17; Mismatches 58; Indels 60; Gaps 11;

QY 20 EGASGFYQADAAHAKASSISGSAKGSFPRISAGYRINDLRFAV-----DYTR----- 67
DB 111 DGAVG-----SLGGAR-----VELEASR-----REFATLDQGYAKSGAESLAA 150

QY 68 -----YKNYKQVPTDFKLSIGASAIYD-FDTQSPVRYIGARLSLRASVDNGS 118
DB 151 ITRDANITETNYFVYKIDETNTSVMLNGCYDYLHTDLVSPYCA--GIGASFVDIS-- 206

QY 119 DFSQSTGLGV--LAGVSYAVTPNVLDAG-----YRNYIGHYNTVKNRSGELS 168
DB 207 ---KQVTKLAYRGKVGISYQFTPEISLVAGGFYHGLFDESRYKNDIPAHNSVK--FSGEAK 261

QY 169 AGVR 172
DB 262 ASVK 265

RESULT 14
US-08-382-184-3
Sequence 3, Application US/08382184
Patent No. 5714593

GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: MICROBACTERIAL PROTEINS,
TITLE OF INVENTION: MICROORGANISMS PRODUCING THEM AND THEIR USE FOR VACCINES
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER &
ADDRESSEE: NEUSTADT, P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/382,184
FILING DATE: 01-FEB-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 22640720
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
US-08-382-184-3

Query Match 9.8%; Score 86; DB 1; Length 286;
Best Local Similarity 27.9%; Pred. No. 0.085;
Matches 43; Conservative 15; Mismatches 60; Indels 36; Gaps 7;

QY 10 ALALPAAALAEASGFYVQADAAHAKASSISGSA-----KGSFPRISAGYRINDLRFA 62

DB 82 SFALPAG-----WVESDAAHFDYGSALSKTTGDPFPFGQPPVA-----NDFTRIY 127

QY 63 VDYTRKKNYKQVPTDFKLSIGASAIYDFTQSPVRYIGARLSLRASVDENGSD--- 119
DB 128 IGRLDQKLYASAETDSK-----AAARLGSMDWGEFMYPGYRINQETVSLDANGVSGSA 182

QY 120 -----SFSQSTGLG-VLAGVSYAVTPNVLDAG 147
DB 183 SYEYKFSDESKPNQIWTGVIGSPANAP-DAG 215

RESULT 15
US-08-641-356-3
Sequence 3, Application US/08641356
Patent No. 5866130

GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: MICROBACTERIAL PROTEINS,
TITLE OF INVENTION: MICROORGANISMS PRODUCING THEM AND THEIR USE FOR VACCINES
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER &
ADDRESSEE: NEUSTADT, P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/641,356
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/382,184
FILING DATE: 01-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 22640720
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
US-08-641-356-3

Query Match 9.8%; Score 86; DB 2; Length 286;
Best Local Similarity 27.9%; Pred. No. 0.085;
Matches 43; Conservative 15; Mismatches 60; Indels 36; Gaps 7;

QY 10 ALALPAAALAEASGFYVQADAAHAKASSISGSA-----KGSFPRISAGYRINDLRFA 62
DB 82 SFALPAG-----WVESDAAHFDYGSALSKTTGDPFPFGQPPVA-----NDFTRIY 127

QY 63 VDYTRKKNYKQVPTDFKLSIGASAIYDFTQSPVRYIGARLSLRASVDENGSD--- 119
DB 128 IGRLDQKLYASAETDSK-----AAARLGSMDWGEFMYPGYRINQETVSLDANGVSGSA 182

QY 120 -----SFSQSTGLG-VLAGVSYAVTPNVLDAG 147

Tue Oct 29 09:23:11 2002

us-09-684-883-4.rai

Page 8

Db 183 SYEYKFSDDPKPNGQIWTGVIGSPANAP-DAG 215

Search completed: October 28, 2002, 16:04:19
Job time : 10.5409 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 28, 2002, 15:58:04 ; Search time 12.5538 Seconds

(without alignments)
1339,485 Million cell updates/sec

Title: US-09-684-883-4

Sequence: 1 MKKALALIALALPAALAE.....VNVKKNRSGELSGAVRVKF 175

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 segs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	838.5	95.9	174	2	B81932 outer membrane pro
2	828.5	94.8	174	2	G81174 outer membrane pro
3	243.5	27.9	260	2	S16611 opacity protein op
4	242	27.7	261	2	S16610 opacity protein op
5	241.5	27.6	283	2	S72343 opacity protein op
6	240.5	27.5	258	2	S16612 opacity protein op
7	240	27.5	237	2	S36343 opacity protein op
8	240	27.5	338	2	S16613 opacity protein op
9	239.5	27.4	254	2	S20043 opacity protein B
10	239	27.3	257	2	S16614 opacity protein op
11	239	27.3	268	1	KONH2C opacity protein P.
12	238.5	27.3	233	2	S36350 opacity protein op
13	237.5	27.2	260	1	KONH0 opacity protein op
14	237.5	27.2	266	2	S16616 opacity protein op
15	236.5	27.1	178	2	F64124 opacity protein ho
16	235.5	26.9	270	2	S04380 opacity protein P.
17	234.5	26.8	261	2	S16619 opacity protein op
18	231	26.4	234	2	S36329 opacity protein op
19	231	26.4	282	2	S16617 opacity protein op
20	230.5	26.4	234	2	S36342 opacity protein op
21	230.5	26.4	234	2	S36341 opacity protein op
22	229.5	26.3	238	2	S36349 opacity protein op
23	226.5	25.9	258	2	S08514 opacity protein-re
24	224.5	25.7	234	1	KONH8 opacity protein V2
25	224.5	25.7	234	2	S36348 opacity protein op
26	223	25.5	243	2	S36346 opacity protein op
27	222.5	25.5	238	2	S36344 opacity protein op
28	219.5	25.1	248	2	P10038 opacity protein D
29	210.5	24.1	239	2	S28630 opacity protein op

30	208	23.8	247	2	S28632 opacity protein op
31	206	23.6	214	2	S44706 opacity protein op
32	196	22.4	235	2	S44707 opacity protein op
33	181	20.7	121	2	S64187 opacity protein ho
34	153	17.5	210	2	S77737 opacity protein op
35	142.5	16.3	187	2	S20044 opacity protein op
36	138.5	15.8	168	2	S08513 opacity protein-re
37	138.5	15.8	170	2	T10256 opacity protein-re
38	129.5	14.8	192	2	S44712 opacity protein-re
39	128.5	14.7	239	2	AH0541 outer surface prot
40	128	14.6	281	2	AH3012 outer surface prot
41	128	14.6	284	2	G98271 hypothetical prote
42	126	14.4	201	2	S16286 opacity protein op
43	124.5	14.2	284	2	AG356 heat resistant agg
44	122.5	14.0	70	2	F6406 heat resistant agg
45	120	13.7	264	2	I54668 heat resistant agg

ALIGNMENTS

RESULT 1

B81932

outer membrane protein NMA0862 [imported] - Neisseria meningitidis (strain Z2491 sero

C/Species: Neisseria meningitidis
C/Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001

C/Accession: B81932

R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mo

Nature 404, 502-506, 2000

A/Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491

A/Reference number: A81775; MUID:20222556

A/Accession: B81932

A/Status: preliminary

A/Molecule type: DNA

A/Residue: 1-174 <PAR>

A/Cross-references: GB:AL162754; GB:AL157959; NID:97379424; PIDN:CA884143.1; PID:9737

A/Experimental source: serogroup A, strain Z2491

C/Genetics:

A/Gene: nspa; NMA0862

Query Match Best Local Similarity 95.9%; Score 838.5; DB 2; Length 174;

Matches 170; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY	1	MKKALALIALALPAALAEASGFYQADAAKAKSSLSGAKGSPRISAGYRINDR	60
DB	1	MKKALALIALALPAALAEASGFYQADAAKAKSSLSGAKGSPRISAGYRINDR	60
QY	61	FAVDYTRKKNYKQVPSTDFKLSIGASATYDFTQSPKPYGARGLSLRASVDFNGSDS	120
DB	61	FAVDYTRKKNYK-APSTDFKLSIGASATYDFTQSPKPYGARGLSLRASVDFNGSDS	119
QY	121	FSQSTGIGLVAGVSAVTPNDLDAGYRNYTGKNTVKNRSGELSGAVRVKF	175
DB	120	FSQSTGIGLVAGVSAVTPNDLDAGYRNYTGKNTVKNRSGELSGAVRVKF	174

RESULT 2

G81174

outer membrane protein NsgA NMB0663 [imported] - Neisseria meningitidis (strain MC58

C/Species: Neisseria meningitidis
C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001

C/Accession: G81174

R:Pettila, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, R.I.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.

Science 287, 1809-1815, 2000

A/Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappunli, R.

A/Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.

A/Reference number: A81000; MUID:20175755

A/Accession: G81174

A/Status: preliminary

	Matches	75;	Conservative	24;	Mismatches	61;	Indels	82;	Gaps	10;
QY	15	AAALLEG-ASGTYVADADAHAKA-----SSSLGSAGK-----FSPRI	50							
Db	21	AAQAASEGGRGGYVADAIYAERITHDYPEPTGAKKGTTISTVSVDYRNIRTHSIHRY	80							
QY	51	SAGYRINLRFPAVDYTRYK--NYKOVS-----TDEK-----LYS	83							
Db	81	SVGYDFGMRLAADYAFARFRKMNNKNYSIKELNKKNGNTDLKAENGCTFHAYSS	140							
QY	84	IGASAIFYEDPQSPVKPYFLGARLSLN--RASVD-----FNCS--	118							
Db	141	LGLSAVYDFPKLNDKRFPYGARGVAAGHVHRSHSDSKTKTEVTTLHGPGTPPTYVGKMT	200							
QY	119	----DSFSQTSTGLGVLAASYAVTPPVNVLDDAGRYNTIGKNTVKWVRSGEISAGVRY	173							
Db	201	QNAHRESDSIRRVGAGVAVGVCIDITPNLLTDAGRHYHHWGRLLENT-RFKTEHASLGARY	259							
QY	174	KF 175								
Db	260	Rf 261								

```

RESULT 5
S72343
opacity protein opaH precursor - Neisseria gonorrhoeae (isolate 15063G)
N:Alternate names: cell invasion protein opaH
C:Species: Neisseria gonorrhoeae
A:Variety: isolate 15063G
C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 26-Aug-1999
C:Accession: S72343
R:Waldbeser, L.S.; Ajlola, R.S.; Merz, A.J.; Puaoli, D.; Lin, L.; Thomas, M.; So, M.;
Mol. Microbiol. 13, 919-928, 1994
A:Title: The opaH locus of Neisseria gonorrhoeae MS11a is involved in epithelial cell in
A:Reference number: S72343; MUID:95115561
A:Accession: S72343
C:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1,283 <MAL>
A:Cross-references: EMBL:U013708; NID:9535357; PIDN:AAA74082.1; PID:9535358
A:Experimental source: isolate 15063G
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
A:Note: expression of opacity proteins is regulated by the number of translated repeat
of repeats. Place the start codon in frame with the rest of the protein
C:Superfamily: opacity protein
C:Keywords: cell surface component; transmembrane protein
F:1-48/Domain: signal sequence #status predicted <SIG>
F:49-283/Product: opacity protein opaH #status predicted <MAT>
F:58-66/Domain: transmembrane #status predicted <TM1>
F:67-98/Domain: extracellular #status predicted <EXT1>
F:75-84/Region: semivariable region
F:99-107/Domain: transmembrane #status predicted <TM2>
F:112-118/Domain: transmembrane #status predicted <TM3>
F:119-135/Domain: extracellular #status predicted <EXT2>
F:125-150/Region: hypervariable region HV1
F:156-170/Domain: transmembrane #status predicted <TM4>
F:176-186/Domain: transmembrane #status predicted <TM5>
F:187-234/Domain: extracellular #status predicted <EXT3>
F:192-240/Region: hypervariable region HV2
F:235-247/Domain: transmembrane #status predicted <TM6>
F:251-259/Domain: transmembrane #status predicted <TM7>
F:260-274/Domain: extracellular #status predicted <EXT4>
F:275-283/Domain: transmembrane #status predicted <TM8>

Query Match 27.6%; Score 241.5; DB 2; Length 283;
Best Local Similarity 28.7%; Pred. No. 9.2e-14;
Matches 70; Conservative 26; Mismatches 69; Indels 79; Gaps 7;

OY 10 ALALPALALGASGFYQADAAHAKA-----SSLSGASG-----FS 47
:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 41 SILSAAQAASLSEMRPFYQADIALPFAERITHTDPEPTTCKGTTSTVSDYRNRITTSVH 100
48 PRISAGYRINDLRFADVATYTRKNY-----KQVPSTDFKLY 82

```

Db	101	PRVSGYDFGGMRLAADYARFKVNNKYSVNIERYOGAHSNRIDLKAEQENQGTPhAAS	160
Qy	83	SIGASAIYDEPTQSPVKPYIGARLSLN--RASVD-----ENG-----	117
Db	161	SLGSAVYDFLNDKFKFYIGARVAIGHVRSIDSTKTKILTSFYGVARKPTTYDIGP	220
Qy	118	-----SDSFQSTQSTGLGLVLAGVSAAVTPNVYDLDAQRYNTGKVNIVKNNVSGELSAGY	171
Db	221	KTQDAHQESNSIRRVGLGVIVAGVFDTPLKLTLDYGRHYHWGRLNTR--FKTHESLGM	279
Qy	172	RYKF 175	
Db	280	KYRF 283	

```

RESULT 6
SI6612
Opacity protein opaE precursor - Neisseria gonorrhoeae (strain MS11) (fragments)
C:Species: Neisseria gonorrhoeae
A:Variety: Strain MS11
C:Date: 04-Jun-1997 #sequence_revision 17-Oct-1997 #text_change 17-Oct-1997
C:Accession: SI6612
R:Bhat, K.S.; Gibbs, C.P.; Barreira, O.; Morrison, S.G.; Jaehrig, F.; Stern, A.; Kupsc
Mol. Microbiol. 5, 1889-1901, 1991
A:Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a f
A:Reference number: SI6610; MUID: 92114767
A:Accession: SI6612.
A:Molecule type: DNA
A:Residues: 1-258 <BHA>
A:Cross-references: EMBL:X52369
A:Experimental source: strain MS11, variant 4.8
A>Note: the authors did not translate the sequence, for the signal peptide
of repeats place the start codon in frame with the rest of the protein
C:Genetics:
A:Gene: opaE
C:Superfamily: opacity protein
C:Keywords: cell surface component; transmembrane protein
F:1-10,11-23/Domain: signal sequence (fragments) #status predicted <Sig>
F:24-258/Product: opacity protein opaE #status predicted <Mat>
F:34-42/Domain: transmembrane #status predicted <TM1>
F:43-74/Domain: extracellular #status predicted <EXT1>
F:50-60/Region: semivariable region
F:75-83/Domain: transmembrane #status predicted <TM2>
F:88-94/Domain: transmembrane #status predicted <TM3>
F:95-131/Domain: extracellular #status predicted <EXT2>
F:101-125/Region: hypervariable region HV1
F:132-146/Domain: transmembrane #status predicted <TM4>
F:152-162/Domain: transmembrane #status predicted <TM5>
F:163-209/Domain: extracellular #status predicted <EXT3>
F:168-215/Region: hypervariable region HV2
F:210-222/Domain: transmembrane #status predicted <TM6>
F:226-234/Domain: transmembrane #status predicted <TM7>
F:235-249/Domain: extracellular #status predicted <EXT4>
F:250-258/Domain: transmembrane #status predicted <TM8>

Query Match 27.5%; Score 240.5; DB 2; Length 258;
Best Local Similarity 28.3%; Pred. No. 1e-13;
Matches 72; Conservative 28; Mismatches 73; Indels 81; Gaps 8;

QY 2 KKALAAALIALPALALEG---ASGFVQDAHA-----KASSIGSAK----- 44
      ||: || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 6 KKPSSLSSLLFSSNAQAAGEDHGGRPYVADLAAYETHIDYDEPTGTRKKDISTVSD 65
      ||: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 45 -----GFSRISAGYRINDLRFADVTRYKN----- 71
      ||: || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 66 YERNIRTSIHPRVSVGDFGWMRIADYARYRKWNQDKYSVDIKELKNQKNRDLKTE 125
      ||: || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 72 KQVPTDKIKYISGASAIYDFDTQSPVKPYIGARSLN--RASVDF----- 115
      ||: || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 126 NOENGTFAHVSLLGISAYIDFKLNDKRPYIGARAYAGVHVSISDTSKTEVTTLHGP 185
      ||: || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```


A:Title: Characterization of the opa (class 5) gene family of *Neisseria meningitidis*.
 A:Reference number: S16286; MUID:92157869
 A:Accession: S20043
 A:Molecule type: DNA
 A:Residues: 1-254 <AH0>
 A:Cross-references: EMBL:X63108
 A:Experimental source: strain FAM18; clone pFIOB1700
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1991
 A:Note: only a part of the translation is shown
 A:Note: expression of opacity proteins is regulated by the number of translated repeat
 C:Genetics:
 A:Gene: opaB
 C:Superfamily: opacity protein
 C:Keywords: cell surface component; transmembrane protein
 F:1-19/Domain: signal sequence (fragment) #status predicted <SIG>
 F:20-254/Product: opacity protein opaB #status predicted <MAT>
 F:21-39/Domain: transmembrane #status predicted <TM1>
 F:40-69/Domain: extracellular #status predicted <EXT1>
 F:48-55/Region: semivariable region
 F:70-78/Domain: transmembrane #status predicted <TM2>
 F:83-89/Domain: transmembrane #status predicted <TM3>
 F:90-126/Domain: extracellular #status predicted <EXT2>
 F:96-121/Region: hypervariable region HV1
 F:127-141/Domain: transmembrane #status predicted <TM4>
 F:147-157/Domain: transmembrane #status predicted <TM5>
 F:158-205/Domain: extracellular #status predicted <EXT3>
 F:163-211/Region: hypervariable region HV2
 F:206-218/Domain: transmembrane #status predicted <TM6>
 F:222-230/Domain: transmembrane #status predicted <TM7>
 F:231-245/Domain: extracellular #status predicted <EXT4>
 F:246-254/Domain: transmembrane #status predicted <TM8>

Query Match 27.4%; Score 239.5; DB 2; Length 254;
 Best Local Similarity 28.7%; Pred. No. 1.2e-13;
 Matches 70; Conservative 29; Mismatches 68; Indels 77; Gaps 7;

QY 8 LIALPAALALPAAALAEAGSGFYVQADAAHAKASSLSGSAKAKGFS 47
 DB 12 LPSMAAGAAASEGSRSPYVQADLVAERITHYPKATGANNSTVSDYFNRIRASHIH 71
 QY 48 PRISAGYRINDLRFAVDYTRYKNYKQVSTDFKLY 82
 DB 72 PVSAGYDGDGMRIADYASYRKMNNKYSVTKELENNKDKLKTENQENGCFPHAS 131
 QY 83 SIGASIVDFDQSPYKPYLGARLSN--RASVD-----FNQS 118
 DB 132 SIGLSAIDFKLNDKFRPYIGARVAVGHVRHSIDSTKRTTEVVTLLHGADTKPTIYNGE 191
 QY 119 -----DSFSQTSGLGVLAGVSAVTPNVDLADGYRYNYIGKVNYSKNGSLSGV 171
 DB 192 STQNAVHSHSIRRLGLGVAVGVGDITPKLLDTGTYRHHMKRLNTR-FKTHVSLSGM 250
 QY 172 RYKF 175
 DB 251 RYHF 254

RESULT 10
 S16614
 opacity protein opaF precursor - *Neisseria gonorrhoeae* (strain MS11) (fragments)
 C:Species: *Neisseria gonorrhoeae*
 A:Variety: strain MS11
 C:Date: 04-Jun-1997 #sequence_revision 17-Oct-1997 #text_change 17-Oct-1997
 C:Accession: S16614
 R:Bhat, K.S.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsch, M.O. Microbiol. 5, 1889-1901, 1991
 A:Title: The opacity proteins of *Neisseria gonorrhoeae* strain MS11 are encoded by a family
 A:Reference number: S16610; MUID:92114767
 A:Molecule type: DNA
 A:Residues: 1-257 <BHA>
 A:Cross-references: EMBL:X52368

A:Experimental source: strain MS11, variant 4.8
 A:Note: the authors translated the codon ACC for residue 206 as Ala and TAT for resid
 A:Note: the authors did not translate the sequence for the signal peptide
 A:Note: expression of opacity proteins is regulated by the number of translated repea
 C:Genetics:
 A:Gene: opaF
 C:Superfamily: opacity protein
 C:Keywords: cell surface component; transmembrane protein
 F:1-10,11-23/Domain: signal sequence (fragments) #status predicted <SIG>
 F:24-257/Product: opacity protein opaF #status predicted <MAT>
 F:34-42/Domain: transmembrane #status predicted <TM1>
 F:43-74/Domain: extracellular #status predicted <EXT1>
 F:51-60/Region: semivariable region
 F:75-83/Domain: transmembrane #status predicted <TM2>
 F:88-94/Domain: transmembrane #status predicted <TM3>
 F:95-131/Domain: extracellular #status predicted <EXT2>
 F:101-126/Region: hypervariable region HV1
 F:132-146/Domain: transmembrane #status predicted <TM4>
 F:152-162/Domain: transmembrane #status predicted <TM5>
 F:163-208/Domain: extracellular #status predicted <EXT3>
 F:209-221/Region: hypervariable region HV2
 F:225-233/Domain: transmembrane #status predicted <TM6>
 F:234-248/Domain: transmembrane #status predicted <EXT4>
 F:249-257/Domain: transmembrane #status predicted <TM8>

Query Match 27.3%; Score 239; DB 2; Length 257;
 Best Local Similarity 28.1%; Pred. No. 1.4e-13;
 Matches 71; Conservative 30; Mismatches 72; Indels 80; Gaps 8;

QY 2 KKALALALPAAALAEAGSGFYVQADAAHAKASSLSGSAK----- 44
 DB 6 KKPILLSLSSILFSSAAQAGEDHGRGPYVQADLVAEHTHYDEPTGKKKISTVSD 65
 QY 45 -----GFSRISAGYRINDLRFAVDYTRYKNY----- 71
 DB 66 YFNIRTHSIHPRVSVGYDGMRIADYARYRKMNNKYSVDIKELNNKDKRLKTE 125
 QY 72 KQVSTDFKLYSIGASIVDFDQSPYKPYLGARLSN--RASVD----- 115
 DB 126 NQENGTHAVSSLSGLSAVDYDFKLNDRKPYIGARVAVGHVRHSIDSTKRTKPLTSSYG 185
 QY 116 -----NCSDFSQTSGLGVLAGVSAVTPNVDLADGYRYNYIGKVNYSKNGSLSGV 162
 DB 186 LNPTVTEENTQNAHNSIRRVGLGVAVGVGDITPKLLDTGTYRHHMKRLNTR-F 244
 QY 163 RSGLSAGVRYKF 175
 DB 245 KTHRASLSGVRYRF 257

RESULT 11
 KONH2C
 opacity protein P.IIC precursor - *Neisseria gonorrhoeae* (strain JS3) (fragments)
 N:Alternate names: outer membrane protein P.IIC
 C:Species: *Neisseria gonorrhoeae*
 A:Variety: strain JS3
 C:Date: 31-Mar-1992 #sequence_revision 17-Oct-1997 #text_change 08-May-1998
 C:Accession: S03095; S16360
 R:van der Ley, P.
 M.O. Microbiol. 2, 797-806, 1988
 A:Title: Three copies of a single protein II-encoding sequence in the genome of *Neiss*
 A:Reference number: S03095; MUID:89096501
 A:Accession: S03095
 A:Molecule type: DNA
 A:Residues: 1-268 <YAN>
 A:Cross-references: EMBL:X12625
 A:Experimental source: strain JS3
 A:Note: 241-Val was also found
 A:Note: expression of opacity proteins is regulated by the number of translated repea
 C:Genetics:
 A:Gene: P.IIC
 A:Note: repeats place the start codon in frame with the rest of the protein
 R:Barltt, D.S.; Schwalbe, R.S.; Klapper, D.G.; Cannon, J.G.

EMBO J. 12, 641-650, 1993

A>Title: Variable opacity (opa) outer membrane proteins account for the cell tropisms of

A:Reference number: S36328; MUID:93178439

A:Accession: S36328

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 25-260 <KUP>

A:Cross-references: EMBL:Z18927; NID:949323; PIDN:CAA79360.1; PID:940789

R:Meyer, T.F.

Submitted to the EMBL Data Library, November 1992

A:Reference number: S28617

A:Accession: S28621

A:Molecule type: DNA

A:Residues: 25-260 <MEY>

A:Cross-references: EMBL:Z18927; NID:949323; PIDN:CAA79360.1; PID:940789

C:Genetics:

A:Gene: opa

C:Superfamily: opacity protein

C:Keywords: cell surface component; transmembrane protein

F:1-11,12-24/Domain: signal sequence (fragments) #status predicted <SIG>

F:25-260/Product: opacity protein opa #status predicted <MAT>

F:35-43/Domain: transmembrane #status predicted <TM1>

F:44-75/Domain: extracellular #status predicted <EXT1>

F:52-61/Region: semivariable region

F:76-84/Domain: transmembrane #status predicted <TM2>

F:89-95/Domain: transmembrane #status predicted <TM3>

F:96-134/Region: extracellular #status predicted <EXT2>

F:102-129/Region: hypervariable region HV1

F:135-149/Domain: transmembrane #status predicted <TM4>

F:155-165/Domain: transmembrane #status predicted <TM5>

F:166-211/Domain: extracellular #status predicted <EXT3>

F:11-217/Region: hypervariable region HV2

F:212-224/Domain: transmembrane #status predicted <TM6>

F:228-236/Domain: transmembrane #status predicted <TM7>

F:237-251/Domain: extracellular #status predicted <EXT4>

F:252-260/Domain: transmembrane #status predicted <TM8>

Query Match

Best Local Similarity 27.2%; Score 237.5; DB 1; Length 260;

Matches 73; Conservative 26; Mismatches 68; Indels 83; Gaps 8;

Db

6

14

48

74

77

134

115

194

166

251

RESULT 14

S16616

opacity protein opa precursor - Neisseria gonorrhoeae (strain MS11) (fragments)

C:Species: Neisseria gonorrhoeae

C:Accession: S16616

C:Date: 04-Jun-1997 #sequence_revision 17-Oct-1997 #text_change 17-Oct-1997

C:Accession: S16616

R:Bhat, K.S.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsch,

Mol. Microbiol. 5, 1889-1901, 1991

A>Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a fam

A:Reference number: S16610; MUID:92114767

A:Accession: S16616

A:Molecule type: DNA

A:Residues: 1-266 <BHA>

A:Cross-references: EMBL:X52372

A:Experimental source: strain MS11, variant 4.8

A>Note: the authors did not translate the sequence for the signal peptide

of repeats place the start codon in frame with the rest of the protein

C:Genetics:

A:Gene: opa

C:Superfamily: opacity protein

C:Keywords: cell surface component; transmembrane protein

F:1-10,11-23/Domain: signal sequence (fragments) #status predicted <SIG>

F:24-266/Product: opacity protein opa #status predicted <MAT>

F:34-42/Domain: transmembrane #status predicted <TM1>

F:43-74/Domain: extracellular #status predicted <EXT1>

F:51-60/Region: semivariable region

F:75-83/Domain: transmembrane #status predicted <TM2>

F:88-94/Domain: transmembrane #status predicted <TM3>

F:95-139/Domain: extracellular #status predicted <EXT2>

F:101-134/Region: hypervariable region HV1

F:140-154/Domain: transmembrane #status predicted <TM4>

F:160-170/Domain: transmembrane #status predicted <TM5>

F:171-217/Domain: extracellular #status predicted <EXT3>

F:176-223/Region: hypervariable region HV2

F:218-230/Domain: transmembrane #status predicted <TM6>

F:234-242/Domain: transmembrane #status predicted <TM7>

F:243-257/Domain: extracellular #status predicted <EXT4>

F:258-266/Domain: transmembrane #status predicted <TM8>

Query Match

Best Local Similarity 27.2%; Score 237.5; DB 2; Length 266;

Matches 76; Conservative 25; Mismatches 72; Indels 89; Gaps 8;

Db

2

6

43

66

79

126

111

186

154

246

RESULT 15

F64124

opacity protein homolog H1457 - Haemophilus influenzae (strain Rd KW20)

C:Species: Haemophilus influenzae

C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 08-Oct-1999

C:Accession: F64124

R:Flerschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage

; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.T.; Glodok, A.; Kelley, J.M.; Weidman

Science 269, 496-512, 1995

A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente

A>Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A:Reference number: A64000; MUID:95350630

A:Accession: F64124

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-178 <TIGR>

A:Cross-references: GB:U32823; GB:U42023; NID:91574281; PIDN:AAC23104.1; PID:91574294

Query Match 27.1%; Score 236.5; DB 2; Length 178;
 Best Local Similarity 35.4%; Pred. No. 1.5e-13;
 Matches 68; Conservative 24; Mismatches 69; Indels 31; Gaps 9;

```

QY 1 MKKALALIALPAAALAEAGSGFYQA-----DAHAKASSLSGAKGFSPTISAG 53
    ||| | : | : ||| | : | : ||| | : | : ||| |
Db 1 MKKLLIYTMFTLALSQAQO---WYVQDGLGASKIDITHVNSSNS---PSFTQRTISVG 52
    ||| | : | : ||| | : | : ||| | : | : ||| |
QY 54 YRIN-DLRFADVTRY-----KNYKQVPTDFFKLYSIGASAIYDEDTQSPVKPYLGARLSL 108
    ||| | : | : ||| | : | : ||| | : | : ||| |
Db 53 YAFDKNRFLAVDTYNGKVTANTADVVDYSLKSGSLGTGFYDFDL-ADFKPYGVGVST 111
    ||| | : | : ||| | : | : ||| | : | : ||| |
QY 109 NRASVDENGSG---DSF-SQTSGLGVLAGVSAVTPNDLDAGYRXNTIGKYNTRYKVR 163
    ||| | : | : ||| | : | : ||| | : | : ||| |
Db 112 NGADVTANARYRIEAFATEFRIGIGALAGVOYKLTDNVALNTNIEYNRL-----ASNVS 166
    ||| | : | : ||| | : | : ||| | : | : ||| |
QY 164 SGEISAGVRYKF 175
    ||| | : | : ||| | : | : ||| | : | : ||| |
Db 167 DVGVAAGLRFESF 178
    ||| | : | : ||| | : | : ||| | : | : ||| |
    
```

Search completed: October 28, 2002, 16:03:35
 Job time : 13.5538 secs

[illegible]

```

Db 125 TEHQENGFHFVAVSSIGLSTIVDFDGSRRPKYRIGRVAVGHNRHQVRSVEQETELITTPP 194
OY 115 FNGSDSFSCOTS-----TGLGVLAGVSAVTPENVDDAGRYNYTKYNT 158
      11 : : 11 : : 11 : : 11 : : 11 : :
Db 195 SNGGCKVSLSSKMPKSRKASHOHSNIRVGLGVLAGVGFEDITPMLTDGRYRHHNMGRLEN 254
OY 159 VKNVRSGLSAGVRYKF 175
      : : : : : : : : : : : : : :
Db 255 TR-FRTHEASLGMYRF 270

RESULT 3
OP67_NEIGO
OP67_NEIGO STANDARD: PRT: 233 AA.
AC 005034;
DF 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DR 01-NOV-1995 (Rel. 32, Last annotation update)
DE Opacity protein OPA67 precursor (Fragment).
OS Neisseria gonorrhoeae.
OC Bacteria, Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=485;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VPI;
RX MEDLINE=931176439; PubMed=8440254;
RA Kupsch E.-M., Knepper B., Kuraki T., Heuer I., Meyer T.F.;
RT "Variable opacity (opa) outer membrane proteins account for the cell
RT tropisms displayed by Neisseria gonorrhoeae for human leukocytes and
RT epithelial cells.";
RL EMBJ J. 12:641-650(1993).
CC -1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
CC VARIATION.
CC -1- SUBCELLULAR LOCATION: Outer membrane.
CC -----
CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on lists
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC CC
CC EMBL: Z18942; CAA79375.1; -.
CC DR PIR: S28625; S28625.
CC DR InterPro: IPR003594; Opacity.
CC DR Pfam: PF02462; Opacity; 1.
CC KW Outer membrane; Multigene family; Signal.
CC FT NON_TER 1 1
CC FT SIGNAL <1 1
CC FT CHAIN 2 >233 POTENTIAL.
CC FT NON_TER 233 233 OPACITY PROTEIN OPA67.
CC SQ SEQUENCE 233 AA; 26039 MW; 6C13A46AB163C67F CRC64;

Query Match 27.3%; Score 238.5; DB 1; Length 233;
Best Local Similarity 28.3%; Pred. No. 3,8e-14;
Matches 66; Conservative 32; Mismatches 56; Indels 77; Gaps 8;

OY 19 AEG-ASGEYVQADAHA-----KASSLSGSAKGF-----SPRISAGY 54
      :| | | | | | :| : : : : : : : : |
Db 2 SEGNGRGPRVQADLAVERITHDYPEATAQKGGTTISVSDYFNIRHVSHPRAVSYG 61
OY 55 RINDRFADVTRYRKNY-----KQVPSDFEKLXSGASALYDFD 93
      :| | | | | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 62 DFGGMRIADADVARYKMNWSKYSVSIKKLQNOYNKKTENQENGTEPHAASLSGVYDFK 121
OY 94 TQSPKPYLIGARLSLN--RASVDF-----NGSDSFSCOST 126
      |||:||||: :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 122 LNDKRKPPIGARVAAGVHRHSIDSRKTTTGFTTTAGAGAAAPTSSPKNTYDADAQESNS 181
      :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
OY 127 ---GLGVLAGVSAVTPENVDDAGRYNYTGVNTVKNVRSGLSAGVRYKF 175

```


Db 182 IRRVGLCVIAGVGFDITPNTLLDAGYRHYHMWGLENTN-RKTHASISGVYRFR 233

RESULT 4

YE57_HAEIN STANDARD; PRT; 178 AA.

AC 057201; 005063;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Protein H11457 precursor.
 GN H11457.
 OS Haemophilus influenzae.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Haemophilus.
 OX NCBI_Taxid=727;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RD/KW20 / ATCC 51907;
 RX MEDLINE=95350630; PubMed=7542800;
 RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
 RA Kervatage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
 RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
 RA Scott J.D., Shirley R., Liu L.-I., Glodok A., Kelley J.M.,
 RA Weidman J.F., Phillips C.A., Spriggs T., Heddlom E., Cotton M.D.,
 RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
 RA Fine L.D., Fritchman J.L., Fritchman J.L., Geoghagen N.S.M.,
 RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
 RA Venter J.C.;
 RT "Whole-genome random sequencing and assembly of Haemophilus
 RT influenzae Rd.";
 RL Science 269:496-512(1995).
 RN [2]
 RP IDENTIFICATION BY MASS SPECTROMETRY.
 RX MEDLINE=20137488; PubMed=10675023;
 RA Langen H., Takacs B., Evers S., Berndt P., Lahm H.W., Wipf B.,
 RA Gray C., Fountoulakis M.;
 RT "Two-dimensional map of the proteome of Haemophilus influenzae.";
 RL Electrophoresis 21:411-429(2000).
 CC -1- SIMILARITY: WEAK, TO N.GONORHOEAE OPACITY PROTEINS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: U32823; AAC3104.1; -
 CC DR TIGR: H11457; -
 CC DR InterPro: IPR003394; Opacity.
 CC DR Pfam: PF02462; Opacity; 1.
 CC KW Signal; Complete proteome.
 CC FT SIGNAL 1 19
 CC FT CHAIN 20 178 PROTEIN H11457
 CC FT SEQUENCE 178 AA; 19470 MW; 15AC5C44FF9A9F CRC64;

Query Match 27.1%; Score 236.5; DB 1; Length 178;
 Best Local Similarity 35.4%; Pred. No. 4.2e-14;
 Matches 68; Conservative 24; Mismatches 69; Indels 31; Gaps 9;

Db 1 MKKALALALALPAALAEAGSGFYQA-----DAHAKASSLSAGSFRISAG 53
 1 MKKLIVYMLFTLASAQOQ-----WYOGDGLASKIDITHVSSNS-----PSFTGRISVG 52
 54 YKIN-DLRFVADYTRY-----KNYKQVPSTDFKYSIGASATYDPTQSGVPRYLGLARSL 108
 53 YAFDKNFRILAVDYTNVGVKATYADVVDYSLKGRSLGLGTFDEPL-ADFKPYGVVRSFT 111
 109 NKASVDENK-----DSF-SQSTGGLGAGSYAVTPVNDLADGARYNYIGKRVNTVKNR 163

Db 112 NGADYANARRYRIEAFETRIIGALAGYQKLTNDVALNTNIEYRNL-----ASNVS 166
 QY 164 SGEISAGVYRFR 175
 Db 167 DVGVRAGLRFSP 178

RESULT 5

OPAH_NEIGO STANDARD; PRT; 238 AA.

AC 004884;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Opacity protein OPA60 precursor (fragment).
 GN OPAH.
 OS Neisseria gonorrhoeae.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_Taxid=485;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MS11 / F3;
 RX MEDLINE=93178439; PubMed=8440254;
 RA Kusch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
 RT "Variable opacity (Opa) outer membrane proteins account for the cell
 RT tropisms displayed by Neisseria gonorrhoeae for human leukocytes and
 RT epithelial cells.";
 RL EMBO J. 12:641-650(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MS11 / V18;
 RX MEDLINE=92114767; PubMed=1815562;
 RA Bhat K.S., Gibbs C.P., Barrera O., Morrison S.G., Jaehnig F.,
 RA Stern A., Kusch E.-M., Meyer T.F., Swanson J.;
 RT "Type opacity proteins of Neisseria gonorrhoeae strain MS11 are
 RT encoded by a family of 11 complete genes.";
 RL Mol. Microbiol. 5:1889-1901(1991).
 RN [3]
 RP ERRATUM.
 RX MEDLINE=92261323; PubMed=1584024;
 RA Bhat K.S., Gibbs C.P., Barrera O., Morrison S.G., Jaehnig F.,
 RA Stern S., Kusch E.-M., Meyer T.F., Swanson J.;
 RL Mol. Microbiol. 6:1073-1076(1992).
 CC -1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
 CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
 CC VARIATION.
 CC -1- SUBCELLULAR LOCATION: Outer membrane.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: Z18939; CAAT9372.1; -
 CC DR EMBL: X60711; CAA43121.1; -
 CC DR PIR: S28631; S28631.
 CC DR InterPro: IPR003394; Opacity.
 CC DR Pfam: PF02462; Opacity; 1.
 CC KW Outer membrane; Multigene family; Signal.
 CC FT NON_TER 1 1
 CC FT SIGNAL 1 1
 CC FT CHAIN 2 238
 CC FT VARIANT 2 4
 CC FT NON_TER 238 238
 CC FT SEQUENCE 238 AA; 27073 MW; 883A3560C2DF1B9F CRC64;

Query Match 26.8%; Score 234.5; DB 1; Length 238;
 Best Local Similarity 28.9%; Pred. No. 8.e-14;
 Matches 69; Conservative 23; Mismatches 66; Indels 81; Gaps 6;

```

OY 17 ALACASGFYQADAAAH-----KASSISGS-----AKFSFRIAGY 54
D 1 ASEDGGRPFYQADLAVAEHITHDYDEPTAPDNKKKISTVSDEYRNRITRSEVHRVSGY 60
OY 55 RINDLRFAVDYTRYKNY-----KQPSIDFKLSTIGAS 87
D 61 DFGGRIADADAFARYKRNMMNKNSVNIENWRIRKENGIRIDRKTEQNGTSHAASISGLS 120
OY 88 AIDPDDTQSPKPYLGARLSLN--RASVDF-----N 116
D 121 AIDPQIDNKKRPYIGARVAAGVHRHSIDTSRKKTILEVTTPSNAPNGAVITTYNTDPKQN 180
OY 117 GSDSFQSTSGTGLGIVAGSYAVTEPNVDADGRINRYICKVNFVKNVNSGELISAGYRKF 175
D 181 DYOSNSIRRVGLGVAGVGFDTPTKLTLDAGRYRHHNMGLNTR-FKTHASLGVRRF 238

RESULT 6
OPAL_NEIGO
AC 004882;
ID OPAL_NEIGO STANDARD; PRT: 237 AA.
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DE 01-NOV-1995 (Rel. 32, Last annotation update)
DE Opacity protein OPA58 precursor (Fragment).
GN OPA.
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=485;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MS11 / F3.
RX MEDLINE=931178439; PubMed=8440254;
RA Kusch C.E.M., Knupper B., Kuroki T., Heuer I., Meyer T.F.;
RT "Variable opacity (Opa) outer membrane proteins account for the cell
RT tropisms displayed by Neisseria gonorrhoeae for human leukocytes and
RT epithelial cells.";
RL EMBL J.12:641-650(1993).
CC -1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
CC VARIATION.
CC -1- SUBCELLULAR LOCATION: Outer membrane.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC DR EMBL; Z18937; CAA79370.1; -.
CC DR PIR; S28624; S28624.
CC DR InterPro; IPR003394; Opacity.
CC DR Pfam; PF02462; Opacity; 1.
CC KW Outer membrane; Multigene family; Signal.
CC FT SIGNAL 1 1
CC FT NON_TER 1 1
CC FT CHAIN 2 >237 POTENTIAL.
CC FT NON_TER 237 237 OPACITY PROTEIN OPA58.
CC SO SEQUENCE 237 AA; 26855 MW; B165033B2CDB6A53 CRC64;

Query Match 26.8%; Score 234; DB 1; Length 237;
Best Local Similarity 28.6%; Pred. No. 9.6e-14;
Matches 66; Conservative 26; Mismatches 59; Indels .80; Gaps
OY 24 GFYVQADAHA-----KASSISGSAGKGS-----PRISAGYRINDLRF 61
D 8 GFYVQADLAVAEHITHDYDEPTDPKRGKISTVSDFYRNRITRSHIRVSVGDFGGMRI 67
OY 62 AVDYTRYKNY-----KQPSIDFKLSTIGASATIDPT 94
D 1 ASEDGGRPFYQADLAVAEHITHDYDEPTAPDNKKKISTVSDEYRNRITRSEVHRVSGY 60

```

[illegible]

Db 1 ASEDGGRGPVQADLAAYEHITHDPKPTDPSKGIISTVDFRNIIRHSHIPRVSGV 60
 QY 55 RINDLRPAVDYTRY-----KNYK---QVSTDFKLISGAS 87
 Db 61 DFGGMIADYARVARKWDSNKYSVSIKNMKRVHKNRNKRLKTENQENSGFHAVSSLGIS 120
 QY 88 AIYDFDQSPVKPYLGRSLN--RASVD-----FN 116
 Db 121 AIYDFQINDKFKPYIGARVAVGHVRSIDSTKKTIGLTTPSPGINSGVYKVLRTPGAR 180
 QY 117 GSDSFQSTGTGLGVSAVTPNDLDAGYRNYIGKNTVKNVRSGLSAGVRYKF 175
 Db 181 ESDSIR--VGLGVINGVGDITPKLTLDAGYRHYHMGRLNTR-FKTHASLGAVRYF 236

RESULT 8
 OPAB_NEIGO STANDARD; PRT: 234 AA.
 AC 004874;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Opacity protein OPA51 precursor (Fragment).
 GN OPAB.
 OS Neisseria gonorrhoeae.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_TaxID=485;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MS11 / F3;
 RX MEDLINE=93178439; PubMed=8440254;
 RA Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
 RT "Variable opacity (Opa) outer membrane proteins account for the cell
 tropisms displayed by Neisseria gonorrhoeae for human leukocytes and
 epithelial cells."
 RL EMO J. 12:641-650(1993).
 CC -1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
 CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
 CC VARIATION.
 CC -1- SUBCELLULAR LOCATION: Outer membrane.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; Z18928; CAA79361.1; -
 DR PIR; S28628; S28628.
 DR PIR; S36329; S36329.
 DR InterPro: IPR003394; Opacity.
 DR Pfam: PF02462; Opacity; 1.
 KW Outer membrane; Multigene family; Signal.
 FT NON_TER 1 1
 FT SIGNAL <1 1 POTENTIAL.
 FT CHAIN 2 >234 OPACITY PROTEIN OPA51.
 FT NON_TER 234 234
 SQ SEQUENCE 234 AA: 26772 MW: 9FEEB5DABBA96CA CRC64;

Query Match 26.4%; Score 231; DB 1; Length 234;
 Best Local Similarity 28.2%; Pred. No. 1.7e-13;
 Matches 66; Conservative 29; Mismatches 61; Indels 78; Gaps 8;

QY 19 AEG-ASGKYQADAAHA-----KASSLSGSAK-----GFSPRISAGYR 55
 Db 2 SGNNGRGPVQADLAAYEHITHDPKPTDPSKGIISTVDFRNIIRHSHIPRVSGV 61
 QY 56 INDLRPAVDYTRYKNY-----KQVSTDFKLISGASAIY 90
 Db 62 FGGMIADYARVARKWDSNKYSVSIKNMKRVHKNRNKRLKTENQENSGFHAVSSLGISAVY 121

QY 91 DEDTQSPVKPYLGRSLN--RASVD-----NGSDSFQST 125
 Db 122 DFKLNGKRFKPYIGARVAVGHVRSIDSTKKTIGLTTPSPGINSGVYKVLRTPGAR 181
 QY 126 T-----GLGVLAGVSAVTPNDLDAGYRNYIGKNTVKNVRSGLSAGVRYKF 175
 Db 182 SIRSRLGVINGVGDITPKLTLDAGYRHYHMGRLNTR-FKTHASLGAVRYF 234

RESULT 9
 OPAB_NEIGO STANDARD; PRT: 234 AA.
 AC 004878;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Opacity protein OPA55 precursor (Fragment).
 GN OPAB.
 OS Neisseria gonorrhoeae.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_TaxID=485;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MS11 / F3;
 RX MEDLINE=93178439; PubMed=8440254;
 RA Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
 RT "Variable opacity (Opa) outer membrane proteins account for the cell
 tropisms displayed by Neisseria gonorrhoeae for human leukocytes and
 epithelial cells."
 RL EMO J. 12:641-650(1993).
 CC -1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
 CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
 CC VARIATION.
 CC -1- SUBCELLULAR LOCATION: Outer membrane.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; Z18933; CAA79366.1; -
 DR PIR; S28632; S28632.
 DR InterPro: IPR003394; Opacity.
 DR Pfam: PF02462; Opacity; 1.
 KW Outer membrane; Multigene family; Signal.
 FT NON_TER 1 1
 FT SIGNAL <1 1 POTENTIAL.
 FT CHAIN 2 >234 OPACITY PROTEIN OPA55.
 FT NON_TER 234 234
 SQ SEQUENCE 234 AA: 26881 MW: 8EBB30B3A774C766 CRC64;

Query Match 26.4%; Score 230.5; DB 1; Length 234;
 Best Local Similarity 28.1%; Pred. No. 1.9e-13;
 Matches 64; Conservative 28; Mismatches 59; Indels 77; Gaps 7;

QY 24 GIFYQADAAHA-----KASSLSGSAK-----GFSPRISAGYRINDLAF 61
 Db 8 GIFYQADLAAYEHITHDPKPTDPSKGIISTVDFRNIIRHSHIPRVSGVDEFGGMI 67
 QY 62 AVDTTRYKNY-----KQVSTDFKLISGASAIYDFDQS 96
 Db 68 AADYARVARKWDSNKYSVSIKNMKRVHKNRNKRLKTENQENSGFHAVSSLGISAVYDEK 127
 QY 97 PVKPYLGRSLN--RASVD-----KSDSFQSTST---G 127
 Db 128 KFKPYIGARVAVGHVRSIDSTKKTIGLTTPSPGINSGVYKVLRTPGAR 187
 QY 128 LGVLAGVSAVTPNDLDAGYRNYIGKNTVKNVRSGLSAGVRYKF 175
 Db 188 LGVLAGVGDITPKLTLDAGYRHYHMGRLNTR-FKTHASLGAVRYF 234

RESULT 10
OPAF_NEIGO STANDARD; PRT; 234 AA.
ID OPAF_NEIGO
AC 004879;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Opacity protein OPA56 precursor (Fragment).
GN OPAF.
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=485;
RN [1]
RM SEQUENCE FROM N.A.
RC STRAIN=MS11 / F3;
RX MEDLINE=93178439; PubMed=8440254;
RA Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
RT "Variable opacity (Opa) outer membrane proteins account for the cell
tropisms displayed by Neisseria gonorrhoeae for human leukocytes and
epithelial cells."
RT EMBL J. 12:641-650(1993).
CC -!- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
CC VARIATION.
CC -!- SUBCELLULAR LOCATION: Outer membrane.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; 218934; CAA79367.1; -.
DR PIR; S28620; S28620.
DR InterPro; IPR003394; Opacity.
DR Pfam; PF02462; Opacity; 1.
KW Outer membrane; Multigene family; Signal.
FT NON_TER 1 1
FT SIGNAL <1 1 POTENTIAL.
FT CHAIN 2 >234 OPACITY PROTEIN OPA56.
FT NON_TER 234 234
SO SEQUENCE 234 AA; 26868 MW; 5175C6606839EFFB CRC64;
Query Match 26.4%; Score 230.5; DB 1; Length 234;
Best Local Similarity 28.1%; Pred. No. 1,9e-13;
Matches 64; Conservative 28; Mismatches 39; Indels 77; Gaps 7;
DY 24 GFYVQADLAHA-----KASSISGSAK-----GPSRISAGYRINDLR 61
DY 8 GFYVQADLAHAAYHITHDPEQGTGKKDISYDVFNRVTHSHPRVSVGIDFGWRI 67
DY 62 AVDYTRYKNY-----KQVSTDFKLYSIGASAIYDFDT 96
DY 68 AADYARFRKMWDSKYVSIDIKELNKNQRDLKTENGSTFHAVSSGLSAVYDFKIND 127
DY 97 PVKPYIGARLSLN--RASVDF-----NCSDFSQTSR---G 127
DY 128 KFRPYIGARVAAGVHSHSIDSTKTKTFLTSSYGLNPTVYEENTONAHOSNSIRRVG 187
DY 128 LGVIAAGVAVTPNDLDAGYRYNYIGKVNTVKNVSGELSGAVRYKF 175
DY 188 LGVIAAGVDFITPKLTLDGGRYHNGRLNTR-FKTHASLSGVRYRF 234
RESULT 11
OP66_NEIGO STANDARD; PRT; 238 AA.
ID OP66_NEIGO
AC 005033;
DT 01-OCT-1993 (Rel. 27, Created)

DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Opacity protein OPA66 precursor (Fragment).
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=485;
RN [1]
RM SEQUENCE FROM N.A.
RC STRAIN=VP1;
RX MEDLINE=93178439; PubMed=8440254;
RA Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
RT "Variable opacity (Opa) outer membrane proteins account for the cell
tropisms displayed by Neisseria gonorrhoeae for human leukocytes and
epithelial cells."
RT EMBL J. 12:641-650(1993).
CC -!- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
CC VARIATION.
CC -!- SUBCELLULAR LOCATION: Outer membrane.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; 218941; CAA79374.1; -.
DR PIR; S28619; S28619.
DR InterPro; IPR003394; Opacity.
DR Pfam; PF02462; Opacity; 1.
KW Outer membrane; Multigene family; Signal.
FT NON_TER 1 1
FT SIGNAL <1 1 POTENTIAL.
FT CHAIN 2 >238 OPACITY PROTEIN OPA66.
FT NON_TER 238 238
SO SEQUENCE 238 AA; 26888 MW; B6E58AF1565263AA CRC64;
Query Match 26.3%; Score 229.5; DB 1; Length 238;
Best Local Similarity 27.2%; Pred. No. 2,4e-13;
Matches 63; Conservative 31; Mismatches 57; Indels 81; Gaps 7;
DY 24 GFYVQADLAHA-----KASSISGSAK-----GPSRISAGYRINDLR 61
DY 8 GFYVQADLAHAAYHITHDPEQGTGKKDISYDVFNRVTHSHPRVSVGIDFGWRI 67
DY 62 AVDYTRYKNY-----KQVSTDFKLYSIGASAIYDFDT 94
DY 68 AADYARFRKMWDSKYVSINKLQRTSNGNRDRKRTENGSTFHAVSSGLSAVYDFK 127
DY 95 QSPVRYIGARLSLN--RASVDF-----NCSDFSQTSR--- 126
DY 128 NDKFRPYIGARVAAGVHSHSIDSTKTKTEFLTAGAGTDPVSSPKYNTQADHOSNSI 187
DY 127 ---GLVIAAGVAVTPNDLDAGYRYNYIGKVNTVKNVSGELSGAVRYKF 175
DY 188 RRVGLVIAAGVDFITPKLTLDAGYRYHNGRLNTR-FKTHASLSGVRYRF 238
RESULT 12
OPRL_NEIMC STANDARD; PRT; 260 AA.
ID OPRL_NEIMC
AC 010170;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Opacity-related protein POPM1.
GN OPR.
OS Neisseria meningitidis (serogroup C).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=135720;
RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN-C1938 / SEROGROUP C;
 RX MEDLINE-88250884; PubMed-2455211;
 RA Stern A., Meyer T.F.;
 RT "Common mechanism controlling phase and antigenic variation in
 pathogenic neisseriae";
 RL Mol. Microbiol. 1:5-12(1987).
 CC -1- SUBCELLULAR LOCATION: Outer membrane.
 CC -1- SIMILARITY: STRONG TO THE OPACITY-RELATED PROTEIN POPM3 AND
 CC REGIONS OF HOMOLOG WITH N. GONORRHOEA (STRAIN MS11) OPA GENE
 CC PRODUCTS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X06445; CAA29748.1; ALT_SEQ.
 DR PIR; S08514; S08514.
 DR InterPro: IPR003394; Opacity.
 DR Pfam; PF02462; Opacity; 1.
 DR Outer membrane.
 KW SEQUENCE 260 AA; 28936 MW; E847A2843B3F037B CRC64;
 SQ
 Query Match 26.0%; Score 227.5; DB 1; Length 260;
 Best Local Similarity 26.8%; Pred. No. 4e-13;
 Matches 69; Conservative 35; Mismatches 68; Indels 85; Gaps 7;
 QY 3 KALALIALALPAALAEAG-----SGFYQADAAHA-----KASSSLG 41
 DB 5 KFFSSILFSSLFSSMAQASEDGSPPYQADALAAERITHNPETGADKDKISTV 64
 QY 42 S-----AKGSPRISAGYRINDLRFADVTRYRNYKQVSTDEKL-----81
 DB 65 SDFFNRIRAHSHIHPRVSGVDEGWMRIADYASYRKKWESNENSTKVEIKDKYKTKT 124
 QY 82 -----YSIGASAIYDFDTQSPVKPYGLARLSLNR-----SYDENFS-----118
 DB 125 EHQGNGSPFATSSLSGLSATYDPLKNDKRPYIGARVAYGHVAKHGVSETKTTVTSPRK 184
 QY 119 -----DSFSQTSSTGLGVLAVSVAYTPNVDDLADAGRYNYIGKYNT 158
 DB 185 GGTTPAGGPYIKTDPKRPYHSHSISLGLGIYAGVGDIPDKLTDGYRTHMGRLEN 244
 QY 159 VKNVRSGLSAGRYVKF 175
 DB 245 TR-FKTHEASLGMRYRF 260
 RESULT 13
 OP28_NEIGO STANDARD; PRT; 234 AA.
 ID OP28_NEIGO
 AC P11297;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Opacity protein V28 precursor (Fragment).
 OS Neisseria gonorrhoeae.
 CC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 CC NCBI_TaxID=485;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-87002493; PubMed-3093085;
 RA Stern A., Brown M., Nickel P., Meyer T.F.;
 RT "Opacity genes in Neisseria gonorrhoeae: control of phase and
 antigenic variation";
 RL Cell 47:61-71(1986).
 CC -1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
 CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
 CC VARIATION.

CC -1- SUBCELLULAR LOCATION: Outer membrane.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M14747; -; NOT_ANNOTATED_CDS.
 DR PIR; B24429; KONH8.
 DR InterPro: IPR003394; Opacity.
 DR Pfam; PF02462; Opacity; 1.
 KW Outer membrane; Multigene family; Signal.
 FT NON_TER 1
 FT SIGNAL 1
 FT CHAIN 2
 FT NON_TER 2
 FT CHAIN 2
 FT NON_TER 2
 FT CHAIN 2
 SQ SEQUENCE 234 AA; 26770 MW; 339ADB09C2FE75E4 CRC64;
 Query Match 25.7%; Score 224.5; DB 1; Length 234;
 Best Local Similarity 28.1%; Pred. No. 6.5e-13;
 Matches 64; Conservative 28; Mismatches 59; Indels 77; Gaps 7;
 QY 24 GFYVQADAAHA-----KASSSLGSAR-----GFSRISAGYRINDLRF 61
 DB 8 GFYVQADALAVYEHITHDHYPEPTGKDKISTVSDYFRNIRTHSHPRVSGVDEGWMRI 67
 QY 62 AVDTTRYRNY-----KQVSTDFELXSIGASAIYDFDTQS 96
 DB 68 AADYARRKKWMDNRYSDYDIKELKNKONKRDJKTENGENGTFHVVSLGLSAYVDFRLND 127
 QY 97 PVKPYGLARLSL-N-RASVDF-----NGSDFSQST-----G 127
 DB 128 KRPYIGARVAYGHVSHSISLSTKTKTTFELSSSGGLNPVYTEENONAHQNSIRRVG 187
 QY 128 LGVLAGSVAYTPNVDDLADAGRYNYIGKYNTVKNVRSGLSAGRYVKF 175
 DB 188 LGVLAGVGFDTPLKTLADAGRYHNMGRLENTR-FKTHEASLGMRYRF 234
 RESULT 14
 OP65_NEIGO STANDARD; PRT; 234 AA.
 ID OP65_NEIGO
 AC Q04885;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Opacity protein OPA65 precursor (Fragment).
 OS Neisseria gonorrhoeae.
 CC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 CC NCBI_TaxID=485;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN-VPI;
 RX MEDLINE-93178439; PubMed-8440254;
 RA Kupsch E.-W., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
 RT "Variable opacity (Opa) outer membrane proteins account for the cell
 tropisms displayed by Neisseria gonorrhoeae for human leukocytes and
 epithelial cells";
 RL EMBO J. 12:641-650(1993).
 CC -1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
 CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
 CC VARIATION.
 CC -1- SUBCELLULAR LOCATION: Outer membrane.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>

or send an email to license@lsb-slb.ch).

CC -----
 CC EMBL: Z18940; CAA79373.1; -
 DR PIR: S28617; S28617.
 DR InterPro: IPR003394; Opacity.
 DR Pfam: PF02462; Opacity; 1. Signal.
 DR Outer membrane; Multigene family; Signal.
 FT SIGNAL 1
 FT NON_TER <1 1
 FT CHAIN 2
 FT NON_TER 234
 FT SEQUENCE 234 AA; 26242 MW; D66A0BA844AC2F1 CRC64;
 SQ

Query Match 25.7%; Score 224.5; DB 1; Length 234;
 Best Local Similarity 28.9%; Pred. No. 6.5e-13;
 Matches 66; Conservative 25; Mismatches 60; Indels 77; Gaps 8;

OY 24 GFYVQADAAHA-----KASSSLGS-----AKGSPRISAGYRINDLRF 61
 DB 8 GPYVQADLAAYAEHITHDYPEPTGKKAQSTVSDYFRNITHTSHIRVSVGYDFGGMRI 67
 OY 62 ADVYARYKRYKQVST-----DFK-----LYSIGASAIYDFPTQSP 97
 DB 68 AADYARYKRWKESNSIKKYTEDIKDNKYETKEHENGTFHVASISGLSTIYDFQISDK 127
 OY 98 VKPYLGARL-----SLNRASVDF-----NGSDSFQSTST-----G 127
 DB 128 IKPYIGVHVGVGHVHRQVRSVQOETIYTPKPKNGTGGPVKSTSPIPAYAHENRSSRLG 187
 OY 128 LGVLGVSVAVTPNVDLDAGRYRYNIGKVTYKRVNSGELSAGYRVKF 175
 DB 188 FGAMAGVGIDVAPGLTLDAGRYRYHMGRLNTR-FKTHEASLSGVYRIF 234

RESULT 15
 OPAD_NEIGO STANDARD: PRT: 243 AA.

AC 004883;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Opacity protein OPA59 precursor (Fragment).
 GN OPAD.
 OS Neisseria gonorrhoeae.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_TaxID=485;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MS11 / F3;
 RX MEDLINE=93178439; PubMed=8440254;
 RA Kupsch E.-W., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
 RT Variable opacity (Opa) outer membrane proteins account for the cell
 RT tropisms displayed by Neisseria gonorrhoeae for human leukocytes and
 RT epithelial cells.";
 RT EMBO J. 12:641-650(1993).
 CC -1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
 CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
 CC VARIATION.
 CC -1- SUBCELLULAR LOCATION: Outer membrane.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-slb.ch/announce/>
 CC or send an email to license@lsb-slb.ch).

DR EMBL: Z18938; CAA79371.1; -
 DR PIR: S28629; S28629.
 DR InterPro: IPR003394; Opacity.
 DR Pfam: PF02462; Opacity; 1. Signal.
 DR Outer membrane; Multigene family; Signal.

FT NON_TER 1 1
 FT SIGNAL <1 1
 FT CHAIN 2 243
 FT NON_TER 243 243
 FT SEQUENCE 243 AA; 27414 MW; 5930C73917436041 CRC64;
 SQ

Query Match 25.5%; Score 223; DB 1; Length 243;
 Best Local Similarity 28.3%; Pred. No. 9.2e-13;
 Matches 67; Conservative 24; Mismatches 60; Indels 86; Gaps 7;

OY 24 GFYVQADAAHA-----KASSSLGSAK-----GSPRISAGYRINDLRF 61
 DB 8 GPYVQADLAAYAEHITHDYPEPTGKTKDKISTVSDYFRNITHTSHIRVSVGYDFGGMRI 67
 OY 62 ADVYARYK-----NYKQVSTD-----FLYSIGASA 88
 DB 68 AADYARYKRWKNNKYSVNIKELLRNDNANSGSHINIKRTEHRENGTFHVASISGLSA 127
 OY 89 IYDFPTQSPFKPYLGARLSLR-----ASYDFNG-----S 118
 DB 128 YVDFDGSFEPKPYLGARVAVGHVHRQVRSVQOETIYTPKPKNGTGGPVKSTSPIPAYAHENRSSRLG 187
 OY 119 DSFSQSTGLGVLAGYSVAVTPNVDLDAGRYRYNIGKVTYKRVNSGELSAGYRVKF 175
 DB 188 ESKRSISLSLFGAVAGVIDITPMLTLDAGRYRYHMGRLNTR-FKTHEASLSGVYRIF 243

Search completed: October 28, 2002, 16:01:11
 Job time : 8.03013 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 28, 2002, 15:56:04 ; Search time 20.0861 Seconds
(without alignments)
1507.218 Million cell updates/sec

Title: US-09-684-883-4
Perfect score: 874
Sequence: 1 MKRALALALALPAAALAE.....VNTKVRSGELSGAVRK 175

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

SPTRMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rviro:*
16: sp_bacteriophage:*
17: sp_archaeap:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	874	100.0	175	2	P95371
2	839.5	96.1	174	2	Q9RP18
3	838.5	95.9	174	16	P95372
4	836.5	95.7	174	2	Q9RP16
5	832.5	95.3	174	2	Q9R21
6	828.5	94.8	174	16	Q9RP17
7	824.5	93.1	174	2	P96943
8	813.5	93.1	174	2	P95343
9	246	28.1	186	16	Q9CM19
10	242.5	27.7	256	2	Q51126
11	242.5	27.7	256	2	Q51124
12	242	27.7	241	2	Q9AEB0
13	241.5	27.6	283	2	Q50943
14	239.5	27.4	262	2	Q07287
15	239.5	27.4	262	2	Q33388
16	238.5	27.3	234	2	Q9R719

17	238.5	27.3	234	2	O07280
18	238.5	27.3	237	2	O31176
19	238.5	27.3	259	2	O51125
20	237.5	27.2	234	2	Q9R718
21	237.5	27.2	235	2	O30753
22	237	27.1	257	2	O50929
23	236.5	27.1	237	2	Q9K4T6
24	236.5	27.1	270	2	Q9RQV4
25	235.5	26.9	241	2	Q9K4T4
26	235	26.9	230	2	Q9R9A7
27	235	26.9	232	2	Q9K4T3
28	235	26.9	241	2	O07274
29	234	26.8	232	2	Q9R3P5
30	234	26.8	241	2	O07912
31	234	26.8	253	2	O51303
32	232.5	26.6	242	2	Q9K4T8
33	232.5	26.6	272	2	O51013
34	231	26.4	232	2	Q9K4T9
35	230.5	26.4	235	2	O30752
36	230.5	26.4	240	2	O07925
37	230.5	26.4	260	2	O33389
38	229.5	26.3	233	2	Q9K4T5
39	229	26.2	241	2	O07273
40	228	26.1	238	2	O31172
41	227	26.0	232	2	Q9R9A9
42	227	26.0	232	2	Q9R9A8
43	226	25.9	242	2	O07279
44	225	25.7	234	2	O30759
45	224.5	25.7	237	2	O31175

ALIGNMENTS

RESULT 1	P95371	PRELIMINARY;	PRT;	175 AA.
ID	P95371			
AC	P95371			
DT	01-MAY-1997 (TREMBL)	03, Created		
DT	01-MAY-1997 (TREMBL)	03, Last sequence update		
DT	01-DEC-2001 (TREMBL)	19, Last annotation update		
DE	OUTER MEMBRANE PROTEIN PRECURSOR.			
OS	Neisseria meningitidis.			
OC	Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.			
OX	NCBI_TaxID=487;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=MCH 88.			
RX	MEDLINE=9386904; PubMed=10456958;			
RA	Cadieux N., Plante M., Rioux C.R., Hamel J., Brodeur B.R., Martin D.,			
RT	"Bactericidal and cross-protective activities of a monoclonal antibody			
RT	directed against Neisseria meningitidis Nspa outer membrane protein."			
RL	Infect. Immun. 67:4955-4959(1999).			
DR	EMBL: U52067; ABA1578.1.			
DR	InterPro: IPR003394; Opacity: 1.			
DR	Pfam: PF02462; Opacity: 1.			
KW	SIGNAL.			
FT	SIGNAL.			
SQ	SEQUENCE	1	19	POTENTIAL.
		175 AA;	18572 MW;	DLEA8F2FEFC22PEA CRC64;
Query Match		100.0%;	Score 874;	DB 2; Length 175;
Best Local Similarity		100.0%;	Pred. No. 1.7e-65;	
Matches 175;	Conservative	0;	Mismatches	0; Indels
			Gaps	0;
QY	1	MKRALALALPAAALAGSGFYQADAAAKSSSGSKGSPRISGRIINDR	60	
DB	1	MKRALALALPAAALAGSGFYQADAAAKSSSGSKGSPRISGRIINDR	60	
QY	61	FAYDYTRKKNYKQVPSTDFKLYSIGASAIYDPTQSPVRYLGAARLSLNASVDENGSDS	120	
DB	61	FAYDYTRKKNYKQVPSTDFKLYSIGASAIYDPTQSPVRYLGAARLSLNASVDENGSDS	120	
QY	121	FSQSTGLGVLAGVSTAVTPNVDLDAGYRINYIGKYNVYKVRSGELSGAVRK 175		

```

Db      121 FSQSTGVLGVLGYSAVTNPVDDAGRYNYIGKVTYKVNVRSGELSGAVRYKF 175
|||||
RESULT 2
ID      09RP18      PRELIMINARY;      PRT;      174 AA.
AC      09RP18;
DT      01-MAY-2000 (TREMBLrel. 13, Created)
DT      01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE      01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE      SURFACE PROTEIN A.
GN      NSPA.
OC      Bacteria: Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX      NCBI_TaxID=487;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=8047;
RA      Moe G.R., Tan S., Granoff D.M.;
RT      "Differences in Surface Expression of Neisserial Surface Protein A
RT      among Neisseria meningitidis Group B strains.";
RL      Infect. Immun. 0:0-0(1999).
DR      EMBL; AF175676; AAD53279.1; -.
DR      InterPro; IPR003394; Opacity.
DR      Pfam; PF02462; Opacity; 1.
SQ      SEQUENCE 174 AA; 18357 MW; 0205AALDA1B7F005 CRC64;

Query Match      96.1%; Score 839.5; DB 2; Length 174;
Best Local Similarity 97.1%; Pred. No. 1.3e-62;
Matches 170; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY      1 MKKALALIALALPAALAEAGSGFYVOADAHAHAKASSLSGAKGSPRISAGYRINDLR 60
      |||||
DB      1 MKKALALIALALPAALAEAGSGFYVOADAHAHAKASSLSGAKGSPRISAGYRINDLR 60

QY      61 FAVDYTRYKNKYKQVPSDFKLYSIGASAIYDFDQSPVKPYLGARLSLNRAVDLGGSDS 120
      |||||
DB      61 FAVDYTRYKNKYK-APSTDFKLYSIGASAIYDFDQSPVKPYLGARLSLNRAVDLGGSDS 119

QY      121 FSQSTGVLGVLGYSAVTNPVDDAGRYNYIGKVTYKVNVRSGELSGAVRYKF 175
      |||||
DB      120 FSQSTGVLGVLGYSAVTNPVDDAGRYNYIGKVTYKVNVRSGELSGAVRYKF 174

RESULT 3
ID      P95372      PRELIMINARY;      PRT;      174 AA.
AC      P95372;
DT      01-MAY-1997 (TREMBLrel. 03, Created)
DT      01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT      01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE      OUTER MEMBRANE PROTEIN PRECURSOR.
GN      NSPA OR NMA0862.
OS      Neisseria meningitidis, and
OS      Neisseria meningitidis (serogroup A).
OC      Bacteria: Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX      NCBI_TaxID=487; 65699;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=24063;
RA      Martin D., Cadieux N., Hamel J., Rioux C., Brodeur B.R.;
RL      Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=22491 / SEROGROUP A / SEROTYPE 4A;
RC      MEDLINE=20222556; PubMed=10761919;
RA      Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
RA      Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA      Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
RA      Jagers K., Leather S., Moule S., Mungall K., Quail M.A.,
RA      Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA      Whitehead S., Spratt B.G., Barrell B.G.;

```

```

RT      "Complete DNA sequence of a serogroup A strain of Neisseria
RT      meningitidis 22491.";
RL      Nature 404:502-506(2000).
DR      EMBL; U52068; AAB41580.1; -.
DR      EMBL; AL162754; CAB84143.1; -.
DR      InterPro; IPR003394; Opacity.
DR      Pfam; PF02462; Opacity; 1.
KW      Signal; Complete proteome.
FT      SIGNAL 1
FT      SEQUENCE 174 AA; 18355 MW; EBA4A1ADA4F6F009 CRC64;

Query Match      95.9%; Score 838.5; DB 16; Length 174;
Best Local Similarity 97.1%; Pred. No. 1.5e-62;
Matches 170; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY      1 MKKALALIALALPAALAEAGSGFYVOADAHAHAKASSLSGAKGSPRISAGYRINDLR 60
      |||||
DB      1 MKKALALIALALPAALAEAGSGFYVOADAHAHAKASSLSGAKGSPRISAGYRINDLR 60

QY      61 FAVDYTRYKNKYKQVPSDFKLYSIGASAIYDFDQSPVKPYLGARLSLNRAVDLGGSDS 120
      |||||
DB      61 FAVDYTRYKNKYK-APSTDFKLYSIGASAIYDFDQSPVKPYLGARLSLNRAVDLGGSDS 119

QY      121 FSQSTGVLGVLGYSAVTNPVDDAGRYNYIGKVTYKVNVRSGELSGAVRYKF 175
      |||||
DB      120 FSQSTGVLGVLGYSAVTNPVDDAGRYNYIGKVTYKVNVRSGELSGAVRYKF 174

RESULT 4
ID      09RP16      PRELIMINARY;      PRT;      174 AA.
AC      09RP16;
DT      01-MAY-2000 (TREMBLrel. 13, Created)
DT      01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT      01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE      SURFACE PROTEIN A.
GN      NSPA.
OS      Neisseria meningitidis.
OC      Bacteria: Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX      NCBI_TaxID=487;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=NG3/88;
RA      Moe G.R., Tan S., Granoff D.M.;
RT      "Differences in Surface Expression of Neisserial Surface Protein A
RT      among Neisseria meningitidis Group B strains.";
RL      Infect. Immun. 0:0-0(1999).
DR      EMBL; AF175681; AAD53284.1; -.
DR      InterPro; IPR003394; Opacity.
DR      Pfam; PF02462; Opacity; 1.
SQ      SEQUENCE 174 AA; 18355 MW; ECF6F38B9268800E CRC64;

Query Match      95.7%; Score 836.5; DB 2; Length 174;
Best Local Similarity 96.6%; Pred. No. 2.3e-62;
Matches 169; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

QY      1 MKKALALIALALPAALAEAGSGFYVOADAHAHAKASSLSGAKGSPRISAGYRINDLR 60
      |||||
DB      1 MKKALALIALALPAALAEAGSGFYVOADAHAHAKASSLSGAKGSPRISAGYRINDLR 60

QY      61 FAVDYTRYKNKYKQVPSDFKLYSIGASAIYDFDQSPVKPYLGARLSLNRAVDLGGSDS 120
      |||||
DB      61 FAVDYTRYKNKYK-APSTDFKLYSIGASAIYDFDQSPVKPYLGARLSLNRAVDLGGSDS 119

QY      121 FSQSTGVLGVLGYSAVTNPVDDAGRYNYIGKVTYKVNVRSGELSGAVRYKF 175
      |||||
DB      120 FSQSTGVLGVLGYSAVTNPVDDAGRYNYIGKVTYKVNVRSGELSGAVRYKF 174

RESULT 5
ID      09R2R1      PRELIMINARY;      PRT;      174 AA.
AC      09R2R1;

```


RESULT 6			
09RP17	09RP17	PRELIMINARY:	PRT: 174 AA.
AC	09RP17;		
DT	01-MAY-2000 (Tremblrel, 13, Created)		
DT	01-MAY-2000 (Tremblrel, 13, last sequence update)		
DT	01-DEC-2001 (Tremblrel, 19, last annotation update)		
DE	SURFACE PROTEIN A (OUTER MEMBRANE PROTEIN NSGA).		
GN	NSPA OR NMB0663		
OS	Neisseria meningitidis, and		
OS	Neisseria meningitidis (serogroup B).		
OC	Bacteria; Proteobacteria; Beta subdivision; Neisseriaceae; Neisseria.		
OX	NCBI_TaxID=487, 491;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	SPRAIN-CU385;		
RA	Moe G.R., Tan S., Granoff D.M.;		
RT	"Differences in Surface Expression of Neisserial Surface Protein A		
RT	among Neisseria meningitidis Group B strains.";		
RL	Infect. Immun. 0:0-0(1999).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	SPRAIN-MC58 / SEROGROUP B;		
RX	MEDLINE=20175755; PubMed=10710307;		
RA	Teteltein H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,		
RA	Elsen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.U.,		
RA	Nelson W.C., Gwyn M.L., Deboy R., Peterson J.D., Hickey E.K.,		
RA	Haft D.H., Salberg S.L., White O., Fleischmann R.D., Dougherty B.A.,		
RA	Mason T., Ciecko A., Parksey D.S., Blair E., Clifton H., Clark E.B.,		
RA	Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,		
RA	Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L.,		
RA	Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;		
RT	"Complete genome sequence of Neisseria meningitidis serogroup B strain		
RL	MC58.";		
	Science 287:1809-1815(2000).		

ID	PRELIMINARY;	PRT;	174 AA.
P96943			
P96943			
01-MAY-1997 (TrEMBLrel. 03, Created)			
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)			
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)			
OTHER MEMBRANE PROTEIN PRECURSOR.			
NSPA.			
Neisseria meningitidis.			
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.			
NCBI_TaxId=487;			
[1]			
SEQUENCE FROM N.A.			
STRAIN=608B:			
MEDLINE=97149429; PubMed=8996237;			
Martin D., Cadieux N., Hamel J., Brodeur B.R.;			
"Costimulation of T cell activation by integrin-associated protein			
(CD47) is an adhesion-dependent, CD28-independent signalling pathway."			
J. Exp. Med. 185:1-11(1997).			
[2]			
SEQUENCE FROM N.A.			
STRAIN=NGP165, M986, AND NG6/88;			
Moe G.R., Tan S., Granoff D.M.;			
"Differences in Surface Expression of Neisserial Surface Protein A			
among Neisseria meningitidis Group B strains."			
Intec. Immun. 0:0-0(1999).			
EMBL; U52066; AAC36000.1; -;			
EMBL; AF175683; AAD53286.1; -;			
EMBL; AF175680; AAD53283.1; -;			
EMBL; AF175682; AAD53285.1; -;			
InterPro: IPR003394; Opacity.			
Pfam: PF02462; Opacity; 1.			
Signal.			
FW			
FT			
SEQUENCE	1	19	POTENTIAL.
174 AA;	18425 MW;	E8B02767DCCF6E19 CRC64;	
Query Match	94.3%;	Score 824.5;	DB 2; Length 174;
Best Local Similarity	95.4%;	Pred. No. 2.3e-61;	
Matches 167; Conservative	0;	Mismatches 7;	Indels 1; Gaps
1 MKKLAALIALALPAALAEAGSGFYQADAAHAKASSLSGAKGSPRSAGYRINDR	60		
1 MKKLAALIALALPAALAEAGSGFYQADAAHAKASSLSGAKGSPRSAGYRINDR	60		
1 MKKLAALIALALPAALAEAGSGFYQADAAHAKASSLSGAKGSPRSAGYRINDR	60		
61 FAVDYTRKNKQVPSDFELKYSIGASAIYDFQTQSPVKEYLIGARLSLNRASVDFNGSDS	120		
61 FAVDYTRKNKQVPSDFELKYSIGASAIYDFQTQSPVKEYLIGARLSLNRASVDFNGSDS	119		

Db 253 RYHF 256

RESULT 11

Q51124 PRELIMINARY; PRT: 256 AA.

AC 051124: 01-NOV-1996 (TREMBLREL. 01, Created)
 DT 01-MAY-1997 (TREMBLREL. 03, last sequence update)
 DT 01-JUN-2001 (TREMBLREL. 17, last annotation update)
 DE OPACITY OUTERMEMBRANE PROTEIN (FRAGMENT).
 GN OPA.
 OS Neisseria meningitidis.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.

NCBI_TaxID=487;
 NCBI_TaxID=487;

RP SEQUENCE FROM N.A.

RC STRAIN=24197;

RA MEDLINE=98129089; PubMed=9467908;

RA Hobbs M.M., Malorny B., Prasad P., Morelli G., Kusecek B.,

Heckels J.E., Cannon J.G., Achtman M.,

"Recombinational reassortment among opa genes from ET-37 complex

Neisseria meningitidis isolates of diverse geographical origins."

RL Microbiology 144:157-166(1998).

DR EMBL: U37255; AAC6101.1; -

DR InterPro: IPR003394; Opacity.

DR Pfam: PF02462; Opacity; 1.

FT NON_TER

SO SEQUENCE 256 AA; 28335 MW; 9DA1C6079C6DD13F CRC64;

Query Match 27.7%; Score 242.5; DB 2; Length 256;

Best Local Similarity 27.9%; Pred. No. 1.3e-12;

Matches 68; Conservative 34; Mismatches 65; Indels 77; Gaps 6;

QY 8 LIALPAAALAGSGFYVQADAAHA-----KASSLSGS-----AKGFS 47

Db 14 LFSAAQAASEDSGHPYVQADLAFAERITHDYPKAGANTSTVSDYFNIRAHSH 73

QY 48 PRISAGYRINDLFAVDYTRYKKNYKQVSTDFKL-----YS 83

Db 74 PRYSVGYDEGGRKADYATYKMKESNSYKVEDIADNFKETKEHQSGSFRHASS 133

QY 84 IGASAIYDFDTOSPVKPYLGARLSLNRA-----SVDFNGS----- 118

Db 134 LGLSAYDEKLNKDFKPYIGARVAGVGHVAVETKTTTYSKPTATSPGGGLIQTD 193

QY 119 -----DSFSQSTGSLGVLAVSYAVTPNVDDAGYRYNYGKVTYKNVSGELSA 171

Db 194 PSKPYHSHSISLGLVAGVGDITPKLTLDGTGRYHNMGRLENTFTHHEVSLGM 252

QY 172 RYVF 175

Db 253 RYRF 256

RESULT 12

Q9AE80 PRELIMINARY; PRT: 241 AA.

AC 09AE80: 01-JUN-2001 (TREMBLREL. 17, Created)

DT 01-JUN-2001 (TREMBLREL. 17, last sequence update)

DT 01-DEC-2001 (TREMBLREL. 19, last annotation update)

DE OPACITY PROTEIN (FRAGMENT).

GN OPA.

OS Neisseria meningitidis.

OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.

NCBI_TaxID=487;

RP SEQUENCE FROM N.A.

RC STRAIN=29620;

RA MEDLINE=21221108; PubMed=11287631;

Zhu P., van der Ende A., Falush D., Brieske N., Morelli G., Bodo L.,

RA Popovic T., Schuurman I.G.A., Adegbola R.A., Zurth K., Gagneux S.,

Platonov A.E., Riou J.Y., Gaugant D.A., Nicolas P., Achtman M.,

"Fit genotypes and escape variants of subgroup III Neisseria

meningitidis during three pandemics of epidemic meningitis."

Proc. Natl. Acad. Sci. U.S.A. 98:5234-5239(2001).

DR EMBL: AJ292238; CAC36361.1; -

DR InterPro: IPR003394; Opacity.

DR Pfam: PF02462; Opacity; 1.

FT NON_TER

SO SEQUENCE 241 AA; 26923 MW; 4923ACF9484BF183 CRC64;

Query Match 27.7%; Score 242; DB 2; Length 241;

Best Local Similarity 30.1%; Pred. No. 1.4e-12;

Matches 72; Conservative 30; Mismatches 57; Indels 80; Gaps 9;

QY 16 AALAGA-SGFYVQADAAHA-----KASSLSGS-----AKGFSRISAGY 54

Db 4 AASEGSRSPYVQADLAFAERITHDYPKASGANTSTVSDYFNIRAHSHIPRSVGY 63

QY 55 RINDLFAVDYTRYKKNY-----KQVSTDFKLSTGAS 87

Db 64 DGDRIADYATYKMKDNKSVNTKKNVQKNSGNRODKTENQENGTFHVAVSSGLS 123

QY 88 AIYDEDTOSPVKPYLGARLSLN--RASVD-----FN-GS----- 118

Db 124 AYDENTGSRFPYAGVAVAGVGHVSHSIDSTKTTNLTVPNTNPGPTIYNGSSTQDA 183

QY 119 --DSFSQSTGSLGVLAVSYAVTPNVDDAGYRYNYGKVTYKNVSGELSA 175

Db 184 YHSHSIRLGLGVAVAGVGDITPKLTLDGTGRYHNMGRLENTFTHHEVSLGVRVF 241

RESULT 13

Q50943 PRELIMINARY; PRT: 283 AA.

AC 050943: 01-NOV-1996 (TREMBLREL. 01, Created)

DT 01-NOV-1996 (TREMBLREL. 01, last sequence update)

DT 01-JUN-2001 (TREMBLREL. 17, last annotation update)

DE OPA15063G.

GN OPA15063G.

OS Neisseria gonorrhoeae.

OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.

NCBI_TaxID=485;

RP SEQUENCE FROM N.A.

RC STRAIN=15063G;

RA MEDLINE=95115561; PubMed=7815949;

RA Waldhiser L.S., Ajlola R.S., Metz A.J., Puaol D., Lin L., Thomas M.,

"The opa locus of Neisseria gonorrhoeae MS11A is involved in

epithelial cell invasion."

Mol. Microbiol. 13:919-928(1994).

DR EMBL: U13708; AAA74082.1; -

DR InterPro: IPR003394; Opacity.

DR Pfam: PF02462; Opacity; 1.

SO SEQUENCE 283 AA; 31877 MW; EBA2AF275316E84B CRC64;

Query Match 27.6%; Score 241.5; DB 2; Length 283;

Best Local Similarity 28.7%; Pred. No. 1.9e-12;

Matches 70; Conservative 26; Mismatches 69; Indels 79; Gaps 7;

QY 10 AALPAAALAGSGFYVQADAAHA-----SSLSGSAK-----FS 47

Db 41 SLISAQAASEAMGPGYVQADLAFAERITHDYPEPTGKGTISYVSDYFNIRAHSHV 100

QY 48 PRISAGYRINDLFAVDYTRYKKNY-----KQVSTDFKLSTGAS 82

Db 101 PRYSVGYDEGGRKADYATYKMKDNKSVNTKKNVQKNSGNRODKTENQENGTFHVA 160

QY 83 SIGASAIYDFDTOSPVKPYLGARLSLN--RASVD-----PNG----- 117

Db 161 SLGSAIYDFDKLNKDFKPYIGARVAGVGHVSHSIDSTKTTKILTISYGVATPTTYDIP 220

QY 118 -----SDSFQSTGTGLAGVSYAVTPNVDLAGRYNTIGKYNVKNRSGELSGV 171
 DB 221 KTDQAHQESNSIRRVGLGVAGVGFDTIPKLTLDGYRYHMGRLNTR-FKTHESLGM 279
 QY 172 RYKF 175
 DB 280 RYKF 283

RESULT 14

007287 PRELIMINARY: PRT: 234 AA.
 AC 007287;
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE OPACITY PROTEIN (FRAGMENT).
 GN OPA OR OPAE.
 OS Neisseria meningitidis.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_TaxID=487;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Achman M., Malorny B., Morelli G.;
 RL Submitted (JUN-1997) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=93915;
 RX MEDLINE=98010345; PubMed=9350862;
 RA Morelli G., Malorny B., Mueller K., Sella A., Wang J.-F.,
 RA del Valle J., Achman M.;
 RT "Clonal descent and microevolution of Neisseria meningitidis during 30
 RT years of epidemic spread";
 RL Mol. Microbiol. 25:1047-1064(1997).
 DR EMBL: AF001204; AAC32725.1; -;
 DR EMBL: AF004823; AAC32684.1; -;
 DR InterPro: IPR003394; Opacity.
 DR Pfam: PF02462; Opacity; 1.
 FT NON_TER 1
 SQ SEQUENCE 234 AA; 25933 MW; 61E375DDE82AFE2 CRC64;

Query Match 27.4%; Score 239.5; DB 2; Length 234;
 Best Local Similarity 30.2%; Pred. No. 2, 1e-12;
 Matches 70; Conservative 30; Mismatches 59; Indels 73; Gaps 8;

QY 16 AALAECA-SGFYVOADAAH-----KASSSLGS-----AKGSPRISAGY 54
 DB 4 AASEDGSRSFYVOADLATAERITHDYPRATGANTSTVSDYFRNIRASHIHPRVSGY 63
 QY 55 RINDLRPAVDYTRKNKQVSTD-----FKLXSIGASATY 90
 DB 64 DFDGWRIRAAIYASRYKKKESSNTNENSTOONRIKIETHGNGSPHAASLGLSATY 123
 QY 91 DFDGSPVRYLGAARLSLNA-----SVDF-----NGS-----DSFQ 123
 DB 124 DFKLNDKFKFYIGARVAYGVKQVQSVESKTKTVTSKPNKGVPKGGPYPKPAYHESNSI 183
 QY 124 TSTGIGLAGVSYAVTPNVDLAGRYNTIGKYNVKNRSGELSGVRYKF 175
 DB 184 SSGGLGVAGVGFDTIPKLTLDGYRYHMGRLNTR-FKTHESLGM 234

RESULT 15
 033388 PRELIMINARY: PRT: 262 AA.
 AC 033388;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE OPA1700 OUTER MEMBRANE PROTEIN PRECURSOR (FRAGMENT).
 GN OPA1700.
 OS Neisseria meningitidis.

OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_TaxID=487;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FAM 18;
 RX MEDLINE=92157869; PubMed=1787795;
 RA Aho E.L., Dempsey J.A., Hobbs M.M., Klapper D.G., Cannon J.G.;
 RT "Characterization of the opa (class 5) gene family of Neisseria
 RT meningitidis";
 RL Mol. Microbiol. 5:1429-1437(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FAM 18;
 RX MEDLINE=98129089; PubMed=9467908;
 RA Hobbs M.M., Malorny B., Prasad P., Morelli G., Kusecek B.,
 RA Heckels J.E., Cannon J.G., Achman M.;
 RT "Recombinational reassortment among opa genes from ET-37 complex
 RT Neisseria meningitidis isolates of diverse geographical origins";
 RL Microbiology 144:157-166(1998).
 DR EMBL: X63108; CAA44822.1; -;
 DR InterPro: IPR003394; Opacity.
 DR Pfam: PF02462; Opacity; 1.
 KW Signal.
 FT NON_TER 1
 FT SIGNAL 27
 FT SEQUENCE 262 AA; 29477 MW; C42511DD6DF6CF97 CRC64;

Query Match 27.4%; Score 239.5; DB 2; Length 262;
 Best Local Similarity 28.7%; Pred. No. 2, 5e-12;
 Matches 70; Conservative 29; Mismatches 68; Indels 77; Gaps 7;

QY 8 LIALALPAALAECA-SGFYVOADAAH-----KASSSLGS-----AKGFS 47
 DB 20 LFSSAQAAASEDGSRSFYVOADLATAERITHDYPRATGANTSTVSDYFRNIRASHIH 79
 QY 48 PRISAGRYNDLRPAVDYTRKNK-----KQVSTDEKLY 82
 DB 80 PRVSGDGFDMRIADYASTRKNNNNKYSYNTKLENNKNNKDKLTENQENGTFHAAS 139
 QY 83 SIGASATYDFDQSPVRYLGAARLSLNA-----RASVD-----FNGS 118
 DB 140 SLGLSATYDFKLNKFKRYIGARVAYGVHRSISSTKTEEVVTSFGADTKPTIYNGE 199
 QY 119 -----DSFQSTGTGLAGVSYAVTPNVDLAGRYNTIGKYNVKNRSGELSGV 171
 DB 200 STONAYHESHSHIRRVGLGVAGVGFDTIPKLTLDGYRYHMGRLNTR-FKTHESLGM 258
 QY 172 RYKF 175
 DB 259 RYKF 262

Search completed: October 28, 2002, 16:02:38
 Job time : 20.0861 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 28, 2002, 15:55:03 ; Search time 24.7145 Seconds

(without alignments)
782.004 Million cell updates/sec

Title: US-09-684-883-6

Perfect score: 868
Sequence: 1 MKKALATLIALALPALALAE.....VNTKVNRSGLSGAVRVK 174

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

```
1: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
2: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
3: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
4: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
5: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
6: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
7: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*
8: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*
9: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
10: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*
11: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*
12: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
13: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
14: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
15: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
16: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*
17: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*
18: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
19: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
20: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
21: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	868	100.0	174	17	AAW04893
2	854	98.4	174	17	AAW04891
3	838.5	96.6	175	17	AAW04892
4	834	96.1	174	17	AAW04894
5	771	88.8	155	22	AA19895
6	735	15.6	170	16	AA19931
7	133	15.3	25	17	AAW04912
8	99	11.4	353	22	AA197447
9	96	11.1	212	22	AAU34556
10	92	10.6	257	22	AAU38252
11	92	10.6	568	17	AA196210

ALIGNMENTS

RESULT 1	AAW04893	standard; Protein; 174 AA.
AC	AAW04893;	
XX		
DT	22-DEC-1996	(first entry)
XX		
DE	Proteinase K resistant N. meningitidis 22 kd surface protein.	
XX		
KW	Proteinase K resistant; Neisseria meningitidis;	
KW	Neisseria gonorrhoeae; antibody; detection; probe; surface protein.	
XX		
OS	Neisseria meningitidis strain 24063.	
XX		
FH	Key	Location/Qualifiers
FT	Peptide	1..19
FT	Protein	/label= sig_peptide
FT		20..174
FT		/label= mat_protein
XX		
PN	W05629412-A1.	
XX		
PD	26-SEP-1996.	
XX		
PF	15-MAR-1996;	96WO-CA00157.
XX		
PR	04-AUG-1995;	95US-0001983.
PR	17-MAR-1995;	95US-0406362.
XX		
PA	(IAPB-) IAF BIO VAC INC.	
XX		
PI	Brodeur BR, Hamel J, Martin D, Rioux C;	
XX		

12	91	10.5	359	16	AA196294	Non-typhable Haemop
13	89.5	10.3	339	21	AA192873	Arabidopsis thalia
14	89.5	10.3	534	21	AA190860	Arabidopsis thalia
15	89	10.3	369	21	AA194589	Virulence gene pro
16	87.5	10.1	162	17	AA196207	Attachment-invasio
17	87	10.0	16	17	AAW04901	N. meningitidis 60
18	87	10.0	350	9	AA192053	Outer membrane pro
19	87	10.0	369	22	AA1959179	Protein associated
20	87	10.0	369	21	AA196098	Actinobacillus ple
21	87	10.0	369	21	AA197900	Actinobacillus ple
22	87	10.0	500	22	AA1965766	Cysteine protease
23	85.5	9.9	221	20	AA1934533	Porphorymonas ging
24	85.5	9.9	221	20	AA1934533	Chlamydia trachoma
25	85	9.8	797	20	AA1934533	Actinobacter pylori
26	84.5	9.7	708	19	AA193022	H. pylori bacteria
27	84.5	9.7	708	21	AA193022	The outer membrane
28	84	9.7	180	21	AA193022	Arabidopsis thalia
29	84	9.7	180	21	AA193022	Virulence gene pro
30	84	9.7	316	21	AA193022	Actinobacillus ple
31	84	9.7	364	21	AA193022	Actinobacillus ple
32	84	9.7	364	21	AA193022	Arabidopsis thalia
33	84	9.7	364	21	AA193022	Arabidopsis thalia
34	84	9.7	511	21	AA193022	Arabidopsis thalia
35	83	9.6	511	21	AA193022	Arabidopsis thalia
36	81.5	9.4	282	19	AA193022	C glutamylum prote
37	81.5	9.4	282	19	AA193022	Anaplasma marginal
38	81.5	9.4	282	19	AA193022	Anaplasma marginal
39	81	9.3	15	17	AAW04194	Major antigenic pr
40	80.5	9.3	215	21	AA196096	N. meningitidis 60
41	80.5	9.3	215	21	AA196096	Actinobacillus ple
42	79.5	9.2	573	19	AA196096	Actinobacillus ple
43	79.5	9.2	581	21	AA196096	M. catarrhalis str
44	79.5	9.2	645	21	AA196096	Arabidopsis thalia
45	79.5	9.2	704	20	AA196096	Arabidopsis thalia

DR WPI: 1996-443187/44.
 DR N-PSDB; AAT39041.
 XX Neisseria meningitidis antigen, highly conserved between different
 PT strains - useful for prodn. of antibodies for immunisation against,
 PT or diagnosis of, N. meningitidis infection
 XX
 PS Claim 7; Fig 9; 117pp; English.
 CC A proteinase K resistant surface protein has been isolated
 CC from 4 strains of N. meningitidis (AAT39039 to AAT39042). The isolated
 CC 22 kD antigen, antigenic fragments of antibodies can be used
 CC in a vaccine for the prevention of infection by N. meningitidis or
 CC by N. gonorrhoeae in humans. The antibodies may also be used
 CC diagnostically to detect N. meningitidis infection. The antigen
 CC may also be used to detect antibodies specific to N. meningitidis
 CC antigen.
 CC DNA sequences encoding the antigen, or their fragments, can be used
 CC as probes for the detection of pathogenic Neisseria bacteria.
 CC
 XX Sequence 174 AA:
 SO
 Query Match 100.0%; Score 868; DB 17; Length 174;
 Best Local Similarity 100.0%; Pred. No. 5.8e-85;
 Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 MKKALATLIALALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 DB 1 MKKALATLIALALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 OY 61 FAVDYTRKKNKAPSTDFKLYSIGASAIYDFPTQSPVRYLCAKRLSLNRAVDLGSDSF 120
 DB 61 FAVDYTRKKNKAPSTDFKLYSIGASAIYDFPTQSPVRYLCAKRLSLNRAVDLGSDSF 120
 OY 121 SQTSTGLGVLGVSVAVTPEVDLDAGYRNYIGKVTYKNNVRSGLSAGVRYKF 174
 DB 121 SQTSTGLGVLGVSVAVTPEVDLDAGYRNYIGKVTYKNNVRSGLSAGVRYKF 174

RESULT 2
 AAW04891
 ID AAW04891 standard; Protein; 174 AA.
 XX
 AC AAW04891;
 XX
 DT 22-DEC-1996 (first entry)
 XX
 DE Proteinase K resistant N. meningitidis 22 kD surface protein.
 XX
 KW Proteinase K resistant; Neisseria meningitidis;
 KW Neisseria gonorrhoeae; antibody; detection; probe; surface protein.
 XX
 OS Neisseria meningitidis strain 608B.
 XX
 FH Key Location/Qualifiers
 FH Peptide 1..19
 FT /label= sig_peptide
 FT Protein 20..174
 FT /label= mat_protein
 FT
 XX W09629412-A1.
 PN
 XX 26-SEP-1996.
 PD
 XX 15-MAR-1996; 96WO-CA00157.
 PF
 XX 04-AUG-1995; 95US-0001983.
 PR 17-MAR-1995; 95US-0406362.
 XX
 PA (IAFB-) IAF BIO VAC INC.
 XX
 PI Brodeur BR, Hamel J, Martin D, Rioux C;
 XX

DR WPI: 1996-443187/44.
 DR N-PSDB; AAT39039.
 XX Neisseria meningitidis antigen, highly conserved between different
 PT strains - useful for prodn. of antibodies for immunisation against,
 PT or diagnosis of, N. meningitidis infection
 XX
 PS Claim 7; Fig 1; 117pp; English.
 CC A proteinase K resistant surface protein has been isolated
 CC from 4 strains of N. meningitidis (AAT39039 to AAT39042). The isolated
 CC 22 kD antigen, antigenic fragments of antibodies can be used
 CC in a vaccine for the prevention of infection by N. meningitidis or
 CC by N. gonorrhoeae in humans. The antibodies may also be used
 CC diagnostically to detect N. meningitidis infection. The antigen
 CC may also be used to detect antibodies specific to N. meningitidis
 CC antigen.
 CC DNA sequences encoding the antigen, or their fragments, can be used
 CC as probes for the detection of pathogenic Neisseria bacteria.
 CC
 XX Sequence 174 AA:
 SO
 Query Match 98.4%; Score 854; DB 17; Length 174;
 Best Local Similarity 98.3%; Pred. No. 1.8e-83;
 Matches 171; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 OY 1 MKKALATLIALALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 DB 1 MKKALATLIALALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 OY 61 FAVDYTRKKNKAPSTDFKLYSIGASAIYDFPTQSPVRYLCAKRLSLNRAVDLGSDSF 120
 DB 61 FAVDYTRKKNKAPSTDFKLYSIGASAIYDFPTQSPVRYLCAKRLSLNRAVDLGSDSF 120
 OY 121 SQTSTGLGVLGVSVAVTPEVDLDAGYRNYIGKVTYKNNVRSGLSAGVRYKF 174
 DB 121 SQTSTGLGVLGVSVAVTPEVDLDAGYRNYIGKVTYKNNVRSGLSAGVRYKF 174

RESULT 3
 AAW04892
 ID AAW04892 standard; Protein; 175 AA.
 XX
 AC AAW04892;
 XX
 DT 22-DEC-1996 (first entry)
 XX
 DE Proteinase K resistant N. meningitidis 22 kD surface protein.
 XX
 KW Proteinase K resistant; Neisseria meningitidis;
 KW Neisseria gonorrhoeae; antibody; detection; probe; surface protein.
 XX
 OS Neisseria meningitidis strain MCH88.
 XX
 FH Key Location/Qualifiers
 FH Peptide 1..19
 FT /label= sig_peptide
 FT Protein 20..175
 FT /label= mat_protein
 FT
 XX W09629412-A1.
 PN
 XX 26-SEP-1996.
 PD
 XX 15-MAR-1996; 96WO-CA00157.
 PF
 XX 04-AUG-1995; 95US-0001983.
 PR 17-MAR-1995; 95US-0406362.
 XX
 PA (IAFB-) IAF BIO VAC INC.
 XX
 PI Brodeur BR, Hamel J, Martin D, Rioux C;
 XX

DR WPI: 1996-443187/44.
 DR N-PSDB; AAT39040.
 XX
 PT Neisseria meningitidis antigen, highly conserved between different
 PT strains - useful for prodn. of antibodies for immunisation against,
 PT or diagnosis of, N. meningitidis infection
 XX
 PS Claim 7; Fig 8; 117pp; English.
 CC
 CC A protease K resistant surface protein has been isolated
 CC from 4 strains of N. meningitidis (AAT39039 to AAT39042). The isolated
 CC 22 kD antigen, antigenic fragments of antibodies can be used
 CC in a vaccine for the prevention of infection by N. meningitidis or
 CC by N. gonorrhoeae in humans. The antibodies may also be used
 CC diagnostically to detect N. meningitidis infection. The antigen
 CC may also be used to detect antibodies specific to N. meningitidis
 CC antigen.
 CC DNA sequences encoding the antigen, or their fragments, can be used
 CC as probes for the detection of pathogenic Neisseria bacteria.
 CC
 XX Sequence 175 AA;
 SQ
 Query Match 96.6%; Score 838.5; DB 17; Length 175;
 Best Local Similarity 97.1%; Pred. No. 8.5e-82;
 Matches 170; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
 QY 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 DB 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 QY 61 FAVDYTRYKKNK-APSDFKLYSIGASAIYDPTQSPVKRYLGLARLSLNKASVDLGGSDS 119
 DB 61 FAVDYTRYKKNKQVPSDFKLYSIGASAIYDPTQSPVKRYLGLARLSLNKASVDLGGSDS 120
 QY 120 FSGTSTGLVAGSYAVTPNVDLDAGYRYNYIGKNTVKNVNSGELSAGYRVKF 174
 DB 121 FSGTSTGLVAGSYAVTPNVDLDAGYRYNYIGKNTVKNVNSGELSAGYRVKF 175
 RESULT 4
 AAM04894
 ID AAM04894 standard; Protein; 174 AA.
 XX
 AC AAM04894;
 XX
 DT 22-DEC-1996 (first entry)
 XX
 DE Protease K resistant N. meningitidis 22 kD surface protein.
 XX
 KW Protease K resistant; Neisseria meningitidis;
 KW Neisseria gonorrhoeae; antibody; detection; probe; surface protein;
 XX
 OS Neisseria meningitidis strain b2.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT /label= sig_peptide
 FT Protein 20..174
 FT /label= mat_protein
 PN W09629412-A1.
 PD 26-SEP-1996.
 PF 15-MAR-1996; 96WO-CA00157.
 PR 04-AUG-1995; 95US-0001983.
 PR 17-MAR-1995; 95US-0406362.
 PA (IAFB-) IAF BIO VAC INC.
 PI Brodeur BR, Hamel J, Martin D, Rioux C;
 XX

DR WPI: 1996-443187/44.
 DR N-PSDB; AAT39042.
 XX
 PT Neisseria meningitidis antigen, highly conserved between different
 PT strains - useful for prodn. of antibodies for immunisation against,
 PT or diagnosis of, N. meningitidis infection
 XX
 PS Claim 7; Fig 10; 117pp; English.
 CC
 CC A protease K resistant surface protein has been isolated
 CC from 4 strains of N. meningitidis (AAT39039 to AAT39042). The isolated
 CC 22 kD antigen, antigenic fragments of antibodies can be used
 CC in a vaccine for the prevention of infection by N. meningitidis or
 CC by N. gonorrhoeae in humans. The antibodies may also be used
 CC diagnostically to detect N. meningitidis infection. The antigen
 CC may also be used to detect antibodies specific to N. meningitidis
 CC antigen.
 CC DNA sequences encoding the antigen, or their fragments, can be used
 CC as probes for the detection of pathogenic Neisseria bacteria.
 CC
 XX Sequence 174 AA;
 SQ
 Query Match 96.1%; Score 834; DB 17; Length 174;
 Best Local Similarity 95.4%; Pred. No. 2.6e-81;
 Matches 166; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
 QY 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 DB 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 QY 61 FAVDYTRYKKNKAPSPDFKLYSIGASAIYDPTQSPVKRYLGLARLSLNKASVDLGGSDS 120
 DB 61 FAVDYTRYKKNKAPSPDFKLYSIGASAIYDPTQSPVKRYLGLARLSLNKASVDLGGSDS 120
 QY 121 SGTSTGLVAGSYAVTPNVDLDAGYRYNYIGKNTVKNVNSGELSAGYRVKF 174
 DB 121 SKTSAGLVAGSYAVTPNVDLDAGYRYNYIGKNTVKNVNSGELSAGYRVKF 174
 RESULT 5
 AAB19895
 ID AAB19895 standard; Protein; 155 AA.
 XX
 AC AAB19895;
 XX
 DT 19-MAR-2001 (first entry)
 XX
 DE Neisseria meningitidis Nspa protein.
 XX
 KW Nspa; infection; diagnosis; therapy; vaccine; meningococcal B.
 KW Neisseria meningitidis.
 XX
 OS Neisseria meningitidis.
 XX
 FH Key Location/Qualifiers
 FT Region 6..17
 FT /note= "transmembrane beta-strand"
 FT Region 18..26
 FT /note= "surface-exposed connecting loop"
 FT Region 27..37
 FT /note= "transmembrane beta-strand"
 FT Region 40..50
 FT /note= "transmembrane beta-strand"
 FT Region 51..62
 FT /note= "surface-exposed connecting loop"
 FT Region 63..74
 FT /note= "transmembrane beta-strand"
 FT Region 78..88
 FT /note= "transmembrane beta-strand"
 FT Region 89..104
 FT /note= "surface-exposed connecting loop"
 FT Region 105..114
 FT /note= "transmembrane beta-strand"
 FT Region 118..130

```

FT      /note="Transmembrane beta-strand"
FT      131..145
FT      /note="surface-exposed connecting loop"
FT      146..155
FT      Region
FT      /note="transmembrane beta-strand"
PN      WO200071725-A2.
XX
XX      30-NOV-2000.
XX
XX      19-MAY-2000; 2000WO-IB00828.
XX
XX      19-MAY-1999; 99GB-0011692.
XX      19-AUG-1999; 99GB-0019705.
XX      09-MAR-2000; 2000GB-0005730.
XX
XX      (CHIR-) CHIRON SPA.
XX
XX      Giuliani MM, Pizzi M, Rappuoli R;
XX      WPI; 2001-025167/03.
XX
XX      Novel composition comprising first and second biological molecules from
XX      a Neisseria bacterium, useful as vaccines or immunogenic compositions
XX      for treating Neisseria infections
XX
XX      Example 12; Fig 32; 126pp; English.
XX
XX      The present sequence is that of the Neisseria meningitidis Nspa
XX      protein, which contains 8 transmembrane beta strands and 4
XX      surface-exposed connected loops. Recombinant Nspa is being
XX      developed as a vaccine for the prevention of meningococcal
XX      disease caused by all serotypes. The invention provides
XX      combination compositions comprising: (i) 2 or more Neisseria
XX      proteins, (ii) 2 or more different Neisseria nucleic acids; or
XX      (iii) mixtures of 1 or more Neisseria protein and 1 or more
XX      Neisseria nucleic acid. The proteins and nucleic acids are
XX      preferably from different Neisseria spp., especially Neisseria
XX      meningitidis and Neisseria gonorrhoeae, but may be from the same
XX      species. A claimed composition includes the Nspa protein,
XX      CC preferably in mature form. The compositions are used e.g. as
XX      immunogenic compositions, vaccines or diagnostic reagents. They
XX      are used to treat or prevent Neisseria infection, to detect the
XX      presence of Neisseria bacteria or of antibodies raised against
XX      Neisseria bacteria, and/or as reagents which can raise antibodies
XX      against Neisseria bacteria.
XX
XX      Sequence 155 AA:
XX
XX      Query Match 88.8%; Score 771; DB 22; Length 155;
XX      Best Local Similarity 98.1%; Pred. No. 1.2e-74;
XX      Matches 152; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX      20 EGASGFVQADAAHAKASSLSGSAKGFSPRISAGYRINDLRFADVDTYRKNYKAPSTDK 79
XX      |||||
XX      DB 1 EGASGFVQADAAHAKASSLSGSAKGFSPRISAGYRINDLRFADVDTYRKNYKAPSTDK 60
XX
XX      QY 80 LYSIGASAIYDFDTQSPVRYKYLGAARLSLNKASVLDGSDSFQSTSTGLGVAGSYAVVP 139
XX      |||||
XX      DB 61 LYSIGASAIYDFDTQSPVRYKYLGAARLSLNKASVLDGSDSFQSTSTGLGVAGSYAVVP 120
XX
XX      QY 140 NVLDAGYRNYTGKYNVYKANSVGLSAGVRYKF 174
XX      |||||
XX      DB 121 NVLDAGYRNYTGKYNVYKANSVGLSAGVRYKF 155
XX
XX      RESULT 6
XX      AAR73911
XX      ID AAR73911 standard; protein; 170 AA.
XX      AC AAR73911;
XX      XX
XX      DT 05-DEC-1995 (first entry)

```

```

XX      XX
XX      DE Neisseria meningitidis opacity related protein POPM3.
XX      XX
XX      KW Neisseria meningitidis; opacity related protein POPM3; vaccine;
XX      KW meningitis related homologous antigenic sequence; MRHAS; RV-1;
XX      KW immunosassay; diagnosis; treatment; prophylactic; bacterial;
XX      KW viral.
XX      XX
XX      OS Neisseria meningitidis.
XX      XX
XX      PN WO9509232-A.
XX      XX
XX      PD 06-APR-1995.
XX      XX
XX      PF 28-SEP-1994; 94WO-CA00516.
XX      XX
XX      PR 28-SEP-1993; 93US-0127499.
XX      XX
XX      PA (SHAR/) SHARMA L R.
XX      PA (VALS/) VAN ALSTYNE D.
XX      XX
XX      PI Sharma LR, Van Alstyne D;
XX      XX
XX      DR WPI; 1995-147431/19.
XX      XX
XX      PT New peptide(s) and corresp. antibodies for the treatment of
XX      PT meningitis - the peptide(s) corresp. to homologous antigenic
XX      PT sites on bacterial and viral agents and on chemokine(s), used for
XX      PT detecting and preventing meningitis
XX      XX
XX      PS Claim 47; Fig 5/10; 98pp; English.
XX      XX
XX      CC AAR73911 is the Neisseria meningitidis opacity related protein POPM3.
XX      CC It contains the meningitis related antigenic sequences (MRHAS)
XX      CC claimed in AAR73889 and AAR73901, which are recognised by a monoclonal
XX      CC antibody from the hybridoma Rubella virus (RV)-1. The claimed MRHAS
XX      CC peptides may be used in immunosassays to diagnose the presence of
XX      CC bacterial and/or viral meningitis agents in a sample, or in
XX      CC prophylactic and therapeutic meningitis treatments. The peptides may
XX      CC also be used as vaccines against meningitis.
XX      CC NB: identified by matching corresponding MRHAS peptides.
XX      XX
XX      SO Sequence 170 AA:
XX
XX      Query Match 15.6%; Score 135; DB 16; Length 170;
XX      Best Local Similarity 26.3%; Pred. No. 1.8e-06;
XX      Matches 41; Conservative 20; Mismatches 47; Indels 48; Gaps 4;
XX
XX      QY 6 ATLINALPAAALAEASGFVQADAAH-----AKASSLSG-----AKG 45
XX      ::::: ||: | :|: ||||| :|: |
XX      DB 15 SSLFSSAAQAASEDRSPYYVQADLAYAERITHDYPOATGANNSTVSDFRNIRAS 74
XX
XX      QY 46 FSPRISAGYRINDLRFADVDTYRKNY-----RAPSTDFK 79
XX      ||: | | | | | :|: |
XX      DB 75 IHPKSVGTDDGGMRIADYASIRKMNKKSIVTKELKHNKKDLKTENDENGTFHA 134
XX
XX      QY 80 LYSIGASAIYDFDTQSPVRYKYLGAARLSLN--RASVD 113
XX      ||: ||||| :|: ||||| :|: |
XX      DB 135 ASSIGLSAIYDFKLGKRFKPYIGARVAVAGVHRHSID 170
XX
XX      RESULT 7
XX      AAM04912
XX      ID AAM04912 standard; protein; 25 AA.
XX      XX
XX      AC AAM04912;
XX      XX
XX      DT 22-DEC-1996 (first entry)
XX      XX
XX      DE N. meningitidis 608B peptide CS-857.
XX      XX
XX      KW Proteinase K resistant; Neisseria meningitidis; epitope; mapping;
XX      KW Neisseria gonorrhoeae; antibody; detection; probe; surface protein.

```



```

XX OS Synthetic.
XX PF WO629412-A1.
XX PN 26-SEP-1996.
XX PD 15-MAR-1996; 96WO-CA00157.
XX PF 04-AUG-1995; 95US-0001983.
XX PR 17-MAR-1995; 95US-0406362.
XX PA (IAFB-) IAF BIO VAC INC.
XX PI Brodeur BR, Hamel J, Martin D, Rioux C;
XX WPI: 1996-443187/44.
XX DR
XX PT Neisseria meningitidis antigen, highly conserved between different
XX PT strains - useful for prodn. of antibodies for immunisation against,
XX PT or diagnosis of, N. meningitidis infection
XX PS Claim 24; Page 84; 117pp; English.
XX CC Example 9 describes the epitope mapping of the 22 kD
XX CC N. meningitidis protein. Identification was accomplished
XX CC using 18 overlapping synthetic peptides (AAW04895 to AAW04912).
XX SQ Sequence 25 AA;
XX Query Match 15.3%; Score 133; DB 17; Length 25;
XX Best Local Similarity 100.0%; Pred. No. 2.3e-07;
XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 61 FAVDYTRYKNYKAPSTDFFLYSIGA 85
DB 1 FAVDYTRYKNYKAPSTDFFLYSIGA 25
RESULT 8
AAB47447
ID AAB47447 standard; Protein; 353 AA.
XX AC AAB47447;
XX DT 31-OCT-2001 (first entry)
XX DE MOMP P5.
XX KW surface exposed loop: major outer membrane protein P5; MOMP P5;
XX KW non-typeable H. influenzae; nH1; LBI(f) peptide; B cell epitope;
XX KW otitis media; sinusitis; conjunctivitis;
XX KW lower respiratory tract infection.
XX OS Haemophilus influenzae.
XX FH Key
XX FT 38..57 Location/Qualifiers
XX FT /label= Loop 1
XX FT /note= "Extracellular domain"
XX FT 89..100
XX FT /label= Loop 2
XX FT /note= "Extracellular domain"
XX FT 136..150
XX FT /label= Loop 3
XX FT /note= "Extracellular domain"
XX FT 181..204
XX FT /label= Loop 4
XX FT /note= "Extracellular domain"
XX PN WO200161013-A1.
XX PD 23-AUG-2001.

```

```

XX XX 13-FEB-2001; 2001WO-EP01556.
XX XX 15-FEB-2000; 2000GB-0003502.
XX XX (SMIK ) SMITHLINE BEECHAM BIOLOGICALS.
XX XX Berthet FJ, Denoel P, Poolman J, Thonnard J;
XX XX WPI: 2001-522599/57.
XX DR
XX PT Recombinant bacterial outer membrane protein where one or more
XX PT surface-exposed loops are modified is useful as a vaccine to prevent or
XX PT treat Haemophilus influenzae infection or associated disease, e.g.,
XX PT otitis media and conjunctivitis -
XX PS Disclosure; Fig 1; 29pp; English.
XX CC This sequence represents the major outer membrane protein P5 of
XX CC non-typeable H. influenzae. One or more surface exposed loops of this
XX CC protein may be replaced with a modified peptide of the invention. Each
XX CC of these peptides contain an LBI(f) peptide which is a 19 amino acid
XX CC peptide derived from the sequence of MOMP P5 from strain nH1128,
XX CC representing amino acids Arg117 to Gly135. This peptide represents the
XX CC third exposed loop of P5 and is a potential B cell epitope. The loops
XX CC of the invention are modified in terms of being in a non-native
XX CC environment in the recombinant outer membrane protein. The modified
XX CC MOMP P5 may be used to induce an immune response in a mammal to
XX CC prevent or treat Haemophilus influenzae infection or associated
XX CC disease, e.g., otitis media, sinusitis, conjunctivitis, or lower
XX CC respiratory tract infection.
XX SQ Sequence 353 AA;
XX Query Match 11.4%; Score 99; DB 22; Length 353;
XX Best Local Similarity 24.8%; Pred. No. 0.035;
XX Matches 53; Conservative 29; Mismatches 92; Indels 40; Gaps 9;
QY 1 MKKALATLIALALPAAALAEAA--SGFYVQADAAHAKASSSGS-----AKGTS 47
DB 1 MKKTAIALVVAAGLAASVAQAAPQENTFYAGVRAAGQASFDGLRALAREKVGYHRRNSFT 60
QY 48 PRISAGYRI--NDLRPAV-----DYTRYKNYKAPSTDFFLYSIGA--SAIYDFDQSPV 97
DB 61 YGVFGGYQILNQNMLGLAVEIDYDFGRAGKREKGVVHTNHGTHLSKGSYEVLEGI 120
QY 98 KPYLGARLSINRASVDGSDSFSQSTG-----LGVLA-GVSYAVYPPNDLDAGY-- 147
DB 121 DYGKAGAVALRSQYKLYNENSTLKKLGGHHRARASGLPFAVGAEYAVLPETLAVRLEYOM 180
QY 148 -----RYNYIGKVTYKNVRS--GELSAGVRYKE 174
DB 181 LTRVGKRYRPQDKPRTALNPNWIGSINAGISYRF 214
RESULT 9
AAU34556
ID AAU34556 standard; Protein; 212 AA.
XX AC AAU34556;
XX DT 14-FEB-2002 (first entry)
XX DE E. coli cellular proliferation protein #137.
XX KW Antisense; prokaryotic cellular proliferation protein;
XX KW antibiotic; antibacterial; drug design.
XX OS Escherichia coli.
XX PN WO200170955-A2.
XX PD 27-SEP-2001.

```

XX 21-MAR-2001; 2001WO-US09180.
 PF 21-MAR-2000; 2000US-191078P.
 XX 23-MAY-2000; 2000US-206848P.
 PR 26-MAY-2000; 2000US-207727P.
 PR 23-OCT-2000; 2000US-242578P.
 PR 27-NOV-2000; 2000US-253625P.
 PR 22-DEC-2000; 2000US-257931P.
 PR 16-FEB-2001; 2001US-269308P.
 XX (ELIT-) ELITRA PHARM INC.
 PA Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
 PI Yamamoto RT, Xu HH;
 XX WPI; 2001-611495/70.
 DR N-PSDB; AAS52415.
 XX New polynucleotides for the identification and development of
 PT antibiotics, comprise sequences of antisense nucleic acids -
 PS Example 3; Seq ID No 10149; 511pp; English.
 XX The invention relates to antisense inhibitors of genes essential to
 CC prokaryotic cellular proliferation, their use in identifying the
 CC genes, their use in the discovery of novel antibiotics, the essential
 CC genes themselves and the encoded proteins. The prokaryotes used are
 CC *Escherichia coli*, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella*
 CC *pneumoniae*, *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The
 CC invention is also useful for the identification of potential new targets
 CC for antibiotic development. The antisense nucleic acids can also be used
 CC to identify proteins used in proliferation, to express these proteins,
 CC and to obtain antibodies capable of binding to the expressed proteins.
 CC The proteins can be used to screen compounds in rational drug discovery
 CC programmes. The antisense nucleic acid sequence is also useful to screen
 CC for homologous nucleic acids which are required for cell proliferation in
 CC a wide variety of organisms. The present sequence represents an
 CC essential prokaryotic cellular proliferation protein.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 CC
 XX Sequence 212 AA:
 SQ
 Query Match 11.1%; Score 96; DB 22; Length 212;
 Best Local Similarity 23.7%; Pred. No. 0.037;
 Matches 53; Conservative 28; Mismatches 77; Indels 66; Gaps 11;
 QY 1 MKKALATLIALA--LPPAALAEAGAGFYVQADAAHAK---ASSLSGSAKFSPRISAGY 54
 DB 1 MKKLTVAALAVTTLLSGSAFAHEAGFEFMRGSAVPTREGAGTGLSGFSV----- 54
 QY 55 RINDLRAVDYTRYKNKA-----PSTDFKLISIGASAIYDF----- 91
 DB 55 -TNNTOGLGTF-----YMAIDNIGVELLAATPFR-HKGTGATGDIATVHLLPPTLMAQW 108
 QY 92 ---DTQSPKPYLYGARLS-----LNRAVDLGGSDSFSQSTGTGLAGVAGSVATPN 140
 DB 109 YFGGSAKSPRYVAGINNTFFDNDGKFKAGLSDLKMSWGAAGGVGVYLIIRD 168
 QY 141 -----VDLAGYRYNYIGKYNVKNVRSGE---LSAGVR 171
 DB 169 WLVNMSVYMDIDTITANYK-LGGAQCHDSVRLDPWFVFMFSGAYR 211
 RESULT 10
 ID AAU38252
 XX AAU38252 standard; Protein; 257 AA.
 AC
 XX

DT 14-FEB-2002 (first entry)
 XX
 DE *Salmonella typhi* cellular proliferation protein #143.
 XX
 KW Antisense: prokaryotic cellular proliferation protein;
 RM antibiotic; antibacterial; drug design.
 XX
 OS *Salmonella typhi*.
 XX
 PN WO200170955-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 21-MAR-2001; 2001WO-US09180.
 XX
 PR 21-MAR-2000; 2000US-191078P.
 PR 23-MAY-2000; 2000US-206848P.
 PR 26-MAY-2000; 2000US-207727P.
 PR 23-OCT-2000; 2000US-242578P.
 PR 27-NOV-2000; 2000US-253625P.
 PR 22-DEC-2000; 2000US-257931P.
 PR 16-FEB-2001; 2001US-269308P.
 XX (ELIT-) ELITRA PHARM INC.
 PA Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
 PI Yamamoto RT, Xu HH;
 XX WPI; 2001-611495/70.
 DR N-PSDB; AAS56111.
 XX New polynucleotides for the identification and development of
 PT antibiotics, comprise sequences of antisense nucleic acids -
 PS Example 3; Seq ID No 13845; 511pp; English.
 XX The invention relates to antisense inhibitors of genes essential to
 CC prokaryotic cellular proliferation, their use in identifying the
 CC genes, their use in the discovery of novel antibiotics, the essential
 CC genes themselves and the encoded proteins. The prokaryotes used are
 CC *Escherichia coli*, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella*
 CC *pneumoniae*, *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The
 CC invention is also useful for the identification of potential new targets
 CC for antibiotic development. The antisense nucleic acids can also be used
 CC to identify proteins used in proliferation, to express these proteins,
 CC and to obtain antibodies capable of binding to the expressed proteins.
 CC The proteins can be used to screen compounds in rational drug discovery
 CC programmes. The antisense nucleic acid sequence is also useful to screen
 CC for homologous nucleic acids which are required for cell proliferation in
 CC a wide variety of organisms. The present sequence represents an
 CC essential prokaryotic cellular proliferation protein.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 CC
 XX Sequence 257 AA:
 SQ
 Query Match 10.6%; Score 92; DB 22; Length 257;
 Best Local Similarity 23.7%; Pred. No. 0.13;
 Matches 53; Conservative 28; Mismatches 77; Indels 66; Gaps 12;
 QY 1 MKKALATLIALA--LPPAALAEAGAGFYVQADAAHAK---ASSLSGSAKFSPRISAGY 54
 DB 27 MKKFTVAALAVTTLLSGSAFAHEAGFEFMRGSAVPTREGAGTGLHNGFD--VS--- 81
 QY 55 RINDLRAVDYTRYKNKA-----PSTDFKLISIGASAIYDF----- 91
 DB 82 ---NNTQGLGTF-----YMAIDNIGVELLAATPFR-HKGTGATGDIATVHLLPPTLMAQW 134
 QY 92 ---DTQSPKPYLYGARLS-----LNRAVDLGGSDSFSQSTGTGLAGVAGSVATPN 140
 DB 135 YFGDSSSKVRYVGVVNTFFDNDGKFKTGLSLSPKDSXGAGGVGVYLIIRD 194

Peyers patch M-cells. The system is not prone to degradation in the gut or early release of histamine.

microbial host / pref. E.coli, Sporodoptera frugiperda or a mucosal

CC pathogen. Fimbria protein (FP) produced by this process is claimed.
CC The FP protein migrates in polyacrylamide gels to a posn. equiv. to
CC a mol. wt. of 25.5 kD or 37.5 kD.

XX Sequence 359 AA;

Query Match 10.5%; Score 91; DB 16; Length 359;

Best Local Similarity 23.68; Pred. No. 0.26; Mismatches 82; Indels 64; Gaps 12;

Matches 54; Conservative 29;

1 MKKATATLIALPAALAEAGA---SGFYVADAA---HAKASSSLGSAKSPRISAG 53

1 MKKTALVAVGLAAASVQAAPQENTFYAGVKAGGSGFHGNNAGIKKGLSS- NYG 59

54 YRINDLRAVDYTRYKNTKAPSTDFKLYSIGASA---IYDF-----DTGSPVAPYL--G 102

60 YRRNFTFYGV---FGGYOILNOD---NFGIAELGYHDEGRAKLRAGKPKAKHTNHG 111

103 ARLSINRASVDLGSDFSGTSTGL-----GVTLA-GVS 134

112 AYLSLKSGTEVLGDIDYGVKAGVALVRSYDFEDANGTRDHKKGRHTARASGLFAVGA 171

135 YAVTPNVDIDAGY-----RYNYIGKVTYKKNRS--GELSAGYRKE 174

172 YAVLELAVRLEYQWLTFRGKXRPQDKPNTAINTNPMWIGINAGISYRF 220

RESULT 13

AAG52873
ID AAG52873 standard; Protein; 339 AA.

AC AAG52873;

DT 18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 67258.

KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

OS Arabidopsis thaliana.

PN EP103405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

XX 05-MAR-1999; 99US-0123180.

XX 09-MAR-1999; 99US-0123548.

XX 23-MAR-1999; 99US-0125788.

XX 25-MAR-1999; 99US-0126264.

XX 29-MAR-1999; 99US-0126785.

XX 01-APR-1999; 99US-0127462.

XX 06-APR-1999; 99US-0128234.

XX 16-APR-1999; 99US-0128714.

XX 19-APR-1999; 99US-0129845.

XX 21-APR-1999; 99US-0130077.

XX 23-APR-1999; 99US-0130449.

XX 23-APR-1999; 99US-0130510.

XX 28-APR-1999; 99US-0130891.

XX 30-APR-1999; 99US-0132048.

XX 30-APR-1999; 99US-0132407.

XX 04-MAY-1999; 99US-0132484.

XX 05-MAY-1999; 99US-0132485.

XX 06-MAY-1999; 99US-0132486.

XX 07-MAY-1999; 99US-0132487.

XX 11-MAY-1999; 99US-0132863.

XX 14-MAY-1999; 99US-0134256.

XX 14-MAY-1999; 99US-0134218.

PR 14-MAY-1999; 99US-0134219.

PR 14-MAY-1999; 99US-0134221.

PR 14-MAY-1999; 99US-0134370.

PR 18-MAY-1999; 99US-0134768.

PR 19-MAY-1999; 99US-0134941.

PR 20-MAY-1999; 99US-0135124.

PR 21-MAY-1999; 99US-0135353.

PR 24-MAY-1999; 99US-0135629.

PR 25-MAY-1999; 99US-0136021.

PR 27-MAY-1999; 99US-0136392.

PR 28-MAY-1999; 99US-0136782.

PR 01-JUN-1999; 99US-0137222.

PR 03-JUN-1999; 99US-0137528.

PR 04-JUN-1999; 99US-0137502.

PR 07-JUN-1999; 99US-0137724.

PR 08-JUN-1999; 99US-0138094.

PR 10-JUN-1999; 99US-0138540.

PR 14-JUN-1999; 99US-0139119.

PR 16-JUN-1999; 99US-0139452.

PR 17-JUN-1999; 99US-0139492.

PR 18-JUN-1999; 99US-0139454.

PR 18-JUN-1999; 99US-0139455.

PR 18-JUN-1999; 99US-0139456.

PR 18-JUN-1999; 99US-0139457.

PR 18-JUN-1999; 99US-0139458.

PR 18-JUN-1999; 99US-0139459.

PR 18-JUN-1999; 99US-0139460.

PR 18-JUN-1999; 99US-0139461.

PR 18-JUN-1999; 99US-0139462.

PR 18-JUN-1999; 99US-0139463.

PR 18-JUN-1999; 99US-0139750.

PR 18-JUN-1999; 99US-0139763.

PR 21-JUN-1999; 99US-0139817.

PR 22-JUN-1999; 99US-0139899.

PR 23-JUN-1999; 99US-0140353.

PR 23-JUN-1999; 99US-0140354.

PR 24-JUN-1999; 99US-0140695.

PR 28-JUN-1999; 99US-0140823.

PR 29-JUN-1999; 99US-0140991.

PR 30-JUN-1999; 99US-0141287.

PR 01-JUL-1999; 99US-0141842.

PR 01-JUL-1999; 99US-0142154.

PR 02-JUL-1999; 99US-0142390.

PR 06-JUL-1999; 99US-0142905.

PR 08-JUL-1999; 99US-0142920.

PR 09-JUL-1999; 99US-0142977.

PR 12-JUL-1999; 99US-0143562.

PR 13-JUL-1999; 99US-0143564.

PR 14-JUL-1999; 99US-0143624.

PR 15-JUL-1999; 99US-0144005.

PR 16-JUL-1999; 99US-0144085.

PR 16-JUL-1999; 99US-0144086.

PR 16-JUL-1999; 99US-0144325.

PR 19-JUL-1999; 99US-0144331.

PR 19-JUL-1999; 99US-0144332.

PR 19-JUL-1999; 99US-0144333.

PR 19-JUL-1999; 99US-0144334.

PR 19-JUL-1999; 99US-0144335.

PR 20-JUL-1999; 99US-0144352.

PR 20-JUL-1999; 99US-0144632.

PR 20-JUL-1999; 99US-0144884.

PR 21-JUL-1999; 99US-0144814.

PR 21-JUL-1999; 99US-0145086.

PR 21-JUL-1999; 99US-0145088.

PR 22-JUL-1999; 99US-0145085.

PR 22-JUL-1999; 99US-0145087.

PR 22-JUL-1999; 99US-0145089.

PR 22-JUL-1999; 99US-0145192.

PR 23-JUL-1999; 99US-0145145.

PR 23-JUL-1999; 99US-0145218.

PR 23-JUL-1999; 99US-0145224.

PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match	10.3%;	Score 89.5;	DB 21;	Length 339;
Best Local Similarity	27.7%;	Pred. NO. 0.35;		
Matches 39;	Conservative 20;	Mismatches 53;	Indels 29;	Gaps 8;

```

QY 39 SLGSAKF-----SPRISAGYRINDLRFANDY--TRYKNYKAPSTDEKLYSIGASAIY 89
    |   | |   | | : | : | | : | : | : | : | : | : |
Db 18 SFSASAKFIESKVESPNVK--YTENEIHSVYDYETIEVHVHEKTVNGCYQWIKPKPIVKY 75

```

```

90 DEFDQSPKRYLGLARSLNRASVDIGSDSFQSTSTGLAVLA---GVSYATPNVDDLAG 146
    ||| ||| | ||| | | | | | | | | | | | | | | | | | | | | | | | |
76 DFKIDIRV-PKLGVAL-----VGLGNGNSTLTA--GVIANKEGISWATKKDYQ---- 121

```

```
QY 147 YRNYIGKVNTVKNVRSGELS 167
      : || | : :: | | :
Db 122 -QANYFGSLTQASSIRVGSFN 141
```

RESULT 14
AAG09860
ID AAG09860 standard; Protein; 534 AA.
VY

DT	17-OCT-2000 (first entry)	XX	Arabidopsis thaliana protein fragment SEQ ID NO: 7956
DE			
XX			

KW hybridisation assay; genetic mapping; gene expression control; termination sequence.

OS *Arabidopsis thaliana*.

PN	EP1033405-A2.
XX	
PD	06-SEP-2000.

PF	25-FEB-2000;	2000EP-0301439.
XX		
PR	25-FEB-1999;	99US-0121825.
PR	05-MAR-1999;	99US-0123180.
PR	09-MAR-1999;	99US-0123388.
PR	23-MAR-1999;	99US-0125788.
PR	23-MAR-1999;	99US-0126264.
PR	29-MAR-1999;	99US-0126785.
PR	01-APR-1999;	99US-0127462.
PR	06-APR-1999;	99US-0128234.
PR	08-APR-1999;	99US-0128714.
PR	16-APR-1999;	99US-0129845.
PR	19-APR-1999;	99US-0130077.
PR	21-APR-1999;	99US-0130449.
PR	23-APR-1999;	99US-0130510.
PR	23-APR-1999;	99US-0130891.
PR	28-APR-1999;	99US-0131448.
PR	30-APR-1999;	99US-0132049.
PR	30-APR-1999;	99US-0132407.
PR	04-MAY-1999;	99US-0132484.
PR	05-MAY-1999;	99US-0132485.
PR	06-MAY-1999;	99US-0132486.
PR	06-MAY-1999;	99US-0132487.
PR	07-MAY-1999;	99US-0132863.
PR	11-MAY-1999;	99US-0134256.

PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 14-JUN-1999; 99US-0138847.
PR 16-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 29-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 02-JUL-1999; 99US-0142154.
PR 06-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 21-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 23-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.

PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 03-AUG-1999; 99US-0146389.
PR 04-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151338.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 08-OCT-1999; 99US-0158369.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.

PR 22-OCT-1999; 99US-0160989.
 PR 25-OCT-1999; 99US-0161404.
 PR 25-OCT-1999; 99US-0161405.
 PR 25-OCT-1999; 99US-0161406.
 PR 26-OCT-1999; 99US-0161359.
 PR 26-OCT-1999; 99US-0161360.
 PR 26-OCT-1999; 99US-0161361.
 PR 28-OCT-1999; 99US-0161920.
 PR 28-OCT-1999; 99US-0161992.
 PR 28-OCT-1999; 99US-0161993.
 PR 29-OCT-1999; 99US-0162142.

Query Match 10.3%; Score 89.5; DB 21; Length 534;
 Best Local Similarity 27.7%; Pred. No. 0.63;

Matches 39; Conservative 20; Mismatches 53; Indels 29; Gaps 8;

QY 39 SLGSAKGF-----SPRISAGYRINDLRPAVDY--TRYKNYKAPSDNFLYSIGASAIY 89
 DB 18 SFSKAKMIESFKVESDNVK--YTENEIHSYDEETTEVYHEKTVNGTYQMYKPKIVKY 75
 QY 90 DEDTQSPVKPYLGARLSLNRAVDLGGSDSFSTSTGLGYLA--GVSVAVTENVDDAG 146
 DB 76 DFKTDIVY-PLGVML-----VGLGNGNSTLTLA--GVIANKEGISMATKDKVQ----- 121
 QY 147 YRYNYIGKVTYKVRSGELS 167
 DB 122 -QANYFGLNQASSIRYGSFN 141

RESULT 15
 AAB44589

ID AAB44589 standard; Protein; 369 AA.

AC AAB44589;

DT 08-FEB-2001 (first entry)

DE Virulence gene protein #69.

XX Virulence gene; antibacterial; vaccine; bacterial infection;

KW septicemia; bronchopneumonia; rhinitis; wound infection.

XX Actinobacillus pleuropneumoniae.

PN WO200061724-A2.

PD 19-OCT-2000.

PF 06-APR-2000; 2000WO-US09218.

PR 09-APR-1999; 99US-0128689.

PR 10-SEP-1999; 99US-0153453.

XX (PHAA) PHARMACIA & UPJOHN INC.

PI Lowery DE, Fuller TE, Kennedy MJ;

DR WPI; 2000-647422/62.

DR N-PSDB; AAC79664.

PT Attenuated Pasteurellaceae bacteria comprising mutations in virulence
 genes, useful as a live attenuated vaccine against bacterial infections

XX Claim 39; Pages 308-309; 322pp; English.

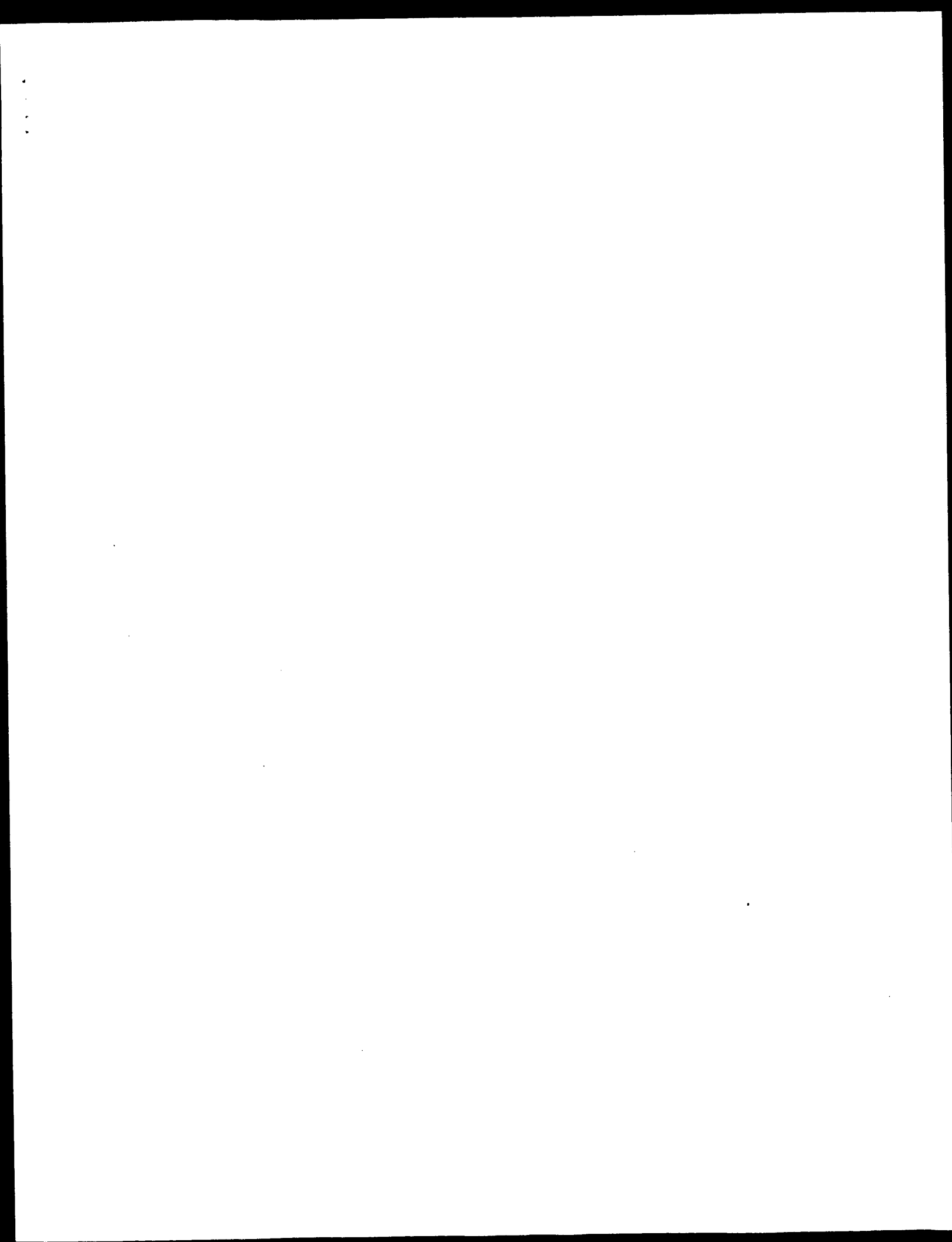
CC The family Pasteurellaceae encompasses several pathogens that infect a
 CC wide variety of animals. The present invention relates to virulence genes
 CC from Pasteurellaceae. The present sequence is a protein encoded by one
 CC such virulence gene. The virulence gene of the present invention may be
 CC mutated in order to produce an inactive gene. The inactive virulence gene
 CC may in turn be used to produce a vaccine, which is useful for treating
 CC bacterial infections such as septicemias, bronchopneumonias, rhinitis and

CC wound infections.
 XX Sequence 369 AA;

Query Match 10.3%; Score 89; DB 21; Length 369;
 Best Local Similarity 21.5%; Pred. No. 0.44;
 Matches 49; Conservative 36; Mismatches 85; Indels 58; Gaps 11;

QY 1 MKKALMTLIALALPAALAEGA--SGFYVQADAAHAKASSISGSAK--GFSPR----- 49
 DB 1 MKKSLVALAVLS--AAAVQAAPQONTFFYAGAKVGQSPFHGVDNLSGSHDRYNDKTRK 58
 QY 50 -----TSAGYRI--NDLRPAVD--TRYKNYKAPSTDRLKLSIGASAIY----- 89
 DB 59 YGINRNSVTYGVFGGTYQLNQNPFGLAELGYDYGRVGNVDEFRYVKSASHGINTALK 118
 QY 90 -DEDTQSPVKPYLGARLSLNRAVDLGGSDSFSTSTGLGYLA--GVSVAVTENVDDAG 141
 DB 119 PSYEVLPPDDVYGVKGIYAVVRNDYKKGAEENTNESTFKHKLKASTIIGAGVEITALP-- 176
 QY 142 DIDAGYRYNYIGKVTYK--VRSG-----ELSGYRVKF 174
 DB 177 ELAARVEYQYLNKAGNLKALVRSSTQDVDFQYAPDISHVYAGISYRF 224

Search completed: October 28, 2002, 16:00:39
 Job time : 25.7145 secs



GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 28, 2002, 15:58:54 ; Search time 9.48637 Seconds

(without alignments)
448.017 Million cell updates/sec

Title: US-09-684-883-6

Sequence: 1 MKKALATLIALPAALAE.....VNTKVNRSGLSGRVK 174

Scoring table: BLOSUM62

GAPOP 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/6C.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/6D.COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	868	100.0	174	4	US-08-913-362-6
2	854	98.4	174	4	US-08-913-362-2
3	847.5	97.6	175	4	US-08-913-362-30
4	838.5	96.6	175	4	US-08-913-362-4
5	834	96.1	174	4	US-08-913-362-8
6	135	15.6	170	1	US-08-127-499A-20
7	135	15.6	170	1	US-08-482-847-20
8	133	15.3	25	4	US-08-913-362-26
9	93	10.7	359	1	US-08-457-997B-2
10	93	10.7	359	3	US-08-467-722A-2
11	92	10.6	568	5	PCT-US95-13749-5
12	87	10.0	16	4	US-08-913-362-15
13	81.5	9.4	282	3	US-08-913-362-6
14	81.5	9.4	282	4	US-08-913-362-6
15	81	9.3	15	4	US-08-913-362-23
16	79.5	9.2	573	4	US-09-336-447A-3
17	79	9.1	15	4	US-08-913-362-18
18	79	9.1	207	2	US-08-381-881-6
19	79	9.1	207	4	US-09-281-221-6
20	79	9.1	610	4	US-09-336-447A-11
21	79	9.1	624	4	US-09-336-447A-7
22	79	9.1	889	4	US-09-336-447A-15
23	78	9.0	15	4	US-08-913-362-14
24	78	9.0	15	4	US-08-913-362-16
25	78	9.0	2123	4	US-08-968-685A-10
26	77.5	8.9	409	4	US-09-066-046-31
27	77.5	8.9	409	4	US-09-066-047-19

28	77	8.9	15	4	US-08-913-362-11	Sequence 11, Appl
29	77	8.9	15	4	US-08-913-362-13	Sequence 13, Appl
30	77	8.9	433	2	US-08-883-515-2	Sequence 2, Appl
31	76	8.8	15	4	US-08-913-362-17	Sequence 17, Appl
32	76	8.8	15	4	US-08-913-362-24	Sequence 24, Appl
33	75.5	8.7	286	1	US-08-382-184-3	Sequence 3, Appl
34	75.5	8.7	286	2	US-08-641-356-3	Sequence 3, Appl
35	75.5	8.7	286	4	US-09-132-528-4	Sequence 4, Appl
36	75.5	8.7	286	4	US-08-875-494-3	Sequence 4, Appl
37	75.5	8.7	286	4	US-08-875-494-3	Sequence 4, Appl
38	75.5	8.7	325	1	US-08-382-184-2	Sequence 2, Appl
39	75.5	8.7	325	2	US-08-641-356-2	Sequence 2, Appl
40	75.5	8.7	325	4	US-09-132-528-2	Sequence 2, Appl
41	75.5	8.7	325	4	US-08-875-494-2	Sequence 2, Appl
42	75.5	8.7	325	4	US-09-559-366-2	Sequence 2, Appl
43	75.5	8.7	325	4	US-09-559-366-3	Sequence 3, Appl
44	75.5	8.7	332	4	US-08-818-112-53	Sequence 53, Appl
45	75.5	8.7	332	4	US-08-818-112-53	Sequence 53, Appl

ALIGNMENTS

RESULT 1
US-08-913-362-6
; Sequence 6, Application US/08913362
; Patent No. 6287574
; GENERAL INFORMATION:
; APPLICANT: Brodeur, Bernard R
; APPLICANT: Martin, Denis
; APPLICANT: Hamel, Josée
; APPLICANT: Rioux, Clement
; TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
; TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/913,362
; FILING DATE: 13-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406,362
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/001,983
; FILING DATE: 04-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29, 768
; REFERENCE/DOCKET NUMBER: 047998/0128
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 174 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
; US-08-913-362-6
Query Match 100.0%; Score 868; DB 4; Length 174;

[illegible]

```

, RESULT 2
, US-08-913-362-2
, Sequence 2, Application US/08913362
, Patent No. 6287574
, GENERAL INFORMATION:
, APPLICANT: Brodeur, Bernard R
, APPLICANT: Martin, Denis
, APPLICANT: Hamel, Josee
, APPLICANT: Rioux, Clement
, TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
, TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
, NUMBER OF SEQUENCES: 30
, CORRESPONDENCE ADDRESS:
, ADDRESSEE: Foley & Lardner
, STREET: 3000 K Street, N.W., Suite 500
, CITY: Washington
, STATE: D.C.
, COUNTRY: USA
, ZIP: 20007-5109
, COMPUTER READABLE FORM:
, MEDIUM TYPE: Floppy disk
, COMPUTER: IBM PC compatible
, OPERATING SYSTEM: PC-DOS/MS-DOS
, SOFTWARE: Patentin Release #1.0, Version #1.30
, CURRENT APPLICATION DATA:
, APPLICATION NUMBER: US/08/913,362
, FILING DATE: 13-NOV-1997
, PRIOR APPLICATION DATA:
, APPLICATION NUMBER: US 08/406,362
, FILING DATE: 17-MAR-1995
, PRIOR APPLICATION DATA:
, APPLICATION NUMBER: US 60/001,983
, FILING DATE: 04-AUG-1995
, ATTORNEY/AGENT INFORMATION:
, NAME: Bent, Stephen A.
, REGISTRATION NUMBER: 29,768
, REFERENCE/DOCKET NUMBER: 047998/0128
, TELECOMMUNICATION INFORMATION:
, TELEPHONE: (202)672-5300
, TELEFAX: (202)672-5399
, TELEX: 904136
, INFORMATION FOR SEQ ID NO: 2:
, SEQUENCE CHARACTERISTICS:
, LENGTH: 174 amino acids
, TYPE: amino acid
, TOPOLOGY: linear
, MOLECULE TYPE: protein
,
, US-08-913-362-2

```

Query Match:	98.4%	Score 854;	DB 4;	Length 174;
Best Local Similarity:	98.3%	Pred. No. 2.3e-90;		
Matches 171;	Conservative	0;	Mismatches 3;	Indels 0;
				Gaps 0;
QY	1	MKKALATLTLALPAALAEAGASGFVYQADAAHAAASSLSAGSGFPRISAGYRINDUR	60	
Db	1	MKKALATLTLALPAALAEAGASGFVYQADAAHAAASSLSAGSGFPRISAGYRINDUR	60	

```

1      RESULT 3
2      US-08-913-362-30
3      : Sequence 30, Application US/08913362
4      : Patent No. 6287574
5      :
6      : GENERAL INFORMATION:
7      :
8      : APPLICANT: Brodeur, Bernard R
9      :
10     : APPLICANT: Martin, Denis
11     :
12     : APPLICANT: Hamel, Josée
13     :
14     : APPLICANT: Rioux, Clement
15     :
16     : TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
17     : TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
18     :
19     : NUMBER OF SEQUENCES: 30
20     :
21     : CORRESPONDENCE ADDRESS:
22     :
23     : ADDRESSEE: Foley & Lardner
24     :
25     : STREET: 3000 K Street, N.W., Suite 500
26     :
27     : CITY: Washington
28     :
29     : STATE: D.C.
30     :
31     : COUNTRY: USA
32     :
33     : ZIP: 20007-5109
34     :
35     : COMPUTER READABLE FORM:
36     :
37     : MEDIUM TYPE: Floppy disk
38     :
39     : COMPUTER: IBM PC compatible
40     :
41     : OPERATING SYSTEM: PC-DOS/MS-DOS
42     :
43     : SOFTWARE: PatentIn Release #1.0, Version #1.30
44     :
45     : CURRENT APPLICATION DATA:
46     :
47     : APPLICATION NUMBER: US/08/913,362
48     :
49     : FILING DATE: 13-NOV-1997
50     :
51     : PRIOR APPLICATION DATA:
52     :
53     : APPLICATION NUMBER: US 08/406,362
54     :
55     : FILING DATE: 17-MAR-1995
56     :
57     : PRIOR APPLICATION DATA:
58     :
59     : APPLICATION NUMBER: US 60/001,983
60     :
61     : FILING DATE: 04-AUG-1995
62     :
63     : ATTORNEY/AGENT INFORMATION:
64     :
65     : NAME: Bent, Stephen A.
66     :
67     : REGISTRATION NUMBER: 29,768
68     :
69     : REFERENCE/DOCKET NUMBER: 047998/0128
70     :
71     : TELECOMMUNICATION INFORMATION:
72     :
73     : TELEPHONE: (202)672-5300
74     :
75     : TELEFAX: (202)672-5399
76     :
77     : TELEX: 904136
78     :
79     : INFORMATION FOR SEQ ID NO: 30:
80     :
81     : SEQUENCE CHARACTERISTICS:
82     :
83     : LENGTH: 175 amino acids
84     :
85     : TYPE: amino acid
86     :
87     : STRANDEDNESS:
88     :
89     : TOPOLOGY: linear
90     :
91     : MOLECULE TYPE: protein
92     :
93     : US-08-913-362-30

```

	Query Match	97.6%;	Score 847.5;	DB 4;	Length 175;
	Best Local Similarity	98.3%;	Pred. No. 1.3e-89;		
	Matches 172;	Conservative	0;	Mismatches 2;	Indels 1; Gaps 1
OY	1 MKKALATLIALPAALAEAGSGEYVQADAAHAKASSLSGASGFSPRISAGYRINDLR 60 				
Dd	1 MKKALATLIALPALAALAEAGSGEVQADAAHAASSLSGASGFSPRISAGYRINDLR 60 				
OY	61 FAVDYTRYKNKYK-APSTDFKLYSIGASAIYDDPTQSPVKPYLGARLSINRASVDLGSDS 119 				
Dd	61 FAVDYTRYKNKKAPSTDFKLYSIGASAIYDPTQSPVKPYLGARLSINRASVDLGSDS 120 				
OY	120 FSSDTSGTGLAGVSAYVPNVLDGGRYRNITGKVNTKYNRSGETLSAGRVRKF 174 				

Db 121 FSQSTGSLGVLAGSYAVTPNVDDAGRYNYIGKVTYKVNKNSGELSGAGRYKF 175

RESULT 4
US-08-913-362-4

; Sequence 4, Application US/08913362
; Patent No. 6287574

GENERAL INFORMATION:

APPLICANT: Brodeur, Bernard R

APPLICANT: Martin, Denis

APPLICANT: Rioux, Clement

TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS

TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/913,362

FILING DATE: 13-NOV-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/406,362

FILING DATE: 17-MAR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/001,983

FILING DATE: 04-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: Bent, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 047998/0128

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 175 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-913-362-4

Query Match 96.6%; Score 838.5; DB 4; Length 175;

Best Local Similarity 97.1%; Pred. No. 1,4e-88;

Matches 170; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

Db 1 MKKALATLIALPAALAEAGSGFYVQADAAHAHAKASSLSGAKGFSRISAGRYNDLR 60

Db 1 MKKALATLIALPAALAEAGSGFYVQADAAHAHAKASSLSGAKGFSRISAGRYNDLR 60

Db 61 FAVDYTRKKNK-APSTDFKLYSGASAIYDFDQSPYKPYLGARLSLNRAVDLGSGSDS 119

Db 61 FAVDYTRKKNK-APSTDFKLYSGASAIYDFDQSPYKPYLGARLSLNRAVDLGSGSDS 119

Db 120 FSQSTGSLGVLAGSYAVTPNVDDAGRYNYIGKVTYKVNKNSGELSGAGRYKF 174

Db 121 FSQSTGSLGVLAGSYAVTPNVDDAGRYNYIGKVTYKVNKNSGELSGAGRYKF 175

Db 121 FSQSTGSLGVLAGSYAVTPNVDDAGRYNYIGKVTYKVNKNSGELSGAGRYKF 175

Db 121 FSQSTGSLGVLAGSYAVTPNVDDAGRYNYIGKVTYKVNKNSGELSGAGRYKF 175

Db 121 FSQSTGSLGVLAGSYAVTPNVDDAGRYNYIGKVTYKVNKNSGELSGAGRYKF 175

Db 121 FSQSTGSLGVLAGSYAVTPNVDDAGRYNYIGKVTYKVNKNSGELSGAGRYKF 175

Db 121 FSQSTGSLGVLAGSYAVTPNVDDAGRYNYIGKVTYKVNKNSGELSGAGRYKF 175

Db 121 FSQSTGSLGVLAGSYAVTPNVDDAGRYNYIGKVTYKVNKNSGELSGAGRYKF 175

Db 121 FSQSTGSLGVLAGSYAVTPNVDDAGRYNYIGKVTYKVNKNSGELSGAGRYKF 175

Db 121 FSQSTGSLGVLAGSYAVTPNVDDAGRYNYIGKVTYKVNKNSGELSGAGRYKF 175

Db 121 FSQSTGSLGVLAGSYAVTPNVDDAGRYNYIGKVTYKVNKNSGELSGAGRYKF 175

Db 121 FSQSTGSLGVLAGSYAVTPNVDDAGRYNYIGKVTYKVNKNSGELSGAGRYKF 175

GENERAL INFORMATION:

APPLICANT: Brodeur, Bernard R

APPLICANT: Martin, Denis

APPLICANT: Rioux, Clement

TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS

TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/913,362

FILING DATE: 13-NOV-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/406,362

FILING DATE: 17-MAR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/001,983

FILING DATE: 04-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: Bent, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 047998/0128

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 174 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-913-362-8

Query Match 96.1%; Score 834; DB 4; Length 174;

Best Local Similarity 95.4%; Pred. No. 4.5e-88;

Matches 166; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Db 1 MKKALATLIALPAALAEAGSGFYVQADAAHAHAKASSLSGAKGFSRISAGRYNDLR 60

Db 1 MKKALATLIALPAALAEAGSGFYVQADAAHAHAKASSLSGAKGFSRISAGRYNDLR 60

Db 61 FAVDYTRKKNK-APSTDFKLYSGASAIYDFDQSPYKPYLGARLSLNRAVDLGSGSDS 120

Db 61 FAVDYTRKKNK-APSTDFKLYSGASAIYDFDQSPYKPYLGARLSLNRAVDLGSGSDS 120

Db 121 FSQSTGSLGVLAGSYAVTPNVDDAGRYNYIGKVTYKVNKNSGELSGAGRYKF 174

Db 121 FSQSTGSLGVLAGSYAVTPNVDDAGRYNYIGKVTYKVNKNSGELSGAGRYKF 174

Db 121 FSQSTGSLGVLAGSYAVTPNVDDAGRYNYIGKVTYKVNKNSGELSGAGRYKF 174

Db 121 FSQSTGSLGVLAGSYAVTPNVDDAGRYNYIGKVTYKVNKNSGELSGAGRYKF 174

Db 121 FSQSTGSLGVLAGSYAVTPNVDDAGRYNYIGKVTYKVNKNSGELSGAGRYKF 174

Db 121 FSQSTGSLGVLAGSYAVTPNVDDAGRYNYIGKVTYKVNKNSGELSGAGRYKF 174

Db 121 FSQSTGSLGVLAGSYAVTPNVDDAGRYNYIGKVTYKVNKNSGELSGAGRYKF 174

Db 121 FSQSTGSLGVLAGSYAVTPNVDDAGRYNYIGKVTYKVNKNSGELSGAGRYKF 174

Db 121 FSQSTGSLGVLAGSYAVTPNVDDAGRYNYIGKVTYKVNKNSGELSGAGRYKF 174

Db 121 FSQSTGSLGVLAGSYAVTPNVDDAGRYNYIGKVTYKVNKNSGELSGAGRYKF 174

Db 121 FSQSTGSLGVLAGSYAVTPNVDDAGRYNYIGKVTYKVNKNSGELSGAGRYKF 174

Db 121 FSQSTGSLGVLAGSYAVTPNVDDAGRYNYIGKVTYKVNKNSGELSGAGRYKF 174

Db 121 FSQSTGSLGVLAGSYAVTPNVDDAGRYNYIGKVTYKVNKNSGELSGAGRYKF 174

Db 121 FSQSTGSLGVLAGSYAVTPNVDDAGRYNYIGKVTYKVNKNSGELSGAGRYKF 174

Db 121 FSQSTGSLGVLAGSYAVTPNVDDAGRYNYIGKVTYKVNKNSGELSGAGRYKF 174

Db 121 FSQSTGSLGVLAGSYAVTPNVDDAGRYNYIGKVTYKVNKNSGELSGAGRYKF 174

Db 121 FSQSTGSLGVLAGSYAVTPNVDDAGRYNYIGKVTYKVNKNSGELSGAGRYKF 174

Db 121 FSQSTGSLGVLAGSYAVTPNVDDAGRYNYIGKVTYKVNKNSGELSGAGRYKF 174

GENERAL INFORMATION:

APPLICANT: Brodeur, Bernard R

APPLICANT: Martin, Denis

APPLICANT: Rioux, Clement

TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS

TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/913,362

FILING DATE: 13-NOV-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/406,362

FILING DATE: 17-MAR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/001,983

FILING DATE: 04-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: Bent, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 047998/0128

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 174 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-913-362-8

Query Match 96.1%; Score 834; DB 4; Length 174;

Best Local Similarity 95.4%; Pred. No. 4.5e-88;

Matches 166; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Db 1 MKKALATLIALPAALAEAGSGFYVQADAAHAHAKASSLSGAKGFSRISAGRYNDLR 60

Db 1 MKKALATLIALPAALAEAGSGFYVQADAAHAHAKASSLSGAKGFSRISAGRYNDLR 60

Db 61 FAVDYTRKKNK-APSTDFKLYSGASAIYDFDQSPYKPYLGARLSLNRAVDLGSGSDS 120

Db 61 FAVDYTRKKNK-APSTDFKLYSGASAIYDFDQSPYKPYLGARLSLNRAVDLGSGSDS 120

Db 121 FSQSTGSLGVLAGSYAVTPNVDDAGRYNYIGKVTYKVNKNSGELSGAGRYKF 174

Db 121 FSQSTGSLGVLAGSYAVTPNVDDAGRYNYIGKVTYKVNKNSGELSGAGRYKF 174

Db 121 FSQSTGSLGVLAGSYAVTPNVDDAGRYNYIGKVTYKVNKNSGELSGAGRYKF 174

Db 121 FSQSTGSLGVLAGSYAVTPNVDDAGRYNYIGKVTYKVNKNSGELSGAGRYKF 174

Db 121 FSQSTGSLGVLAGSYAVTPNVDDAGRYNYIGKVTYKVNKNSGELSGAGRYKF 174

Db 121 FSQSTGSLGVLAGSYAVTPNVDDAGRYNYIGKVTYKVNKNSGELSGAGRYKF 174

Db 121 FSQSTGSLGVLAGSYAVTPNVDDAGRYNYIGKVTYKVNKNSGELSGAGRYKF 174

Db 121 FSQSTGSLGVLAGSYAVTPNVDDAGRYNYIGKVTYKVNKNSGELSGAGRYKF 174

Db 121 FSQSTGSLGVLAGSYAVTPNVDDAGRYNYIGKVTYKVNKNSGELSGAGRYKF 174

Db 121 FSQSTGSLGVLAGSYAVTPNVDDAGRYNYIGKVTYKVNKNSGELSGAGRYKF 174

Db 121 FSQSTGSLGVLAGSYAVTPNVDDAGRYNYIGKVTYKVNKNSGELSGAGRYKF 174

Db 121 FSQSTGSLGVLAGSYAVTPNVDDAGRYNYIGKVTYKVNKNSGELSGAGRYKF 174

Db 121 FSQSTGSLGVLAGSYAVTPNVDDAGRYNYIGKVTYKVNKNSGELSGAGRYKF 174

Db 121 FSQSTGSLGVLAGSYAVTPNVDDAGRYNYIGKVTYKVNKNSGELSGAGRYKF 174

Db 121 FSQSTGSLGVLAGSYAVTPNVDDAGRYNYIGKVTYKVNKNSGELSGAGRYKF 174

Db 121 FSQSTGSLGVLAGSYAVTPNVDDAGRYNYIGKVTYKVNKNSGELSGAGRYKF 174

Db 121 FSQSTGSLGVLAGSYAVTPNVDDAGRYNYIGKVTYKVNKNSGELSGAGRYKF 174

Db 121 FSQSTGSLGVLAGSYAVTPNVDDAGRYNYIGKVTYKVNKNSGELSGAGRYKF 174

[illegible]

REFERENCE/DOCKET NUMBER: 047998/0128
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Neisseria meningitidis
STRAIN: 608B
US-08-913-362-26

Query Match 15.3%; Score 133; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.8e-09;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 FAVDYTRYKNYKAPSTDFKLYSIGA 85
DB 1 FAVDYTRYKNYKAPSTDFKLYSIGA 25

RESULT 9
US-08-457-997B-2
Sequence 2, Application US/08457997B
Patent No. 576608
GENERAL INFORMATION:
APPLICANT: Kolattukudy, P. E.
TITLE OF INVENTION: Otitis Media Vaccine
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calfee, Halter and Griswold
STREET: Suite 1800 800 Superior Avenue
CITY: Cleveland
STATE: Ohio
COUNTRY: U.S.A.
ZIP: 44114-2688
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,997B
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Gollick, Mary E.
REGISTRATION NUMBER: 34,829
REFERENCE/DOCKET NUMBER: 22727/00102
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 622-8458
TELEFAX: (216) 241-0816
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-457-997B-2

Query Match 10.7%; Score 93; DB 1; Length 359;
Best Local Similarity 23.6%; Pred. No. 0.017;
Matches 54; Conservative 28; Mismatches 83; Indels 64; Gaps 11;

QY 1 MKKALATLIALAPAAALAEGA---SGFYVOADAA---HAKASSISGSAKGFSPRISAG 53
DB 1 MKKTAIALVAVAGLAASVAQAAPQENFTYAGVKAQSGSFHGINNKAIGKISSS---NYG 59
QY 54 YRINDLRFAVDYTRYKNYKAPSTDFKLYSIGASAIYDFD-----TQSPVKPYL-----G 102

DB 60 YRRNTFTYGV-----FGYQLNOD---NFGLAELGYDDFGRAKLRBAGKPKAKHTNHG 111
QY 103 ARLSLNRASVDLGSDSFQSTSTGL-----GVLA-GVS 134
DB 112 AYLSLKGSYEVLDDGLDYGKAGVALVRSDYKFEEDANGTRDHRKGRHTRASGLFVAGAE 171
QY 135 YAVTPNVLDLAGY-----RYNYIGKVTYKNVRS--GELSAGYRVK 174
DB 172 YAVLPBLAVLEQWLTFRVGYKRPQDKPMTAIVNPMWICINAGISYRF 220

RESULT 10
US-08-467-722A-2
Sequence 2, Application US/08467722A
Patent No. 6030626
GENERAL INFORMATION:
APPLICANT: Kolattukudy, P. E.
TITLE OF INVENTION: Otitis Media Vaccine
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calfee, Halter and Griswold
STREET: Suite 1800 800 Superior Avenue
CITY: Cleveland
STATE: Ohio
COUNTRY: U.S.A.
ZIP: 44114-2688
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,722A
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Gollick, Mary E.
REGISTRATION NUMBER: 34,829
REFERENCE/DOCKET NUMBER: 22727/00102
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 622-8458
TELEFAX: (216) 241-0816
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-467-722A-2

Query Match 10.7%; Score 93; DB 3; Length 359;
Best Local Similarity 23.6%; Pred. No. 0.017;
Matches 54; Conservative 28; Mismatches 83; Indels 64; Gaps 11;

QY 1 MKKALATLIALAPAAALAEGA---SGFYVOADAA---HAKASSISGSAKGFSPRISAG 53
DB 1 MKKTAIALVAVAGLAASVAQAAPQENFTYAGVKAQSGSFHGINNKAIGKISSS---NYG 59
QY 54 YRINDLRFAVDYTRYKNYKAPSTDFKLYSIGASAIYDFD-----TQSPVKPYL-----G 102
DB 60 YRRNTFTYGV-----FGYQLNOD---NFGLAELGYDDFGRAKLRBAGKPKAKHTNHG 111
QY 103 ARLSLNRASVDLGSDSFQSTSTGL-----GVLA-GVS 134
DB 112 AYLSLKGSYEVLDDGLDYGKAGVALVRSDYKFEEDANGTRDHRKGRHTRASGLFVAGAE 171
QY 135 YAVTPNVLDLAGY-----RYNYIGKVTYKNVRS--GELSAGYRVK 174
DB 172 YAVLPBLAVLEQWLTFRVGYKRPQDKPMTAIVNPMWICINAGISYRF 220

RESULT 11

PCT-US95-13749-5
Sequence 5, Application PC/TUS9513749
GENERAL INFORMATION:
APPLICANT: Amgen Inc.
TITLE OF INVENTION: COMPOSITIONS FOR INCREASED
BIOAVAILABILITY OF ORALLY DELIVERED THERAPEUTIC AGENTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavenland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13749
FILING DATE:
CLASSIFICATION:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 568 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
PCT-US95-13749-5

Query Match 10.6%; Score 92; DB 5; Length 568;
Best Local Similarity 25.8%; Pred. No. 0.043;
Matches 48; Conservative 28; Mismatches 70; Indels 40; Gaps 9;

QY 12 ALPAALAGASGFYVOADAHAKASSLSGSA-----KGFSPRISAGYRI 56
DB 396 SVPGRSIGRSVNY---AASSSISIGYASHKENGTYLDDMPKGFN--LKYRYEL 450
QY 57 NDL-----RPAVDYTR-----YKNTKAPSTDPKLSIASAIYDPDQSPYKPYLGRL 105
DB 451 DDMMGVIGSFA--YTHQGYDFYGSNKGHGVDDYISVTMGPSFRINEYVSLYGLGAH 508
QY 106 SLNRASVDDGSDSFQSTGLGLAGVSAAVTPNYVDLDAGRYNYIGKVTNKNVRSGE 165
DB 509 GKTKASV---FDSISASKSNMAYGAGVQFNPLPNVIDASYEYS---KLDSIK-VGTWM 561
QY 166 LSAGVR 171
DB 562 LGAGYR 567

RESULT 12
US-08-913-362-15
Sequence 15, Application US/08913362
Patent No. 6287574
GENERAL INFORMATION:
APPLICANT: Brodeur, Bernard R
APPLICANT: Hamel, Josee
APPLICANT: Rioux, Clement
TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/001,983
FILING DATE: 04-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 047998/0128
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Neisseria meningitidis
STRAIN: 608B
US-08-913-362-15

Query Match 10.0%; Score 87; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.00077;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 FAVDYTRYKNTKAPST 76
DB 1 FAVDYTRYKNTKAPST 16

RESULT 13
US-08-733-230-6
Sequence 6, Application US/08733230
Patent No. 602538
GENERAL INFORMATION:
APPLICANT: Barbel, Anthony F.
APPLICANT: Ganta, Roman Reddy
APPLICANT: McGuire, Travis C.
APPLICANT: Burridge, Michael J.
APPLICANT: Nyika, Aceme
APPLICANT: Rurangitwa, Fred R.
APPLICANT: Mahan, Suman M.
TITLE OF INVENTION: Nucleic Acid Vaccines Against
Rickettsial Diseases and Methods of Use
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,230
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:

```
Query Match          9.48; Score 81.5; DB 4; Length 282;  
Best Local Similarity    25.2%; Pctd No. 0.24;  
Matches   52; Conservative     22; Mismatches   75; Indels      57; Gaps       12;
```

```
3 KALMTLLAIPAAALAEG-----ÄSGFYVADAHAKASSLSAGKCFSPRISAGRIN 57  
|||:::||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::  
80 KSINT-IDVSFAFMSGSITFAFSKNLITSFGGA--VGSLGGAR--VELERASTYR- 130  
DLPRA-----VDTRYKKNTKAPESTDRLKLSTIASAIIV-PFTQS 95
```

[illegible]

Tue Oct 29 09:23:17 2002

us-09-684-883-6.rail

Page 8

Search completed: October 28, 2002, 16:04:20
Job time : 10.4864 secs

1

A:Molecule type: DNA
 A:Residues: 1-174 <TEXT>
 A:Cross-references: GB:AE002420; GB:AE002098; NID:97225876; PID:AA41081.1; PID:9722588
 A:Experimental source: serogroup B, strain MC58
 C:Genetics:
 A:Gene: NMB063

Query Match 98.8%; Score 858; DB 2; Length 174;
 Best Local Similarity 98.9%; Pred. No. 2,2e-68;
 Matches 172; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB 1 MKKALATLIALALPAALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
 DB 1 MKKALATLIALALPAALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
 QY 61 FAVDYTRYKRYKAPSTDFLYSIGASATDEPTOSPYRYLGARLSLRASVDLGSDSF 120
 DB 61 FAVDYTRYKRYKAPSTDFLYSIGASATDEPTOSPYRYLGARLSLRASVDLGSDSF 120
 QY 121 SQTSTGLVLAGVSYAVTPNVDLAGRYRYNIGKVTYVNVSGELSGAVRYKF 174
 DB 121 SQTSTGLVLAGVSYAVTPNVDLAGRYRYNIGKVTYVNVSGELSGAVRYKF 174

RESULT 3

S16610
 opacity protein opak precursor - Neisseria gonorrhoeae (strain MS11) (fragments)

N:Alternate names: outer membrane protein opak
 C:Species: Neisseria gonorrhoeae

A:Variety: strain MS11

C:Date: 13-Jan-1995 #sequence_revision 17-Oct-1997 #text_change 17-Oct-1997

C:Accession: S16610

R:Bhat, K.S.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsch, M.; Microbiol. 5, 1889-1901, 1991

A:Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a fam

A:Reference number: S16610; MUID:92114767

A:Accession: S16610

A:Molecule type: DNA

A:Residues: 1-261 <BHA>

A:Cross-references: EMBL:X52364

A:Experimental source: strain MS11, variant 4.8

A>Note: the authors did not translate the sequence for the signal peptide

A>Note: expression of opacity proteins is regulated by the number of translated repeat

A:Note: place the start codon in frame with the rest of the protein

C:Genetics:

A:Gene: opak

C:Superfamily: opacity protein

C:Keywords: cell surface component; transmembrane protein

F:1-10,11-23/Domain: signal sequence (fragments) #status predicted <SIG>

F:24-261/Product: opacity protein opak #status predicted <MAT>

F:34-42/Domain: transmembrane #status predicted <TM1>

F:43-75/Domain: extracellular #status predicted <EXT1>

F:51-61/Region: semivariable region

F:76-84/Domain: transmembrane #status predicted <TM2>

F:89-95/Domain: transmembrane #status predicted <TM2>

F:96-134/Domain: extracellular #status predicted <EXT2>

F:102-129/Region: hypervariable region HV1

F:135-149/Domain: transmembrane #status predicted <TM4>

F:155-165/Domain: transmembrane #status predicted <TM5>

F:166-212/Domain: extracellular #status predicted <EXT3>

F:171-218/Region: hypervariable region HV2

F:213-225/Domain: transmembrane #status predicted <TM6>

F:229-237/Domain: transmembrane #status predicted <TM7>

F:238-252/Domain: extracellular #status predicted <EXT4>

F:253-261/Domain: transmembrane #status predicted <TM8>

Query Match 28.1%; Score 243.5; DB 2; Length 261;
 Best Local Similarity 30.3%; Pred. No. 4.2e-14;
 Matches 74; Conservative 24; Mismatches 59; Indels 87; Gaps 10;

QY 15 AALAAES-ASGFYVQADAAHAKA-----SSLSGAKG-----FSPRI 50
 DB 21 AQAASBSGNGKPYQADLAAERITHDYPEPTGAKKGTITISVDFPNIRKISHIPRY 80

QY 51 SAGYRINDLRFADVTRYKRY-----KAPSTDFK-----LYS 82
 DB 81 SVGDFEGWMIADYAVYARKNNKYSVSIKELLRRKNGNFRDLEAENGCTFAVVS 140
 QY 83 IGASATYDPTOSPYRYLGARLSN--RASVD-----LCG-----116
 DB 141 LGLSAVYDFTKLNDFKPYIGARVAGVHRHSIDSTFKTTEVTILHGPGTPPYRGKNT 200
 QY 117 -----SDSFSQSTGLVLAGVSYAVTPNVDLAGRYRYNIGKVTYVNVSGELSGAV 170
 DB 201 QNAHRESDSIR--VGLGAVAGVIGIDITPMLTDAGTRYHMGRLNTR-FKTHEASLGV 257

RESULT 4

S16611
 opacity protein opak precursor - Neisseria gonorrhoeae (strain MS11) (fragments)

N:Alternate names: outer membrane protein opak8

C:Species: Neisseria gonorrhoeae

A:Variety: strain MS11

C:Date: 04-Jun-1997 #sequence_revision 17-Oct-1997 #text_change 26-Aug-1999

C:Accession: S16611; S36345; S28624

R:Bhat, K.S.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsc

Mol. Microbiol. 5, 1889-1901, 1991

A:Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a f

A:Reference number: S16610; MUID:92114767

A:Accession: S16611

A:Molecule type: DNA

A:Residues: 1-260 <BHA>

A:Cross-references: EMBL:X52371

A:Experimental source: strain MS11, variant 4.8

A>Note: the authors did not translate the sequence for the signal peptide

A>Note: expression of opacity proteins is regulated by the number of translated repea

A>Note: place the start codon in frame with the rest of the protein

C:Genetics:

A:Title: Variable opacity (Opa) outer membrane proteins account for the cell trophisms

A:Reference number: S36328; MUID:93178439

A:Accession: S36345

A:Molecule type: DNA

A:Residues: 24-260 <RUP>

A:Cross-references: EMBL:Z18937; NID:949333; PID:CAA79370.1; PID:9940799

A:Experimental source: strain MS11, variant F3

A>Note: expression of opacity proteins is regulated by the number of translated repea

A:Note: place the start codon in frame with the rest of the protein

C:Genetics:

A:Gene: opak

C:Superfamily: opacity protein

C:Keywords: cell surface component; transmembrane protein

F:1-10,11-23/Domain: signal sequence (fragments) #status predicted <SIG>

F:24-260/Product: opacity protein opak #status predicted <MAT>

F:34-42/Domain: transmembrane #status predicted <TM1>

F:43-74/Domain: extracellular #status predicted <EXT1>

F:51-60/Region: semivariable region

F:75-83/Domain: transmembrane #status predicted <TM2>

F:88-94/Domain: transmembrane #status predicted <TM3>

F:95-133/Domain: extracellular #status predicted <EXT2>

F:101-128/Region: hypervariable region HV1

F:134-148/Domain: transmembrane #status predicted <TM4>

F:154-164/Domain: transmembrane #status predicted <TM5>

F:165-211/Domain: extracellular #status predicted <EXT3>

F:217-224/Domain: hypervariable region HV2

F:228-236/Domain: transmembrane #status predicted <TM6>

F:237-251/Domain: extracellular #status predicted <EXT4>

F:252-260/Domain: transmembrane #status predicted <TM8>

Query Match 27.8%; Score 241; DB 2; Length 260;
 Best Local Similarity 29.8%; Pred. No. 7e-14;

Matches 77; Conservative 25; Mismatches 68; Indels 88; Gaps 10;

QY 2 KKAATLALPAAALAE---ASGFYVQADAAH-----KASSSLGSAKGS- 47

Db 6 KKPSTLFLSSAAAGEDHGRGPVQADLAAYEHITHDYDEPTGKKKSTVSD 65

QY 48 -----PRISAGYRINDLRFADVITYRK-----KAPSTDFK 79

Db 66 YFRNIRTHSHPRVSVGDFGGMRIADYARYRKNNKYSVSIKELLRNKNGNRTRDK 125

QY 80 -----LYSIGASAIYDFDTQSPVKPYLGARLSLN--RASVD-----LG 115

Db 126 TENQNGTFHVVSLGSAVYDFKLNKFKRYIGARVAYGVHRSIDSTKTTTETVTLH 185

QY 116 G-----SDSFSQSTGTGLVAGVYAVTPNVVDADAGYRNYKGVN 156

Db 186 GPGTTPYVPGKNTQDAHRESDSIR--VGIGAVAGVGDITPMLTLDAGYRHYWGRLE 243

QY 157 TVKNVSGELSGYRVK 174

Db 244 NTR-FKTHEASLGYRVK 260

RESULT 5

S16613

Opacity protein opab precursor - Neisseria gonorrhoeae (strain MS11) (fragments)

C:Species: Neisseria gonorrhoeae

A:Variety: strain MS11

C>Date: 04-Jun-1997 #sequence_revision 17-Oct-1997 #text_change 17-Oct-1997

C:Accession: S16613

R:Bhat, K.S.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsch, M.; Microbiol. 5, 1989-1991, 1991

A:Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a fam

A:Reference number: S16610; MUID:92114767

A:Accession: S16613

A:Molecule type: DNA

A:Residues: 1-338 <BHA>

A:Cross-references: EMBL:X52373

A:Experimental source: strain MS11, variant 4.8

A:Note: the authors did not translate the sequence for the signal peptide

C:Genetics:

A:Gene: opab

C:Superfamily: opacity protein

C:Keywords: cell surface component; transmembrane protein

F:1-13/14-104/Domain: signal sequence (fragments) #status predicted <SIG>

F:105-338/Product: opacity protein opab #status predicted <MAT>

F:115-123/Domain: transmembrane #status predicted <TM1>

F:124-155/Domain: extracellular #status predicted <EXT1>

F:132-141/Region: semivariable region

F:166-164/Domain: transmembrane #status predicted <TM2>

F:169-175/Domain: transmembrane #status predicted <TM3>

F:176-212/Domain: extracellular #status predicted <EXT2>

F:182-207/Region: hypervariable region HV1

F:213-227/Domain: transmembrane #status predicted <TM4>

F:224-289/Domain: extracellular #status predicted <EXT3>

F:233-243/Domain: transmembrane #status predicted <TM5>

F:249-295/Region: hypervariable region HV2

F:290-302/Domain: transmembrane #status predicted <TM6>

F:306-314/Domain: transmembrane #status predicted <TM7>

F:315-329/Domain: extracellular #status predicted <EXT4>

F:330-338/Domain: transmembrane #status predicted <TM8>

Query Match 27.7%; Score 240.5; DB 2; Length 338;
Best Local Similarity 30.5%; Pred. No. 1e-13;
Matches 74; Conservative 23; Mismatches 67; Indels 79; Gaps 9;

QY 10 ALALPAAALAE---ASGFYVQADAAH-----KASSSLGSAKGS- 46

Db 97 SLFLPAAALAE---ASGFYVQADAAH-----KASSSLGSAKGS- 156

QY 47 SPRISAGYRINDLRFADVITYRK--NYKAPSTDFK-----L 80

Db 157 HPRVSVGDFGGMRIADYARYRKNNKYSVDIKLENNKNNKRDLTENQNGTFHAY 216

QY 81 YSIGASAIYDFDTQSPVKPYLGARLSLN--RASVD-----LG- 116

Db 217 SSLGLSAVYDFKLNKFKRYIGARVAYGVHRSIDSTKTTTETVTLH 276

QY 117 -----SDSFSQSTGTGLVAGVYAVTPNVVDADAGYRNYKGVN 171

Db 277 TVNAHNSNIRRVGLGVAGVGFDTPKLTDYGRHYWGRLENT-RFKTHEASLGYR 335

QY 172 VKF 174

Db 336 YRF 338

RESULT 6

S16612

Opacity protein opab precursor - Neisseria gonorrhoeae (strain MS11) (fragments)

C:Species: Neisseria gonorrhoeae

A:Variety: strain MS11

C>Date: 04-Jun-1997 #sequence_revision 17-Oct-1997 #text_change 17-Oct-1997

C:Accession: S16612

R:Bhat, K.S.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsc M.; Microbiol. 5, 1989-1991, 1991

A:Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a f

A:Reference number: S16610; MUID:92114767

A:Accession: S16612

A:Molecule type: DNA

A:Residues: 1-258 <BHA>

A:Cross-references: EMBL:X52369

A:Experimental source: strain MS11, variant 4.8

A:Note: the authors did not translate the sequence for the signal peptide

C:Genetics:

A:Gene: opab

C:Superfamily: opacity protein

C:Keywords: cell surface component; transmembrane protein

F:1-10/11-23/Domain: signal sequence (fragments) #status predicted <SIG>

F:124-258/Product: opacity protein opab #status predicted <MAT>

F:134-42/Domain: transmembrane #status predicted <TM1>

F:143-174/Domain: extracellular #status predicted <EXT1>

F:50-60/Region: semivariable region

F:75-83/Domain: transmembrane #status predicted <TM2>

F:88-94/Domain: transmembrane #status predicted <TM3>

F:95-131/Domain: extracellular #status predicted <EXT2>

F:101-125/Region: hypervariable region HV1

F:132-146/Domain: transmembrane #status predicted <TM4>

F:152-162/Domain: transmembrane #status predicted <TM5>

F:163-209/Domain: extracellular #status predicted <EXT3>

F:168-215/Region: hypervariable region HV2

F:210-222/Domain: transmembrane #status predicted <TM6>

F:226-234/Domain: transmembrane #status predicted <TM7>

F:235-249/Domain: extracellular #status predicted <EXT4>

F:250-258/Domain: transmembrane #status predicted <TM8>

Query Match 27.6%; Score 240; DB 2; Length 258;
Best Local Similarity 30.1%; Pred. No. 8.5e-14;
Matches 77; Conservative 24; Mismatches 65; Indels 86; Gaps 10;

QY 2 KKAATLALPAAALAE---ASGFYVQADAAH-----KASSSLGSAK- 44

Db 6 KKPSTLFLSSAAAGEDHGRGPVQADLAAYEHITHDYDEPTGKKKISTVSD 65

QY 45 -----GFPRISAGYRINDLRFADVITYRK--NYKAPSTDFK- 79

Db 66 YFRNIRTHSHPRVSVGDFGGMRIADYARYRKNNKYSVDIKLENNKNNKRDLTKE 125

QY 80 -----LYSIGASAIYDFDTQSPVKPYLGARLSLN--RASVD-----LG- 116

Db 126 NOENGTFAVSVSLGSAVYDFKLNKFKRYIGARVAYGVHRSIDSTKTTTETVTLHGP 185

OY 117 -----SDSFQSTGSLAGVAYATPNVDLDAGRYNYIGKVTMV 158
 DB 186 GTTPPYPPKKNODAREDSIR--VGLGAVAGVIGDITPLTLTDAGRYNYMGRLENT 243
 OY 159 KNRSGELSGAVRYKF 174
 DB 244 R-FKTHASISLGVRYRF 258

RESULT 7

Opacity protein opac precursor - Neisseria gonorrhoeae (strain MS11) (fragments)
 N:Alternate names: opacity protein V0; triosephosphate dehydrogenase
 C:Species: Neisseria gonorrhoeae
 A:Variety: strain MS11
 C>Date: 31-Mar-1989 #sequence_revision 17-Oct-1997 #text_change 16-Jul-1999
 C:Accession: S16618; A24429; S36328; S28621
 R:Bhat, K.S.; Gidbbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehning, F.; Stern, A.; Kupsch, M.; Microbiol. 5, 1889-1901, 1991
 A:Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a fam
 A:Reference number: S16618; MUID:92114767
 A:Accession: S16618
 A:Molecule type: DNA
 A:Residues: 1-260 <BHA>
 A:Cross-references: EMBL:X52370
 A:Experimental source: strain MS11, variant 4.8
 A:Note: the authors translated the codon CCA for residue 32 as Thr
 A:Note: the authors did not translate the sequence for the signal peptide
 A:Note: expression of opacity proteins is regulated by the number of translated repeat
 A:Note: repeats place the start codon in frame with the rest of the protein
 R:Stern, A.; Brown, M.; Nickel, P.; Meyer, T.F.
 Cell 47, 61-71, 1986
 A:Title: Opacity genes in Neisseria gonorrhoeae: control of phase and antigenic variatio
 A:Reference number: A90887; MUID:87002493
 A:Accession: A24429
 A:Molecule type: DNA
 A:Residues: 25-260 <STB>
 A:Note: this protein is synthesized as a precursor; however, the authors are uncertain a
 uncoding
 R:Kupsch, E.M.; Knepper, B.; Kuroki, T.; Heuer, I.; Meyer, T.F.
 EMBO J. 12, 641-650, 1993
 A:Title: Variable opacity (Opa) outer membrane proteins account for the cell tropisms di
 A:Reference number: S36328; MUID:93178439
 A:Accession: S36328
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 25-260 <KUP>
 A:Cross-references: EMBL:Z18927; NID:949323; PIDN:CAA79360.1; PID:9440789
 R:Meyer, T.F.
 submitted to the EMBL Data Library, November 1992
 A:Reference number: S28617
 A:Accession: S28621
 A:Molecule type: DNA
 A:Residues: 25-260 <MEY>
 A:Cross-references: EMBL:Z18927; NID:949323; PIDN:CAA79360.1; PID:9440789
 C:Genetics:
 A:Gene: opac
 C:Superfamily: opacity protein
 C:Keywords: cell surface component; transmembrane protein
 F:1-11,12-24/Domain: signal sequence (fragments) #status predicted <SIG>
 F:25-260/Product: opacity protein opac #status predicted <MAT>
 F:35-43/Domain: transmembrane #status predicted <EXT1>
 F:44-75/Domain: extracellular #status predicted <TM1>
 F:52-61/Region: semivariable region
 F:76-84/Domain: transmembrane #status predicted <TM2>
 F:89-95/Domain: transmembrane #status predicted <TM3>
 F:96-134/Domain: extracellular #status predicted <EXT2>
 F:102-129/Region: hypervariable region HV1
 F:135-149/Domain: transmembrane #status predicted <TM4>
 F:155-165/Domain: transmembrane #status predicted <TM5>
 F:166-211/Domain: extracellular #status predicted <EXT3>
 F:171-217/Region: hypervariable region HV2
 F:212-224/Domain: transmembrane #status predicted <TM6>

F:228-236/Domain: transmembrane #status predicted <TM7>
 F:237-251/Domain: extracellular #status predicted <EXT4>
 F:252-260/Domain: transmembrane #status predicted <TM8>

Query Match 27.6%; Score 240; DB 1; Length 260;
 Best Local Similarity 29.2%; Pred. No. 8, 5e-14;
 Matches 73; Conservative 28; Mismatches 65; Indels 84; Gaps 9;

OY 6 ATLIALPAALAEASGAGFYVODAAH-----KASSLSAKGFS----- 47
 DB 14 SLLPSSAQAASRDGGKGPVODLVAIEHTHDYPTDPSKGIISVDFRNIRF 73
 OY 48 ----PRISAGRIINDLRFAYDYTRY-----KNYRAPSTD-- 77
 DB 74 HSIHPRVSVGDFPGCWRIADYARVAKMSDNKYSVSIKNRVKHNKNRKLTKENG 133
 OY 78 --FKYISGASATYDFTQSPVRYLARSLSN--RASVP-----LGG- 116
 DB 134 SFHAYSSISLSATYDFINDKFKYIGARVAYGVHRSIDSTKRTGLTTPGIMSGV 193
 OY 117 -----SDSFQSTGSLAGVAYATPNVDLDAGRYNYIGKVTMV 164
 DB 194 YKVLRTPGAHRESDSIR--VGLGVINGVGFDTIPKLTLDAGRYNYMGRLENT-RKTH 250
 OY 165 ELSAGVRYKF 174
 DB 251 EASLGVRVRF 260

RESULT 8

Opacity protein opa57 - Neisseria gonorrhoeae (strain MS11) (fragment)
 N:Alternate names: outer membrane protein opa57
 C:Species: Neisseria gonorrhoeae
 A:Variety: strain MS11
 C>Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 26-Aug-1999
 C:Accession: S36343; S28626
 R:Kupsch, E.M.; Knepper, B.; Kuroki, T.; Heuer, I.; Meyer, T.F.
 EMBO J. 12, 641-650, 1993
 A:Title: Variable opacity (Opa) outer membrane proteins account for the cell tropisms
 A:Reference number: S36328; MUID:93178439
 A:Accession: S36343
 A:Molecule type: DNA
 A:Residues: 1-237 <KUP>
 A:Cross-references: EMBL:Z18935; NID:949331; PIDN:CAA79368.1; PID:9440797
 A:Experimental source: strain MS11, variant F3
 A:Note: expression of opacity proteins is regulated by the number of translated repea
 of repeats place the start codon in frame with the rest of the protein
 C:Genetics:
 A:Gene: opa57
 C:Superfamily: opacity protein
 C:Keywords: cell surface component; transmembrane protein
 F:1-237/Product: opacity protein opa57 #status predicted <MAT>
 F:11-19/Domain: transmembrane #status predicted <TM1>
 F:20-51/Domain: extracellular #status predicted <EXT1>
 F:28-37/Region: semivariable region
 F:52-60/Domain: transmembrane #status predicted <TM2>
 F:65-71/Domain: transmembrane #status predicted <TM3>
 F:72-110/Domain: extracellular #status predicted <EXT2>
 F:78-105/Region: hypervariable region HV1
 F:111-125/Domain: transmembrane #status predicted <TM4>
 F:131-141/Domain: transmembrane #status predicted <TM5>
 F:142-188/Domain: extracellular #status predicted <EXT3>
 F:147-194/Region: hypervariable region HV2
 F:189-201/Domain: transmembrane #status predicted <TM6>
 F:205-213/Domain: transmembrane #status predicted <TM7>
 F:214-228/Domain: extracellular #status predicted <EXT4>
 F:229-237/Domain: transmembrane #status predicted <TM8>

Query Match 27.6%; Score 239.5; DB 2; Length 237;
 Best Local Similarity 30.0%; Pred. No. 8, 5e-14;
 Matches 72; Conservative 24; Mismatches 59; Indels 85; Gaps 9;

QY 17 ALAAGSGFYVQADAAH-----KASSLSGS-----AKGSPRISAGY 54
 Db 1 ASDEGGGFPYQADLAAYEHITHDYPEPTAPKMKIISTVSDYFNIRTRSPVRSVCG 60
 QY 55 RINDLRFAVDYTRYKVN-----KAPSTDFK-----LVSIGAS 86
 Db 61 DFGGWRIAADYARYRRKNNKYSVSIKELLRKNGNRIDLAKNOENGTFFHAIVSSLSGS 120
 QY 87 AITDFPTQSPVRYLGAARLSLN--RASVD-----LGG----- 116
 Db 121 AAYDFKLNDFKFKPYIGARVAVGHVRHSIDSTKTKTEVTITLLHGPGTTPVYDGKNTQDAH 180
 QY 117 --SDSPQSTGTGLAGVSYATPNVDLDAGRYNYTGKNTKVNKRGESLACVRYK 174
 Db 181 RESDSIR--VGLGAVAGVIGIDITPMLTLDAGRYHYRWLENT-RFKTHASLGVRYR 237

RESULT 9
 S16614
 Opacity protein opaf precursor - Neisseria gonorrhoeae (strain MS11) (fragments)

C:Species: Neisseria gonorrhoeae
 A:Variety: strain MS11
 C:Date: 04-Jun-1997 #sequence_revision 17-Oct-1997 #text_change 17-Oct-1997
 C:Accession: S16614
 R:Bhat, K.S.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehmig, F.; Stern, A.; Kupsch, M.; Microbiol. 5, 1989-1901, 1991
 A:Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a fam1
 A:Reference number: S16610; MUID:92114767
 A:Accession: S16614
 A:Molecule type: DNA
 A:Residues: 1-257 <BHA>
 A:Cross-references: EMBL:X52368
 A:Experimental source: strain MS11, variant 4.8
 A>Note: the authors translated the codon ACC for residue 206 as Ala and TAT for residue
 A>Note: the authors did not translate the sequence for the signal peptide
 A>Note: expression of opacity proteins is regulated by the number of translated repeat e
 C:Genetics:
 A:Gene: opaf
 C:Superfamily: Opacity protein
 C:Keywords: cell surface component; transmembrane protein
 F:1-10,11-23/Domain: signal sequence (fragments) #status predicted <SIG>
 F:24-257/Product: opacity protein opaf #status predicted <MAT>
 F:34-42/Domain: transmembrane #status predicted <TM1>
 F:43-74/Domain: extracellular #status predicted <EXT1>
 F:51-60/Region: semivariable region
 F:51-83/Domain: transmembrane #status predicted <TM2>
 F:88-94/Domain: transmembrane #status predicted <TM2>
 F:95-131/Domain: extracellular #status predicted <TM3>
 F:101-126/Region: hypervariable region HV1
 F:132-146/Domain: transmembrane #status predicted <TM4>
 F:153-162/Domain: transmembrane #status predicted <TM5>
 F:163-208/Domain: extracellular #status predicted <EXT3>
 F:168-214/Region: hypervariable region HV2
 F:209-221/Domain: transmembrane #status predicted <TM6>
 F:223-233/Domain: transmembrane #status predicted <TM7>
 F:234-248/Domain: extracellular #status predicted <EXT4>
 F:249-257/Domain: transmembrane #status predicted <TM8>

Query Match 27.6%; Score 239.5; DB 2; Length 257;
 Best Local Similarity 29.6%; Pred. No. 9.3e-14;
 Matches 75; Conservative 24; Mismatches 73; Indels 81; Gaps 9;

QY 2 KKAATLIALALPAALAE--ASGFYQADAAH-----KASSLSGS----- 44
 Db 6 KKPILLSLFFSSAAQAGDHGRGPYQADLAAYEHITHDYPEPTGTRKDKISTVSD 65
 QY 45 -----GSPRISAGRYNDRFAVDYTRYK--NYKAPSTDFK----- 79
 Db 66 YFNIRTHSHIPRVSVDGFGWRIAADYARYRRKNNKYSVDIKELRNKNNKRDILKTE 125
 QY 80 -----LVSIGASATYDFDTPSPVRYLGAARLSLN--RASVD-----LGG 116

Db 126 NOENGTFFHAIVSSLSGSAYDFKLNDFKFKPYIGARVAVGHVRHSIDSTKTKTKFLTSYCG 185
 QY 117 -----SDSPQSTGTGLAGVSYATPNVDLDAGRYNYTGKNTKVNK 161
 Db 186 LNPVYTEENTQMAHQNSIRRVGLVAGVGIDITPMLTLDAGRYHYRWLENT-R 244
 QY 162 RSGELAGVRYK 174
 Db 245 KTHASLGVRYR 257

RESULT 10
 S16616

Opacity protein opaf precursor - Neisseria gonorrhoeae (strain MS11) (fragments)

C:Species: Neisseria gonorrhoeae
 A:Variety: strain MS11
 C:Date: 04-Jun-1997 #sequence_revision 17-Oct-1997 #text_change 17-Oct-1997
 C:Accession: S16616
 R:Bhat, K.S.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehmig, F.; Stern, A.; Kupsch, M.; Microbiol. 5, 1989-1901, 1991
 A:Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a f
 A:Reference number: S16610; MUID:92114767
 A:Accession: S16616
 A:Molecule type: DNA
 A:Residues: 1-266 <BHA>
 A:Cross-references: EMBL:X52372
 A:Experimental source: strain MS11, variant 4.8
 A>Note: the authors did not translate the sequence for the signal peptide
 A>Note: expression of opacity proteins is regulated by the number of translated repea
 C:Genetics:
 A:Gene: opaf
 C:Superfamily: Opacity protein
 C:Keywords: cell surface component; transmembrane protein
 F:1-10,11-23/Domain: signal sequence (fragments) #status predicted <SIG>
 F:24-266/Product: opacity protein opaf #status predicted <MAT>
 F:34-42/Domain: transmembrane #status predicted <TM1>
 F:43-74/Domain: extracellular #status predicted <EXT1>
 F:51-60/Region: semivariable region
 F:51-83/Domain: transmembrane #status predicted <TM2>
 F:88-94/Domain: transmembrane #status predicted <TM2>
 F:95-131/Domain: extracellular #status predicted <TM3>
 F:101-134/Region: hypervariable region HV1
 F:140-154/Domain: transmembrane #status predicted <TM4>
 F:160-170/Domain: transmembrane #status predicted <TM5>
 F:171-217/Domain: extracellular #status predicted <EXT3>
 F:176-223/Region: hypervariable region HV2
 F:218-230/Domain: transmembrane #status predicted <TM6>
 F:234-242/Domain: transmembrane #status predicted <TM7>
 F:243-257/Domain: extracellular #status predicted <EXT4>
 F:258-266/Domain: transmembrane #status predicted <TM8>

Query Match 27.4%; Score 238; DB 2; Length 266;
 Best Local Similarity 29.4%; Pred. No. 1.3e-13;
 Matches 77; Conservative 24; Mismatches 71; Indels 90; Gaps 8;

QY 2 KKAATLIALALPAALAE--ASGFYQADAAH-----KASSLSGS----- 42
 Db 6 KKPILLSLFFSSAAQAGDHGRGPYQADLAAYEHITHDYPEPTGTRKDKISTVSD 65
 QY 43 -----AKGSPRISAGRYNDRFAVDYTRYK----- 69
 Db 66 YFNIRTHSHIPRVSVDGFGWRIAADYARYRRKNNKYSVDIKELLRNANNGSGSHL 125
 QY 70 NYKAPSTDFK-----LVSIGASATYDFDTPSPVRYLGAARLS----- 107
 Db 126 NIKTRKTHRENTFFHAASLSGSAYDIDTSPKRYLGMVAVAGHVRHVRYSVOETI 185
 QY 108 -----NRASV-----DLGSDSPQSTGTGLAGVSYATPNVDLDAGRYNY 152
 Db 186 AVTYTPQNAASVTYNAPTRKLPHEHSRISISLGVAGVAGIDITPMLTLDAGRYRNM 245
 QY 153 GKVNIVKNNVRSGLSAGVRYK 174

MOL. Microbiol. 3, 663-671, 1989
 A>Title: Expression of gonococcal protein II in *Escherichia coli* by translational fusion
 A/Reference number: S04380; MUID:89343653
 A/Accession: S04380
 A/Molecule type: DNA
 A/Residues: 1-270 <PAL>
 A/Cross-references: EMBL:X15760
 A/Experimental source: Strain F62-SF, serogroup IB-3; clone F62-SF1
 A/Note: the authors did not translate the sequence of the signal peptide
 A/Note: expression of opacity proteins is regulated by the number of translated repeat
 R:Raha, M.K.; So, M.; Seifert, H.S.; Bilyard, E.; Marchal, C.
 EMOJ. 7, 4367-4378, 1988
 A>Title: Pili expression in *Neisseria gonorrhoeae* is under both positive and negative t
 A/Reference number: S02017; MUID:89210824
 A/Accession: S16504
 A/Status: translation not shown
 A/Molecule type: DNA
 A/Residues: 259-270 <TAH>
 A/Cross-references: EMBL:X13965
 A/Experimental source: strain MS11A
 A/Note: expression of opacity proteins is regulated by the number of translated repeat
 C:Genetics: place the start codon in frame with the rest of the protein
 A/Genes: opa1
 C:Superfamily: opacity protein
 C/Keywords: cell surface component; transmembrane protein
 F:1-10,11-23/Domain: signal sequence (fragments) #status predicted <SIG>
 F:24-270/Product: opacity protein opa #status predicted <MAT>
 F:34-42/Domain: transmembrane #status predicted <TM1>
 F:43-75/Domain: extracellular #status predicted <EXT1>
 F:51-61/Region: semivariable region
 F:76-84/Domain: transmembrane #status predicted <TM2>
 F:89-95/Domain: transmembrane #status predicted <TM3>
 F:96-141/Domain: extracellular #status predicted <EXT2>
 F:102-136/Region: hypervariable region HV1
 F:142-156/Domain: transmembrane #status predicted <TM4>
 F:162-176/Domain: transmembrane #status predicted <TM5>
 F:173-221/Domain: extracellular #status predicted <EXT3>
 F:178-227/Region: hypervariable region HV2
 F:222-234/Domain: transmembrane #status predicted <TM6>
 F:238-246/Domain: transmembrane #status predicted <TM7>
 F:247-261/Domain: extracellular #status predicted <EXT4>
 F:262-270/Domain: transmembrane #status predicted <TM8>

Query Match 27.2%; Score 236; DB 2; Length 270;
 Best Local Similarity 27.4%; Pred. No. 2e-13;
 Matches 73; Conservative 31; Mismatches 68; Indels 94; Gaps 8;

2 KRALATLALPAALAE--ASGFYVADAAH-----AKASSLSGSAK 44
 6 KPSILFSSLAQAAGBNGRPYQADLAAYEHITHDPKPKGAKKGTITSVS 65
 45 GP-----SPRISAGYRINDLRFAYDYTRYK----- 69
 66 DFNIRHSHVPRVSVGDFGMRIDYARFKMNNKYSVSIKELGRDMSASVGRG 125
 70 --NYKASDFDK-----LVSIGASATYDDPTGSPYKPYIGARLSL----- 107
 126 HNIOTQTEHDENTFPAASSLGLSTIYDFDTSRFRPYGARVAHVHQRVSYEOE 185
 108 -----NRASVDLGG-----DSFSQSTGLGVLGAGVAVTPVNDAGYR 148
 186 TEIVTTPREQNVAPSPRIGAPTKRPAHNEBSRISLSLGFAGVAGVGDITPNTLLDAGYR 245
 149 YNYICKVMTVNVRSGLSAGYRKF 174
 246 YHNGRELENTN-FTHEASLGVRRF 270

RESULT 14
 K0NH2C
 opacity protein P.IIC precursor - *Neisseria gonorrhoeae* (strain JS3) (fragments)

N/Alternate names: outer membrane protein P.IIC
 C/Species: *Neisseria gonorrhoeae*
 A/Variety: strain JS3
 C/Date: 31-Mar-1992 #sequence_revision 17-Oct-1997 #text_change 08-May-1998
 C/Accession: S03095; S16360
 R:van der Ley, P.
 MOL. Microbiol. 2, 797-806, 1988
 A>Title: Three copies of a single protein II-encoding sequence in the genome of *Neis*
 A/Reference number: S03095; MUID:89096501
 A/Accession: S03095
 A/Molecule type: DNA
 A/Residues: 1-268 <VAN>
 A/Cross-references: EMBL:X12625
 A/Experimental source: strain JS3
 A/Note: 241-Val was also found
 A/Note: expression of opacity proteins is regulated by the number of translated repea
 R:Barritt, D.S.; Schwalbe, R.S.; Klapper, D.G.; Cannon, J.G.
 Infect. Immun. 55, 2026-2031, 1987
 A>Title: Antigenic and structural differences among six proteins II expressed by a sl
 A/Reference number: S16360; MUID:87306843
 A/Accession: S16360
 A/Status: Preliminary
 A/Molecule type: protein
 A/Residues: 24-34 <BAR>
 C:Genetics: P.IIC
 C:Superfamily: opacity protein
 C/Keywords: cell surface component; transmembrane protein
 F:1-10,11-23/Domain: signal sequence (fragments) #status predicted <SIG>
 F:24-268/Product: opacity protein P.IIC #status experimental <MAT>
 F:34-42/Domain: transmembrane #status predicted <TM1>
 F:43-74/Domain: extracellular #status predicted <EXT1>
 F:51-60/Region: semivariable region
 F:75-83/Domain: transmembrane #status predicted <TM2>
 F:88-94/Domain: transmembrane #status predicted <TM3>
 F:95-140/Domain: extracellular #status predicted <EXT2>
 F:101-135/Region: hypervariable region HV1
 F:141-155/Domain: transmembrane #status predicted <TM4>
 F:161-171/Domain: transmembrane #status predicted <TM5>
 F:172-219/Domain: extracellular #status predicted <EXT3>
 F:177-225/Region: hypervariable region HV2
 F:220-232/Domain: transmembrane #status predicted <TM6>
 F:236-244/Domain: transmembrane #status predicted <TM7>
 F:245-259/Domain: extracellular #status predicted <EXT4>
 F:260-268/Domain: transmembrane #status predicted <TM8>

Query Match 27.1%; Score 235.5; DB 1; Length 268;
 Best Local Similarity 27.2%; Pred. No. 2e-13;
 Matches 70; Conservative 30; Mismatches 68; Indels 89; Gaps 8;

6 ATLIALPAALAEASGFYVADAAHAKA-----SSLSGSAK----- 44
 13 SLSLSSAARASDGGRGPPYQADLAAYERITHDPKPKGTGKKNISTVSDFNIRT 72
 45 -GPSRISAGYRINDLRFAYDYTRYK-----NYKAPS 75
 73 HSHVPRVSVGDFGSMRIDYARFKMNNKYSVSIKELRDNDSAGVGRHLNIOQOK 132
 76 TDPK-----LVSIGASATYDDPTGSPYKPYIGARLSLRA-----SYDL----- 114
 133 TEHDENTFPAVSSLGLSTIYDFDTSRFRPYIGMVAAGVHQRVSYEOETEITTPY 192
 115 -----GGSDFSQ-----TSTGLGVLGAGVAVTPVNDAGYRNYIGKVT 157
 193 SNGGKYSLSKMPKPSAHNQSIRRVGLGVLGAGVGFITPNTLLDTGYRYHNGRELE 252
 158 YKAVRSGLSAGYRKF 174
 253 TR-FTHEASLGMRRF 268

RESULT 15

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 28, 2002, 15:55:44 ; Search time 6.98996 Seconds

(without alignments)
963.840 Million cell updates/sec

Title: US-09-684-883-6

Sequence: 1 MKKALATLIALALPAALAE.....VNTVKNVSGELSGAVRYKF 174

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	239.5	27.6	237	1	OPAK_NEIGO
2	238	27.4	260	1	OPRI_NEIMC
3	235.5	27.1	270	1	OPMC_NEIGO
4	234	27.0	236	1	OPAC_NEIGO
5	231.5	26.7	234	1	OPAB_NEIGO
6	231.5	26.7	237	1	OPAJ_NEIGO
7	231	26.6	234	1	OPAE_NEIGO
8	231	26.6	234	1	OPAF_NEIGO
9	230	26.5	233	1	OP67_NEIGO
10	225	25.9	234	1	OP28_NEIGO
11	225	25.9	234	1	OP65_NEIGO
12	225	25.9	238	1	OP66_NEIGO
13	225	25.9	238	1	OPAH_NEIGO
14	223.5	25.7	243	1	OPAD_NEIGO
15	223	25.7	244	1	OPAL_NEIGO
16	220	25.3	178	1	VER57_HAEN
17	219	25.2	238	1	OP68_NEIGO
18	214	24.7	239	1	OPAA_NEIGO
19	205.5	23.7	247	1	OPAG_NEIGO
20	177.5	20.4	121	1	OPAH_HAEN
21	135	15.6	170	1	OPR3_NEIMC
22	122.5	14.1	70	1	VAL14_HAEN
23	113	13.0	182	1	ATL_YERPS
24	100	11.5	353	1	OM52_HAEN
25	99	11.4	353	1	OM51_HAEN
26	98.5	11.3	350	1	OMPA_SALTY
27	98	11.3	521	1	TSAS_RICIS
28	97	11.2	213	1	OM25_BRUB
29	96	11.1	178	1	ATL_YEREN
30	96	11.1	212	1	OMFW_ECOTI
31	93.5	10.8	341	1	OMP7_VIBCH
32	93.5	10.8	428	1	OM67_PASBU
33	93	10.7	359	1	OM53_HAEN

34	89	10.3	213	1	OM25_BRUSU	O45689 brucella su
35	88.5	10.2	346	1	OMPA_ECOTI	P02934 escherichia
36	87	10.0	213	1	OM25_BRUME	O45321 brucella me
37	87	10.0	349	1	OMPA_BUCAT	P57414 brucella ap
38	87	10.0	350	1	PORF_PSEAE	P13794 pseudomonas
39	84.5	9.7	995	1	YI09_YEAST	P40442 saccharomyc
40	84	9.7	511	1	INO1_ARATH	P42801 arabidopsis
41	84	9.7	511	1	INO1_PHAVU	O41107 phaseolus v
42	83.5	9.6	350	1	OMPA_ENDAE	P09146 enterobacte
43	83	9.6	201	1	OM25_BRUV	O45335 brucella ov
44	83	9.6	213	1	OM25_BRUCA	O45110 brucella ca
45	82	9.4	172	1	OMPF_ENTCL	P25253 enterobacte

ALIGNMENTS

RESULT 1	OPAK_NEIGO	STANDARD	PRT	237 AA
ID	OPAK_NEIGO			
AC	Q04880			
DT	01-OCT-1993 (Rel. 27, Created)			
DT	01-OCT-1993 (Rel. 27, Last sequence update)			
DT	01-NOV-1995 (Rel. 32, Last annotation update)			
DE	Opacity protein OPA57 precursor (Fragment).			
GN	OPAK.			
OS	Neisseria gonorrhoeae.			
CC	Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.			
OX	NCBI_TaxID=485;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=MS11 / F3;			
RX	MEDLINE=93178439; PubMed=8440254;			
RA	Kirsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;			
RT	"Variable opacity (Opa) outer membrane proteins account for the cell			
RT	topisms displayed by Neisseria gonorrhoeae for human leukocytes and			
RT	epithelial cells."			
RL	EMBO J. 12:641-650(1993).			
CC	-I- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA			
CC	PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE			
CC	VARIATION.			
CC	-I- SUBCELLULAR LOCATION: Outer membrane.			
CC	-----			
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sdb.ch/announce/			
CC	or send an email to license@sdb-sdb.ch).			
CC	-----			
DR	EMBL; Z18935; CAA79368.1; -			
DR	PIR; S28626; S28626.			
DR	InterPro; IPR003394; Opacity.			
DR	Pfam; PF02462; Opacity; 1.			
KW	Outer membrane; Multigene family; Signal.			
FT	NON_TER	1		
FT	SIGNAL	<1		
FT	CHAIN	2	>237	POTENTIAL.
FT	NON_TER	237		OPACITY PROTEIN OPA57.
SQ	SEQUENCE	237 AA; 26703 MW; F8B1A0FB5C7EBCAD CRC64;		
Query Match	27.6%;	Score 239.5; DB 1; Length 237;		
Best local similarity	30.0%;	Pred. No. 1,6e-14;		
Matches	72; Conservative	24; Mismatches 59; Indels 85; Gaps 9;		
DB	17 ALAEGASGFVQADAAHA-----KASSSLGS-----AKGFSPTISAGY 54			
DB	1 ASEGGGGRPYQADLAYAYEHITHDYPEPPAPKNKISTVSDYFRNIRRSVHPRVSVGY 60			
DB	55 RINDLRPAVYVTRKNV-----KAPSTDEK-----LVSIGAS 86			
DB	61 DFGWRIRADYATYATKRWNNKYSYSIKELIRKNGNRTDLAENQENGTFAVSVSLGIS 120			

```

QY 87 AYDFPDSQSPKPYLGARLSLN--RASVD-----LGG----- 116
DB 121 AYDFKLNKFKPKYIGARVAYGVRHSIDSTKKTTEVTTLHGPGTTPVYDEKNTQAH 180
QY 117 -SDSEQSTGTGLGAGVAVTAPNVDDAGRYNYICKVNTVKVNSGELSGAGVRKF 174
DB 181 RESDSIRK--VGLGAVAGVGIDITPNLTLDAGYRHYWGRLEWTR-FKTHEASLGVRYKF 237

RESULT 2
ID OPRI_NEIMC STANDARD: PRT: 260 AA.
AC P10170;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Opacity-related protein POPM1.
GN OPR.
OS Neisseria meningitidis (serogroup C).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=135720;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C1938 / SEROGROUP C;
RX MEDLINE=88260884; PubMed=2455211;
RA Stern A., Meyer T.F.;
RT "Common mechanism controlling phase and antigenic variation in
RT pathogenic neisseriae."
RL Mol. Microbiol. 1:5-12(1987).
CC - SUBCELLULAR LOCATION: Outer membrane.
CC - SIMILARITY: STRONG TO THE OPACITY-RELATED PROTEIN POPM3 AND
CC REGIONS OF HOMOLOGY WITH N.GONORRHOEA (STRAIN MS11) OPA GENE
CC PRODUCTS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC
CC EMBL: X06445; CAA29748.1; ALF_SEQ.
CC PIR: S08514; S08514.
CC InterPro: IPR003394; Opacity.
CC Pfam: PF02462; Opacity; 1.
CC Outer membrane.
CC KW
CC SEQUENCE 260 AA; 28936 MW; EB47A2843B3F037B CRC64;

Query Match 27.4%; Score 238; DB 1; Length 260;
Best Local Similarity 28.0%; Pred. No. 2.4e-14;
Matches 72; Conservative 32; Mismatches 67; Indels 86; Gaps 8;

QY 3 KALATLALPAAALAEAG-----SGFYVQADAAHA-----KASSSLG 41
DB 5 KTFSSLLFSSLSAQAASEDSRSPYVQADLAVERITHNTPEPTGADKDXISYV 64
QY 42 S-----AKGSPRISAGRYNDLRFADVTRYK-----NYKAPST 76
DB 65 SDYRNIRAHISIHPRVSVGDFGQWRITADYASRKMKESNFSKVTETIKNYETKT 124
QY 77 DFK-----LYSGASATIDFDTQSPKPYLGARLSLN-----ASVDL 114
DB 125 EHONGNSFHATSSLGSLATYDFKLNDFKPKYIGARVAVGVHVKQHVSVETKTTVNSKPK 184
QY 115 GGS-----DSEQSTGTGLGAGVAVTAPNVDDAGRYNYICKVNT 157
DB 185 GGTAGGPPVTKTDPKSPKPYHSHSISLGLGVAGVGFDITPKLTDTGRIHNMGRLEN 244
QY 158 VKNVRSGLSGAGVRKF 174
DB 245 TR-FKTHEASLGMRYRF 260

```

```

RESULT 3
ID OMFPC_NEIGO STANDARD: PRT: 270 AA.
AC P09888;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DE 01-FEB-1994 (Rel. 28, Last annotation update)
DE Outer membrane protein P.IIC precursor (Protein IIC).
GN PIIC.
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=485;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=J53;
RX MEDLINE=89096501; PubMed=3145386;
RA van der Ley P.;
RT "Three copies of a single protein II-encoding sequence in the genome
RT of Neisseria gonorrhoeae J53: evidence for gene conversion and gene
RT duplication."
RL Mol. Microbiol. 2:797-806(1988).
CC - FUNCTION: THIS PROTEIN SERVES AS A PORIN.
CC - SUBUNIT: HOMOTRIMER.
CC - SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC
CC EMBL: X12625; CAA31144.1; -.
CC PIR: S03095; KONH2C.
CC InterPro: IPR003394; Opacity.
CC Pfam: PF02462; Opacity; 1.
CC Outer membrane; Porin; Transmembrane; Antigen; Signal.
CC KW
CC SIGNAL 1 25
CC CHAIN 26 270
CC TRANSMEM 36 44 OUTER MEMBRANE PROTEIN P. IIC.
CC TRANSMEM 77 85 POTENTIAL.
CC TRANSMEM 90 96 POTENTIAL.
CC TRANSMEM 143 157 POTENTIAL.
CC TRANSMEM 163 173 POTENTIAL.
CC TRANSMEM 222 234 POTENTIAL.
CC TRANSMEM 238 246 POTENTIAL.
CC TRANSMEM 262 270 POTENTIAL.
CC SEQUENCE 270 AA; 30269 MW; FEB448373830A50D CRC64;

Query Match 27.1%; Score 235.5; DB 1; Length 270;
Best Local Similarity 27.2%; Pred. No. 4.2e-14;
Matches 70; Conservative 30; Mismatches 68; Indels 89; Gaps 8;

QY 6 ATTLALPAAALAGSGFYVQADAAHAKA-----SSSLGSAK----- 44
DB 15 SLLFSSAARASASEDGGGPGYVQADLAVERITHDYKPKGTGKNKISTVSDYERNIRT 74
QY 45 -GFSPRISAGRYNDLRFADVTRYK-----NYKAPS 75
DB 75 HSYHPRVSVGDFGQWRITADYARTRKNNNNKYSYSIKELLRNDSAGVGHNLDTOK 134
QY 76 TDFK-----LYSGASATIDFDTQSPKPYLGARLSLN-----SVDL 114
DB 135 THQENGTFHAAVSSLGSLTITDFDTSKPKYIGARVAVGVHVKQHVSVDEQETELITTP 194
QY 115 ---GSDSEFQ-----TSTGLGVLGAVAVTAPNVDDAGRYNYICKVNT 157
DB 195 SNGGKRVSLSSKMPKSAHOSNSIRRVGLGVAGVGFDITPNLTDTGRIHNMGRLEN 254
QY 158 VKNVRSGLSGAGVRKF 174

```

DB 255 TR-FKTHESLGMRYRF 270

RESULT 4

OPAC_NEIGO STANDARD: PRT: 236 AA.

AC P11296; 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Opacity protein OPA50 precursor (OPA30) (VO) (Fragment).
 GN OPAC.
 OS Neisseria gonorrhoeae.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_TaxID=485;
 RN [1]
 RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
 RC STRAIN=MS11 / VO;
 RX MEDLINE=87002493; PubMed=3093085;
 RA Stern A., Brown M., Nickel P., Meyer T.F.;
 RT "Opacity genes in Neisseria gonorrhoeae: control of phase and antigenic variation.";
 RL Cell 47:61-71(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MS11 / F3;
 RX MEDLINE=93178439; PubMed=8440254;
 RA Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
 RT "Variable opacity (Opa) outer membrane proteins account for the cell tropisms displayed by Neisseria gonorrhoeae for human leukocytes and epithelial cells.";
 RL EMO J. 12:641-650(1993).

-1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE VARIATION.

-1- SUBCELLULAR LOCATION: Outer membrane.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC EMBL; M14746; -; NOT_ANNOTATED_CDS.

DR EMBL; Z18927; CA79360.1; -

DR PIR; A24429; KONHO.

DR PIR; S28621; S28621.

DR PIR; S36328; S36328.

DR InterPro; IPR003394; Opacity.

DR Pfam; PF02462; Opacity.1.

KW Outer membrane; Multigene family; Signal.

FT NON_TER 1 1

FT SIGNAL <1 1

FT CHAIN 2 >236

FT NON_TER 236 236

FT SEQUENCE 236 AA; 26685 MW; 68DC237692183398 CRC64;

Query Match 27.0%; Score 234; DB 1; Length 236;

Best Local Similarity 29.7%; Pred. 5e-14;

Matches 71; Conservative 24; Mismatches 60; Indels 84; Gaps 9;

QY 17 ALAAGSGFYVQADAAHA-----KASSLSGSAKGS-----PRISAGY 54
 DB 1 ASEGGGPGPYQADLAAYEHITHDYKPTDPSKGIKSTVSDYFRNIRTHSHPRVSGV 60
 QY 55 RINDRFVADTRY-----KTKKASTD-----FKLYSIGAS 86
 DB 61 DFGGRIMADYARFKKMSDNKYSIKNMRYVHKHNSKRNKLTENQSGSFHVAVSLGLS 120
 QY 87 AIYDFDQSPVKPYLGARSLN--RASVD-----LGG----- 116

DB 121 AIYDFQINDKFKPYIGARVAYGVHRSHIDSTKKTITGLTSTPGIMSGYKVLRTPGAHR 180
 QY 117 -SDSFSQSTGIVAGVAVTPNVDDAGRYRNYTKVNTYKANKVRSGLSGYVRF 174
 DB 181 ESDSIR--VGLGVAGVGFDTTPKLTLDAGYRHHMGRLENTR-FKTHESLGMRYRF 236

RESULT 5

OPAB_NEIGO STANDARD: PRT: 234 AA.

AC Q04874; 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Opacity protein OPA51 precursor (Fragment).
 GN OPAB.
 OS Neisseria gonorrhoeae.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_TaxID=485;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MS11 / F3;
 RX MEDLINE=93178439; PubMed=8440254;
 RA Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
 RT "Variable opacity (Opa) outer membrane proteins account for the cell tropisms displayed by Neisseria gonorrhoeae for human leukocytes and epithelial cells.";
 RL EMO J. 12:641-650(1993).

-1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE VARIATION.

-1- SUBCELLULAR LOCATION: Outer membrane.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

DR EMBL; Z18928; CA79361.1; -

DR PIR; S28628; S28628.

DR PIR; S36329; S36329.

DR InterPro; IPR003394; Opacity.

DR Pfam; PF02462; Opacity.1.

KW Outer membrane; Multigene family; Signal.

FT NON_TER 1 1

FT SIGNAL <1 1

FT CHAIN 2 >234

FT NON_TER 234 234

FT SEQUENCE 234 AA; 26772 MW; 9FEF5B5DABA6CA CRC64;

Query Match 26.7%; Score 231.5; DB 1; Length 234;

Best Local Similarity 29.9%; Pred. No. 8.2e-14;

Matches 70; Conservative 23; Mismatches 62; Indels 79; Gaps 9;

QY 19 AEG-ASGFYVQADAAHA-----KASSLSGSAK-----GFSRISAGR 55
 DB 2 SEGGGPGPYQADLAAYEHITHDYKPTDPSKGIKSTVSDYFRNIRTHSHPRVSGV 61
 QY 56 INDIRFVADTRYK--NYKASTDFK-----LYSIGASATY 89
 DB 62 FGGWRIMADYARFKKMSDNKYSIKNMRYVHKHNSKRNKLTENQSGSFHVAVSLGLS 121
 QY 90 DFTQSPVKPYLGARSLN--RASVD-----LGG-----SDSF 120
 DB 122 DFKLNGKFRPYIGARVAYGVHRSHIDSTKKTITGLTSSYGCINPVTYTEENTQNAHHSN 181
 QY 121 SQSTGIVAGVAVTPNVDDAGRYRNYTKVNTYKANKVRSGLSGYVRF 174
 DB 182 SIKRVGLGVAGVGFDTTPKLTLDAGYRHHMGRLENTR-FKTHESLGMRYRF 234

RESULT 6
OPAF_NEIGO STANDARD; PRT; 237 AA.
AC 004882;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Opacity protein OPA58 precursor (Fragment).
GN OPA5.
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=485;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MS11 / F3;
RX MEDLINE=93178439; PubMed=8440254;
RA Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
RT "Variable opacity (Opa) outer membrane proteins account for the cell
RT tropisms displayed by Neisseria gonorrhoeae for human leukocytes and
RT epithelial cells";
RL EMO J. 12:641-650(1993).
CC -1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
CC VARIATION.
CC -1- SUBCELLULAR LOCATION: Outer membrane.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z18937; CAAT9370.1; -
DR PIR; S28624; S28624.
DR InterPro; IPR003394; Opacity.
DR Pfam; PF02462; Opacity; 1.
KW Outer membrane; Multigene family; Signal.
FT NON_TER 1 1
FT SIGNAL <1 1 POTENTIAL.
FT CHAIN 2 >237 OPACITY PROTEIN OPA58.
FT NON_TER 237 237
SQ SEQUENCE 237 AA; 26855 MW; B165033B2CDBA53 CRC64;
Query Match 26.7%; Score 231.5; DB 1; Length 237;
Best Local Similarity 30.0%; Pred. No. 8.3e-14;
Matches 70; Conservative 23; Mismatches 35; Indels 85; Gaps 9;
QY 24 GPYVQADAAHA-----KASSLSGSAKPS-----PRISAGYRINDLRF 61
DB 8 GPYVQADLAAYAEHITHDYPQGTGPKDKISTVSDYFRNIRKTHSHPRVSVYDGFQGMRI 67
QY 62 AVDYTRKNT-----KAPSTDFK-----LYSIGSAIYDEPTOS 93
DB 68 AADYARARKMNDNKKYSVSIKELRNKRVNGNRKTKTENDENGTFHVAVSSLSGSAVYDFKL 127
QY 94 QSPYKPYLGARLSLN--RASVD-----LGG-----SDSPS 121
DB 128 NDKFKPYIGARVAVGAVRHSHIDSTKKTTEVTTLHGPGITTPYPPKNTQDAHRESDSIR 187
QY 122 QSTGGLAVAGSVAVTPVNDLAGRYNTYKNTVKNVRSGLSAGYRVKE 174
DB 188 R-VGLGAVAGVGDITPNTLDAGRYHYHWGLRLENT-R-FKTHEASLGVRVRF 237
RESULT 7
OPAF_NEIGO STANDARD; PRT; 234 AA.
AC 004878;
DT 01-OCT-1993 (Rel. 27, Created)

DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Opacity protein OPA55 precursor (Fragment).
GN OPA5.
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=485;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MS11 / F3;
RX MEDLINE=93178439; PubMed=8440254;
RA Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
RT "Variable opacity (Opa) outer membrane proteins account for the cell
RT tropisms displayed by Neisseria gonorrhoeae for human leukocytes and
RT epithelial cells";
RL EMO J. 12:641-650(1993).
CC -1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
CC VARIATION.
CC -1- SUBCELLULAR LOCATION: Outer membrane.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z18933; CAAT9366.1; -
DR PIR; S28632; S28632.
DR InterPro; IPR003394; Opacity.
DR Pfam; PF02462; Opacity; 1.
KW Outer membrane; Multigene family; Signal.
FT NON_TER 1 1
FT SIGNAL <1 1 POTENTIAL.
FT CHAIN 2 >234 OPACITY PROTEIN OPA55.
FT NON_TER 234 234
SQ SEQUENCE 234 AA; 26881 MW; 8EEB30B3A774C766 CRC64;
Query Match 26.6%; Score 231; DB 1; Length 234;
Best Local Similarity 29.8%; Pred. No. 9.1e-14;
Matches 68; Conservative 22; Mismatches 60; Indels 78; Gaps 8;
QY 24 GPYVQADAAHA-----KASSLSGSAK-----GSPRISAGYRINDLRF 61
DB 8 GPYVQADLAAYAEHITHDYPQGTGPKDKISTVSDYFRNIRKTHSHPRVSVYDGFQGMRI 67
QY 62 AVDYTRKNT-----KAPSTDFK-----LYSIGSAIYDEPTOS 95
DB 68 AADYARARKMNDNKKYSVSIKELRNKRVNGNRKTKTENDENGTFHVAVSSLSGSAVYDFKL 127
QY 96 PYKPYLGARLSLN--RASVD-----LGG-----SDSPSQTSTG 126
DB 128 KFKPYIGARVAVGAVRHSHIDSTKKTTRKLTSSYGLNPTVTEENTQNAHQSISIRRG 167
QY 127 LGVLAGVAVTPVNDLAGRYNTYKNTVKNVRSGLSAGYRVKE 174
DB 188 LGVIAGVFDTIPKLTLDGTGRYHYHWGLRLENT-R-FKTHEASLGVRVRF 234
RESULT 8
OPAF_NEIGO STANDARD; PRT; 234 AA.
AC 004879;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Opacity protein OPA56 precursor (Fragment).
GN OPA6.
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=485;

```

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MS11 / F3;
RX MEDLINE=93178439; PubMed=8440254;
RA Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
RT "Variable opacity (Opa) outer membrane proteins account for the cell
RT tropisms displayed by Neisseria gonorrhoeae for human leukocytes and
RT epithelial cells.";
RL EMBL J. 12:641-650(1993).
CC -1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
CC VARIATION.
CC -1- SUBCELLULAR LOCATION: Outer membrane.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; 218934; CAA79367.1; -.
DR PIR; S28620; S28620.
DR InterPro; IPR003394; Opacity.
DR Pfam; PF02462; Opacity; 1.
KM Outer membrane; Multigene family; Signal.
FT SIGNAL 1 1
FT NON_TER 1 1
FT CHAIN 2 >234 POTENTIAL.
FT NON_TER 234 234 OPACITY PROTEIN OPA56.
SQ SEQUENCE 234 AA; 26868 MW; 5175C6606839EFFB CRC64;

Query Match
Best Local Similarity 26.6%; Score 231; DB 1; Length 234;
Matches 67; Conservative 23; Mismatches 60; Indels 78; Gaps 8;

QY 24 GFYVQADAAHA-----KASSSLGSAK-----GPSRISAGYRINDLRF 61
DB 8 GPYVQADLAAYEHITHDPEQTGTRKKDKISTVDFRNVRTHSHIPRVSVYDQGWRI 67
QY 62 ANDYTRYKNYKAP--STDFK-----LYSIGASAIYDFDQS 95
DB 68 AADYATYRRKMDKYSVDIKELENNQNRKDLKTENQENGTFHAYSLGSLAVYDFKLAND 127
QY 96 PVKPYTGARLSLN--RASVD-----LGC-----SDSFQSTSTG 126
DB 128 KRPPIYGARVAAGVHRHSIDSTKTKTTLTSSYGGINPTVTEENTONAHHSIRRVG 187
QY 127 LCVLAGVSAYAVPNVDLDAGYRYNYIGKYNVKNVRSGLSAGVRYKF 174
DB 188 LCVIAGVGFDIPKLTLDGYRYRHHWGRLENTR-FKTHASLSGVYRFF 234

RESULT 9
OP67_NEIGO STANDARD; PRT; 233 AA.
AC Q05034;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Opacity protein OPA67 precursor (Fragment).
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=485;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VPI;
RX MEDLINE=93178439; PubMed=8440254;
RA Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
RT "Variable opacity (Opa) outer membrane proteins account for the cell
RT tropisms displayed by Neisseria gonorrhoeae for human leukocytes and
RT epithelial cells.";

```

```

RL EMBL J. 12:641-650(1993).
CC -1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
CC VARIATION.
CC -1- SUBCELLULAR LOCATION: Outer membrane.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; 218942; CAA79375.1; -.
DR PIR; S28625; S28625.
DR InterPro; IPR003394; Opacity.
DR Pfam; PF02462; Opacity; 1.
KM Outer membrane; Multigene family; Signal.
FT SIGNAL 1 1
FT NON_TER 1 1
FT CHAIN 2 >233 POTENTIAL.
FT NON_TER 233 233 OPACITY PROTEIN OPA67.
SQ SEQUENCE 233 AA; 26039 MW; 6C13A46AB163C67F CRC64;

Query Match
Best Local Similarity 26.5%; Score 230; DB 1; Length 233;
Matches 65; Conservative 29; Mismatches 61; Indels 78; Gaps 7;

QY 19 AEG-ASGYVQADAAHA-----KASSSLGSAKG-----SPRISAGY 54
DB 2 SEGNGRGPYVQADLAAYERITHDYPEATAQKKGTITISVDYRNIRTHSVHPRVSVG 61
QY 55 RINDRFAPVDYTRYKNY-----KAPSDFKLYSIGSAIYDFD 92
DB 62 DGGKRIADYARIRKMNKSYVSISKLNQYKKTENQENGTFHASSLSGSAVYDFK 121
QY 93 TQSPKPYTGARLSLN--RASVDL-----GGSDFS 121
DB 122 LNDKFKPYIGARVAAGVHRHSIDSTKTKTGLTTAGARGAAPVSSPYKNTQADHQSNS 181
QY 122 QTSGLGVLAGVSAYAVPNVDLDAGYRYNYIGKYNVKNVRSGLSAGVRYKF 174
DB 182 IRRVGLVIAAGVGFDIPNLTLDAGYRYHWWGRLENTR-FKTHASLSGVYRFF 233

RESULT 10
OP68_NEIGO STANDARD; PRT; 234 AA.
AC P11297;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Opacity protein V28 precursor (Fragment).
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=485;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87002493; PubMed=3093085;
RA Stern A., Brown M., Nickel P., Meyer T.F.;
RT "opacity genes in Neisseria gonorrhoeae: control of phase and
RT antigenic variation.";
RL Cell 47:61-71(1986).
CC -1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
CC VARIATION.
CC -1- SUBCELLULAR LOCATION: Outer membrane.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way

```

modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

DR EMBL: M14747; NOT_ANNOTATED_CDS.

DR PIR: B24429; K0N8.

DR InterPro: IPR003394; Opacity: 1.

DR Pfam: PF02462; Opacity: 1.

DR Outer membrane; Multigene family: Signal.

FT SIGNAL 1 1 POTENTIAL.

FT CHAIN 2 >234 OPACITY PROTEIN V28.

FT NON_TER 234 234

SEQUENCE 234 AA; 26770 MW; 339AE09C2FE75E4 CRC64;

Query Match 25.9%; Score 225; DB 1; Length 234;

Best Local Similarity 29.8%; Pred. No. 3.1e-13;

Matches 68; Conservative 22; Mismatches 60; Indels 78; Gaps 8;

QY 24 GYVQADAAHA-----KASSLSGSAK-----GSPRISAGYRINDLR 61

DB 8 GYVQADAAHAERHTHDYDEPTGKDKISTVSDYFRNIRTHSHIPRVSGYDFGGMRI 67

QY 62 AVDYTRK--NYKAPSTDEK-----LYSGASAIYDPTQSP 95

DB 68 AADYARFKRKNDKYSVDIKELKNKNDKTDENGTFHNVSLGSLAVYDFKIND 127

QY 96 PVKPYLGARLSLN--RASVD-----LGG-----SDFSQSTSG 126

DB 128 KKPPIYGAIVAAVGHVHSDYSTRKTKTFLTSSYGLINPTVTEENTONAHNSISIRRV 187

QY 127 LGVLAGSVAVTPNVDDAGYRNYIGKVTYKVNRSGLSAGYRVKF 174

DB 188 LGVLAGVGDITPKLTLADAGYRHYHMGLENTFRTHASLGVRYRF 234

RESULT 11

OP66_NEIGO STANDARD; PRT; 234 AA.

AC 004885;

DT 01-OCT-1993 (Rel. 27, Created)

DT 01-OCT-1993 (Rel. 27, Last sequence update)

DT 01-NOV-1995 (Rel. 32, Last annotation update)

DE Opacity protein OPA65 precursor (Fragment).

OS Neisseria gonorrhoeae.

OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.

OX NCBI_TaxID=485;

RN (1)

RP SEQUENCE FROM N.A.

RC STRAIN=VPI;

RX MEDLINE=93178439; PubMed=8440254;

RA Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;

RT "Variable opacity (Opa) outer membrane proteins account for the cell

tropisms displayed by Neisseria gonorrhoeae for human leukocytes and

epithelial cells.";

RL EMBO J. 12:641-650(1993).

-1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA

PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE

VARIATION.

-1- SUBCELLULAR LOCATION: Outer membrane.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

between the Swiss Institute of Bioinformatics and the EMBL outstation -

the European Bioinformatics Institute. There are no restrictions on its

use by non-profit institutions as long as its content is in no way

modified and this statement is not removed. Usage by and for commercial

entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC EMBL: Z18940; CAA79374.1; -

DR PIR: S28617; S28617.

DR InterPro: IPR003394; Opacity.

DR Pfam: PF02462; Opacity; 1.

KW Outer membrane; Multigene family; Signal.

FT NON_TER 1 1 POTENTIAL.

FT SIGNAL 2 >234 OPACITY PROTEIN OPA65.

FT CHAIN 234 234

FT NON_TER 234 234

SEQUENCE 234 AA; 26242 MW; D66A0BA8424C2F1 CRC64;

Query Match 25.9%; Score 225; DB 1; Length 234;

Best Local Similarity 28.5%; Pred. No. 3.1e-13;

Matches 65; Conservative 26; Mismatches 59; Indels 78; Gaps 8;

QY 24 GYVQADAAHA-----KASSLSGSAK-----AKGSPRISAGYRINDLR 61

DB 8 GYVQADAAHAERHTHDYDEPTGAKKAQLSTVSDYFRNIRTHSHIPRVSGYDFGGMRI 67

QY 62 AVDYTRK--NYKAPSTDEK-----LYSGASAIYDPTQSP 96

DB 68 AADYARFKRKESNSIKKYTEDIKDKYKTEKTEHOENGTFHNVSLGSLSTYDFQISDK 127

QY 97 VKPYLGARL-----SLNRSAYDL-----GG-----SDFSQSTSG 126

DB 128 IKPYIGRVAGVGHVHSDYSTRKTKTFLTSSYGLINPTVTEENTONAHNSISIRRV 187

QY 127 LGVLAGSVAVTPNVDDAGYRNYIGKVTYKVNRSGLSAGYRVKF 174

DB 188 FGAMAGVGDIVAPGLTLADAGYRHYHMGLENTFRTHASLGVRYRF 234

RESULT 12

OP66_NEIGO STANDARD; PRT; 238 AA.

AC 005033;

DT 01-OCT-1993 (Rel. 27, Created)

DT 01-OCT-1993 (Rel. 27, Last sequence update)

DT 01-NOV-1995 (Rel. 32, Last annotation update)

DE Opacity protein OPA66 precursor (Fragment).

OS Neisseria gonorrhoeae.

OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.

OX NCBI_TaxID=485;

RN (1)

RP SEQUENCE FROM N.A.

RC STRAIN=VPI;

RX MEDLINE=93178439; PubMed=8440254;

RA Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;

RT "Variable opacity (Opa) outer membrane proteins account for the cell

tropisms displayed by Neisseria gonorrhoeae for human leukocytes and

epithelial cells.";

RL EMBO J. 12:641-650(1993).

-1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA

PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE

VARIATION.

-1- SUBCELLULAR LOCATION: Outer membrane.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

between the Swiss Institute of Bioinformatics and the EMBL outstation -

the European Bioinformatics Institute. There are no restrictions on its

use by non-profit institutions as long as its content is in no way

modified and this statement is not removed. Usage by and for commercial

entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC EMBL: Z18941; CAA79374.1; -

DR PIR: S28619; S28619.

DR InterPro: IPR003394; Opacity.

DR Pfam: PF02462; Opacity; 1.

KW Outer membrane; Multigene family; Signal.

FT SIGNAL 1 1 POTENTIAL.

FT CHAIN 2 >238 OPACITY PROTEIN OPA66.

FT NON_TER 238 238

SEQUENCE 238 AA; 26888 MW; B6E38AF1585263AA CRC64;

Query Match 25.9%; Score 225; DB 1; Length 238;

Best Local Similarity 28.9%; Pred. No. 3.2e-13;
Matches 67; Conservative 25; Mismatches 58; Indels 82; Gaps 8;

QY 24 GFVYQADAAHA-----KASSSLGSAKF-----SPRISAGYRINDLR 61
D 8 GPYVQADLAAYEHITHDYPKPTDPSKGLSTVDYFRNRTSHIRPVSGVDEGWRK 67
QY 62 AVDYTRK--NYKAPSDER-----LYSIGASAIYDFDT 93
D 68 AADARTRKRNDSKYSVSTINLQRTSNGNRDRKTENDENGSEFHAVSSIGLSAVYDFKL 127
QY 94 QSPVPPYLGARLSLN--RASVD-----LGSPD-----SFGQ 122
D 128 NDKFKPYIGARVAYGVRHSIDSTKKTETITAGARGTDPYVSPYKNTQAHQESNSI 187
QY 123 TSGGLVAGVSAVTPNDLDAGRYNNTGKYNVKNVRSGLSAGVRYKF 174
D 188 RRVGLVAGVGPDIPTNLTLDAGRYHNMGRLENTF--FTHASLSGVRYRF 238

RESULT 13

OPAD_NEIGO STANDARD; PRT; 238 AA.

AC 004884;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Opacity protein OPA60 precursor (Fragment).
GN OPAH.
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=485;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MS11 / F3;
RX MEDLINE=93178439; PubMed=8440254;
RA Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
RT "Variable opacity (Opa) outer membrane proteins account for the cell
RT tropisms displayed by Neisseria gonorrhoeae for human leukocytes and
RT epithelial cells."
RL EMO J. 12:641-650(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MS11 / V18;
RX MEDLINE=92114767; PubMed=1815562;
RA Bhat K.S., Gibbs C.P., Barrera O., Morrison S.G., Jaehnis F.,
RA Stern A., Kupsch E.-M., Meyer T.F., Swanson J.;
RT "The opacity proteins of Neisseria gonorrhoeae strain MS11 are
RT encoded by a family of 11 complete genes."
RL Mol. Microbiol. 5:1889-1901(1991).
RN [3]
RP ERRATUM.
RX MEDLINE=92261323; PubMed=1584024;
RA Bhat K.S., Gibbs C.P., Barrera O., Morrison S.G., Jaehnis F.,
RA Stern A., Kupsch E.-M., Meyer T.F., Swanson J.;
RL Mol. Microbiol. 6:1073-1076(1992).

-1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
VARIATION.
-1- SUBCELLULAR LOCATION: Outer membrane.

This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

DR EMBL; Z18939; CAA79372.1; -;
DR EMBL; X60711; CAA43121.1; -;
DR PIR; S28631; S28631.
DR InterPro; IPR003394; Opacity.

DR Pfam; PF02462; Opacity; 1.
KW Outer membrane; Multigene family; Signal.

FT NON_TER 1 1
FT SIGNAL <1 1
FT CHAIN 2 >238 POTENTIAL.
FT VARIANT 2 4 OPACITY PROTEIN OPA60.
FT VARIANT 234 234 SED -> MLKA (IN MS11 / V18).
FT NON_TER 238 238 V -> M (IN MS11 / V18).
SQ SEQUENCE 238 AA: 27073 MW: 883A3560C2DF1B9F CRC64;

Query Match

Best Local Similarity 25.9%; Score 225; DB 1; Length 238;
Matches 67; Conservative 24; Mismatches 66; Indels 82; Gaps 6;

QY 17 ALAEGASGFYQADAAHA-----KASSSLG-----AKGSPRISAGY 54
D 1 ASEDGGRPYQADLAAYEHITHDYPEPTAPNNKISTVDYFRNRTSHIRPVSGV 60
QY 55 RINDLRFAVDYTRKKNY-----KAPSTDFKLYSIGAS 86
D 61 DFGWRRIADYARVKKNNKNSVNIENVRIRKENGIRIDKKTENDENGTFHAVSSIGLS 120
QY 87 AIYDDTQSPVPPYLGARLSLN--RASVD-----LG 115
D 121 AIYFQINDKRPYIGARVAYGVRHSIDSTKKTETITVPSNAPNGAVTYNTDPKTON 180
QY 116 GDSFSTSTGGLVAGVSAVTPNDLDAGRYNNTGKYNVKNVRSGLSAGVRYKF 174
D 181 DYGSNIRVGLVAGVGPDIPTNLTLDAGRYHNMGRLENTF--FTHASLSGVRYRF 238

RESULT 14

OPAD_NEIGO STANDARD; PRT; 243 AA.

AC 004883;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Opacity protein OPA59 precursor (Fragment).
GN OPAD.
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=485;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MS11 / F3;
RX MEDLINE=93178439; PubMed=8440254;
RA Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
RT "Variable opacity (Opa) outer membrane proteins account for the cell
RT tropisms displayed by Neisseria gonorrhoeae for human leukocytes and
RT epithelial cells."
RL EMO J. 12:641-650(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MS11 / V18;
RX MEDLINE=92114767; PubMed=1815562;
RA Bhat K.S., Gibbs C.P., Barrera O., Morrison S.G., Jaehnis F.,
RA Stern A., Kupsch E.-M., Meyer T.F., Swanson J.;
RT "The opacity proteins of Neisseria gonorrhoeae strain MS11 are
RT encoded by a family of 11 complete genes."
RL Mol. Microbiol. 5:1889-1901(1991).
RN [3]
RP ERRATUM.
RX MEDLINE=92261323; PubMed=1584024;
RA Bhat K.S., Gibbs C.P., Barrera O., Morrison S.G., Jaehnis F.,
RA Stern A., Kupsch E.-M., Meyer T.F., Swanson J.;
RL Mol. Microbiol. 6:1073-1076(1992).

-1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
VARIATION.

This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

DR EMBL; Z18938; CAA79371.1; -;
DR PIR; S28629; S28629.
DR InterPro; IPR003394; Opacity.
DR Pfam; PF02462; Opacity; 1.
KW Outer membrane; Multigene family; Signal.
FT NON_TER 1 1
FT SIGNAL <1 1
FT CHAIN 2 >243 POTENTIAL.
FT CHAIN 2 >243 OPACITY PROTEIN OPA59.

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 28, 2002, 15:56:04 ; Search time 19.9713 Seconds
(without alignments)
1507.218 Million cell updates/sec

Title: US-09-684-883-6

Perfect score: 1 MKKALTLRLALPAAALAE.....VNTVKNVSGELSGVRYKF 174

Sequence: 1 MKKALTLRLALPAAALAE.....VNTVKNVSGELSGVRYKF 174

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SP. Archaea: *
2: SP. Bacteria: *
3: SP. Fungi: *
4: SP. Human: *
5: SP. Invertebrate: *
6: SP. Mammal: *
7: SP. Mhc: *
8: SP. Organelle: *
9: SP. Phage: *
10: SP. Plant: *
11: SP. Rodent: *
12: SP. Virus: *
13: SP. Vertebrate: *
14: SP. Unclassified: *
15: SP. Virus: *
16: SP. Bacteriophage: *
17: SP. Archaeop: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	868	100.0	174	16	P95372
2	866	99.8	174	2	Q9RP16
3	862	99.3	174	2	Q9R2R1
4	860	99.1	174	2	Q9RP18
5	858	98.8	174	16	Q9RP17
6	854	98.4	174	2	P96943
7	838.5	96.6	175	2	P95371
8	834	96.1	174	2	P95343
9	246	28.3	256	2	051124
10	243.5	28.1	186	16	Q9C819
11	243.5	28.1	241	2	Q9A80
12	243	28.0	234	2	Q9R719
13	243	28.0	234	2	007280
14	242	27.9	234	2	Q9R718
15	240.5	27.7	232	2	Q9K4F9
16	240	27.6	237	2	031176

17	239.5	27.6	230	2	Q9R9A7	Q9R9A7 neisseria m
18	239	27.5	241	2	Q9K4T4	Q9K4T4 neisseria l
19	239	27.5	256	2	051126	051126 neisseria m
20	239	27.5	259	2	051125	051125 neisseria m
21	238.5	27.5	232	2	Q9R3P5	Q9R3P5 neisseria m
22	238	27.4	270	2	Q9R0V4	Q9R0V4 neisseria m
23	237.5	27.4	257	2	Q50929	Q50929 neisseria m
24	237	27.3	234	2	007287	007287 neisseria f
25	236.5	27.2	241	2	007274	007274 neisseria m
26	236	27.2	262	2	033388	033388 neisseria m
27	235.5	27.1	232	2	Q9K4T3	Q9K4T3 neisseria s
28	235.5	27.1	241	2	007912	007912 neisseria s
29	235	27.1	283	2	Q50943	Q50943 neisseria m
30	233	26.8	240	2	007925	007925 neisseria m
31	233	26.8	272	2	051013	051013 neisseria m
32	232.5	26.8	253	2	051303	051303 neisseria s
33	232	26.7	233	2	Q9K4T5	Q9K4T5 neisseria l
34	232	26.7	235	2	030753	030753 neisseria l
35	231.5	26.7	232	2	Q9R9A9	Q9R9A9 neisseria m
36	231.5	26.7	232	2	Q9R9A8	Q9R9A8 neisseria m
37	231	26.6	237	2	Q9K4T6	Q9K4T6 neisseria l
38	230.5	26.6	241	2	007273	007273 neisseria m
39	230	26.5	235	2	030752	030752 neisseria m
40	228.5	26.3	232	2	Q9K4T7	Q9K4T7 neisseria l
41	227	26.2	242	2	Q9K4T8	Q9K4T8 neisseria l
42	226.5	26.1	238	2	031172	031172 neisseria m
43	226.5	26.1	243	2	007278	007278 neisseria m
44	226	26.0	237	2	031175	031175 neisseria m
45	226	26.0	260	2	033389	033389 neisseria m

ALIGNMENTS

RESULT 1
P95372 PRELIMINARY; PRT; 174 AA.
ID P95372;
AC 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE OUTER MEMBRANE PROTEIN PRECURSOR.
GN NSPA OR NMA0862.
OS Neisseria meningitidis, and
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487, 65699;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=24063;
RA Martin D., Cadieux N., Hamel J., Rioux C., Brodeur B.R.;
RN Submitted (MAR-1996) to the EMBL/Genbank/DBJ databases.
RP SEQUENCE FROM N.A.
RC STRAIN=22491 / SEROGROUP A / SEROTYPE 4A;
RX MEDLINE=20222556; PubMed=10761919;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Feltham T., Hamlin N., Holtroyd S.,
RA Jagers K., Leather S., Moule S., Mungall K., Quail M.A.,
RA Rajadaram M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrell B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22491."
RT Nature 404:502-506 (2000).
DR EMBL: U52068; AAB41580.1; -;
DR EMBL: AL162754; CAB84143.1; -;
DR InterPro: IPR003394; Opacity: 1.
DR Pfam: PF02462; Opacity: 1.
KM Signal: Complete proteome.
FT SIGNAL. 1 19 POTENTIAL.
SQ SEQUENCE 174 AA; 18355 MW; E8A4A1ADAFA6F009 CRC64;

```

Query Match          100.0%; Score 866; DB 16; Length 174;
Best Local Similarity 100.0%; Pred. No. 1.2e-64;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MKKALATLIALALPAALAEAGSGFYVOADAHAHAKASSLSGSAKGFSPRISAGYRINDLR 60
    |||||||
DB 1 MKKALATLIALALPAALAEAGSGFYVOADAHAHAKASSLSGSAKGFSPRISAGYRINDLR 60

OY 61 FAVDYTRYKKNYKAPSTDPEKLYSIGASAIYDFDTQSPVKPYLGARLSLNRAVDLGSDSF 120
    |||||||
DB 61 FAVDYTRYKKNYKAPSTDPEKLYSIGASAIYDFDTQSPVKPYLGARLSLNRAVDLGSDSF 120

OY 121 SQTSTGLGVLAGVSYAVTPNVDDLADAGYRNYIGKVTNVKVRSGELSGAGYRVKF 174
    |||||||
DB 121 SQTSTGLGVLAGVSYAVTPNVDDLADAGYRNYIGKVTNVKVRSGELSGAGYRVKF 174

RESULT 2
O9RP16 PRELIMINARY; PRT; 174 AA.
AC O9RP16;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, last annotation update)
DE SURFACE PROTEIN A.
GN NSPA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NG3/88;
RA Moe G.R., Tan S., Granoff D.M.;
RT "Differences in Surface Expression of Neisserial Surface Protein A
    among Neisseria meningitidis Group B strains.";
RL Infect. Immun. 0:0-0(1999).
DR EMBL; AF175681; AAD53284.1; -.
DR InterPro; IPR003394; Opacity.
DR Pfam; PF02462; Opacity; 1.
SQ SEQUENCE 174 AA; 18355 MW; ECF6F38B9286800E CRC64;

Query Match          99.8%; Score 866; DB 2; Length 174;
Best Local Similarity 99.4%; Pred. No. 1.8e-64;
Matches 173; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 MKKALATLIALALPAALAEAGSGFYVOADAHAHAKASSLSGSAKGFSPRISAGYRINDLR 60
    |||||||
DB 1 MKKALATLIALALPAALAEAGSGFYVOADAHAHAKASSLSGSAKGFSPRISAGYRINDLR 60

OY 61 FAVDYTRYKKNYKAPSTDPEKLYSIGASAIYDFDTQSPVKPYLGARLSLNRAVDLGSDSF 120
    |||||||
DB 61 FAVDYTRYKKNYKAPSTDPEKLYSIGASAIYDFDTQSPVKPYLGARLSLNRAVDLGSDSF 120

OY 121 SQTSTGLGVLAGVSYAVTPNVDDLADAGYRNYIGKVTNVKVRSGELSGAGYRVKF 174
    |||||||
DB 121 SQTSTGLGVLAGVSYAVTPNVDDLADAGYRNYIGKVTNVKVRSGELSGAGYRVKF 174

RESULT 3
O9R2R1 PRELIMINARY; PRT; 174 AA.
AC O9R2R1;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
DE SURFACE PROTEIN A.
GN NSPA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M136, AND B232;

```

```

RA Moe G.R., Tan S., Granoff D.M.;
RT "Differences in Surface Expression of Neisserial Surface Protein A
    among Neisseria meningitidis Group B strains.";
RL Infect. Immun. 0:0-0(1999).
DR EMBL; AF175679; AAD53282.1; -.
DR EMBL; AF175677; AAD53280.1; -.
DR InterPro; IPR003394; Opacity.
DR Pfam; PF02462; Opacity; 1.
SQ SEQUENCE 174 AA; 18385 MW; ECF6F39A9286910E CRC64;

Query Match          99.3%; Score 862; DB 2; Length 174;
Best Local Similarity 98.9%; Pred. No. 3.8e-64;
Matches 172; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 MKKALATLIALALPAALAEAGSGFYVOADAHAHAKASSLSGSAKGFSPRISAGYRINDLR 60
    |||||||
DB 1 MKKALATLIALALPAALAEAGSGFYVOADAHAHAKASSLSGSAKGFSPRISAGYRINDLR 60

OY 61 FAVDYTRYKKNYKAPSTDPEKLYSIGASAIYDFDTQSPVKPYLGARLSLNRAVDLGSDSF 120
    |||||||
DB 61 FAVDYTRYKKNYKAPSTDPEKLYSIGASAIYDFDTQSPVKPYLGARLSLNRAVDLGSDSF 120

OY 121 SQTSTGLGVLAGVSYAVTPNVDDLADAGYRNYIGKVTNVKVRSGELSGAGYRVKF 174
    |||||||
DB 121 SQTSTGLGVLAGVSYAVTPNVDDLADAGYRNYIGKVTNVKVRSGELSGAGYRVKF 174

RESULT 4
O9RP18 PRELIMINARY; PRT; 174 AA.
AC O9RP18;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
DE SURFACE PROTEIN A.
GN NSPA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=8047;
RA Moe G.R., Tan S., Granoff D.M.;
RT "Differences in Surface Expression of Neisserial Surface Protein A
    among Neisseria meningitidis Group B strains.";
RL Infect. Immun. 0:0-0(1999).
DR EMBL; AF175676; AAD53279.1; -.
DR InterPro; IPR003394; Opacity.
DR Pfam; PF02462; Opacity; 1.
SQ SEQUENCE 174 AA; 18357 MW; 0205A1DA1B7F005 CRC64;

Query Match          99.1%; Score 860; DB 2; Length 174;
Best Local Similarity 98.9%; Pred. No. 5.5e-64;
Matches 172; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 MKKALATLIALALPAALAEAGSGFYVOADAHAHAKASSLSGSAKGFSPRISAGYRINDLR 60
    |||||||
DB 1 MKKALATLIALALPAALAEAGSGFYVOADAHAHAKASSLSGSAKGFSPRISAGYRINDLR 60

OY 61 FAVDYTRYKKNYKAPSTDPEKLYSIGASAIYDFDTQSPVKPYLGARLSLNRAVDLGSDSF 120
    |||||||
DB 61 FAVDYTRYKKNYKAPSTDPEKLYSIGASAIYDFDTQSPVKPYLGARLSLNRAVDLGSDSF 120

OY 121 SQTSTGLGVLAGVSYAVTPNVDDLADAGYRNYIGKVTNVKVRSGELSGAGYRVKF 174
    |||||||
DB 121 SQTSTGLGVLAGVSYAVTPNVDDLADAGYRNYIGKVTNVKVRSGELSGAGYRVKF 174

RESULT 5
O9RP17 PRELIMINARY; PRT; 174 AA.
AC O9RP17;
DT 01-MAY-2000 (TREMBLrel. 13, Created)

```

DT 01-MAY-2000 (Tremblrel. 13, last sequence update)
 DE SURFACE PROTEIN A (OUTER MEMBRANE PROTEIN NSGA).
 GN NSGA OR NMB0663.
 OS Neisseria meningitidis, and
 OC Neisseria meningitidis (serogroup B).
 RX Neisseria meningitidis; beta subdivision; Neisseriaceae; Neisseria.
 NX NCBI_TaxID=487, 491;
 RP SEQUENCE FROM N.A.
 RC STRAIN=CU385;
 RA Moe G.R., Tan S., Granoff D.M.;
 RT "Differences in Surface Expression of Neisserial Surface Protein A
 among Neisseria meningitidis Group B strains.";
 RL Infect. Immun. 0:0-0(1999).
 RN [12]
 SQ SEQUENCE FROM N.A.
 RC STRAIN=MC58 / SEROGROUP B;
 RX MEDLINE=20175755; PubMed=10710307;
 RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
 Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
 Nelson W.C., Gill M.U., Deboy R., Peterson J.D., Hickey E.K.,
 Hart D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
 Mason T., Glecko A., Parksey D.S., Blair E., Cifton H., Clark E.B.,
 Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,
 Gill J., Scarlato V., Maignani V., Pizzi M., Grandi G., Sun L.,
 Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
 RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
 MC58.";
 RL Science 287:1809-1815 (2000).
 DR EMBL: AF175678; AAD53281.1;
 DR EMBL: AE002420; AAF41081.1;
 DR TIGR: NMB0663;
 DR InterPro: IPR003394; Opacity.
 DR Pfam: PF02462; Opacity; 1.
 KW Complete proteome.
 SQ SEQUENCE 174 AA; 18397 MW; E8B02767DDC6E109 CRC64;

Query Match 98.8%; Score 858; DB 16; Length 174;
 Best Local Similarity 98.9%; Pred. No. 8.1e-64;
 Matches 172; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MKKALATLIALALPAALAEAGSGFYQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
 DB 1 MKKALATLIALALPAALAEAGSGFYQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
 QY 61 FAVDYTRYKNYKAPSTDFTKLYSIGASAIYDPTQSPVKPYLGARLSLNRAVDLGSDSF 120
 DB 61 FAVDYTRYKNYKAPSTDFTKLYSIGASAIYDPTQSPVKPYLGARLSLNRAVDLGSDSF 120
 QY 121 SOTSTGLVLAGSYAVTPNVLDAGYRNYIGKNTYKNSGELSGAVRVK 174
 DB 121 SOTSTGLVLAGSYAVTPNVLDAGYRNYIGKNTYKNSGELSGAVRVK 174

RESULT 6
 ID P96943 PRELIMINARY; PRT; 174 AA.
 AC P96943;
 DT 01-MAY-1997 (Tremblrel. 03, Created)
 DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE OUTER MEMBRANE PROTEIN PRECURSOR.
 GN NSGA.
 OS Neisseria meningitidis.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_TaxID=487;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=608B;
 RX MEDLINE=97149429; PubMed=8996237;
 RA Martin D., Cadieux N., Hamel J., Brodeur B.R.;
 RT "Costimulation of T cell activation by integrin-associated protein

RT (CD47) is an adhesion-dependent, CD28-independent signaling pathway.";
 RL J. Exp. Med. 185:1-11(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NGP165, M986, AND NG6/88;
 RA Moe G.R., Tan S., Granoff D.M.;
 RT "Differences in Surface Expression of Neisserial Surface Protein A
 among Neisseria meningitidis Group B strains.";
 RL Infect. Immun. 0:0-0(1999).
 DR EMBL: AF175683; AAD53286.1;
 DR EMBL: AF175680; AAD53283.1;
 DR EMBL: AF175682; AAD53285.1;
 DR InterPro: IPR003394; Opacity.
 DR Pfam: PF02462; Opacity; 1.
 KW Signal.
 FT SIGNAL.
 SQ SEQUENCE 174 AA; 18425 MW; E8B02767DDC6E19 CRC64;

Query Match 98.4%; Score 854; DB 2; Length 174;
 Best Local Similarity 98.3%; Pred. No. 1.7e-63;
 Matches 171; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKKALATLIALALPAALAEAGSGFYQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
 DB 1 MKKALATLIALALPAALAEAGSGFYQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
 QY 61 FAVDYTRYKNYKAPSTDFTKLYSIGASAIYDPTQSPVKPYLGARLSLNRAVDLGSDSF 120
 DB 61 FAVDYTRYKNYKAPSTDFTKLYSIGASAIYDPTQSPVKPYLGARLSLNRAVDLGSDSF 120
 QY 121 SOTSTGLVLAGSYAVTPNVLDAGYRNYIGKNTYKNSGELSGAVRVK 174
 DB 121 SOTSTGLVLAGSYAVTPNVLDAGYRNYIGKNTYKNSGELSGAVRVK 174

RESULT 7
 ID P95371 PRELIMINARY; PRT; 175 AA.
 AC P95371;
 DT 01-MAY-1997 (Tremblrel. 03, Created)
 DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE OUTER MEMBRANE PROTEIN PRECURSOR.
 OS Neisseria meningitidis.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_TaxID=487;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MCH 88;
 RX MEDLINE=99386904; PubMed=10456958;
 RA Cadieux N., Plante M., Rioux C.R., Hamel J., Brodeur B.R., Martin D.;
 RT "Bactericidal and cross-protective activities of a monoclonal antibody
 directed against Neisseria meningitidis Nspa outer membrane protein.";
 RL Infect. Immun. 67:4955-4959(1999).
 DR EMBL: U52067; AAB41579.1;
 DR InterPro: IPR003394; Opacity.
 DR Pfam: PF02462; Opacity; 1.
 KW Signal.
 FT SIGNAL.
 SQ SEQUENCE 175 AA; 18572 MW; D1E8F2F55C2FEA CRC64;

Query Match 96.6%; Score 838.5; DB 2; Length 175;
 Best Local Similarity 97.1%; Pred. No. 3.4e-62;
 Matches 170; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 MKKALATLIALALPAALAEAGSGFYQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
 DB 1 MKKALATLIALALPAALAEAGSGFYQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
 QY 61 FAVDYTRYKNYKAPSTDFTKLYSIGASAIYDPTQSPVKPYLGARLSLNRAVDLGSDSF 119
 DB 61 FAVDYTRYKNYKAPSTDFTKLYSIGASAIYDPTQSPVKPYLGARLSLNRAVDLGSDSF 120

QY 120 FSGTSTGLGVLGAGSYAVTPNVDDAGRYNYIGKVTYKVRSGELSGAGYRVK 174
 DB 121 FSGTSTGLGVLGAGSYAVTPNVDDAGRYNYIGKVTYKVRSGELSGAGYRVK 175

RESULT 8
 P95343 PRELIMINARY; PRT: 174 AA.

AC P95343;
 DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE OUTER MEMBRANE PROTEIN PRECURSOR.
 OS Neisseria gonorrhoeae.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_TaxID=485;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B2;
 RX MEDLINE=99270944; PubMed=10338491;
 RA Plante M., Cadieux N., Rioux C.R., Hamel J., Brodeur B.R., Martin D.;
 RT "Antigenic and molecular conservation of the gonococcal Nspa
 protein.";
 RL Infect. Immun. 67:2855-2861(1999).
 DR EMBL: U52069; AAB41581.1; -;
 DR InterPro: IPR003394; Opacity.
 DR Pfam: PF02462; Opacity; 1.
 KW Signal.
 FT SIGNAL.
 SQ SEQUENCE 174 AA; 18337 MW; 1B558EC8A040841A CRC64;

Query Match 96.1%; Score 834; DB 2; Length 174;
 Best Local Similarity 95.4%; Pred. No. 8e-62; Mismatches 6; Indels 0; Gaps 0;
 Matches 166; Conservative 2;

QY 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
 DB 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60

QY 61 FAVDYTRYKRYKAPSTDFKITYSGASAIYDFQSPYKPYLIGARLSLNASVDLGSDSF 120
 DB 61 FAVDYTRYKRYKAPSTDFKITYSGASAIYDFQSPYKPYLIGARLSLNASVDLGSDSF 120

QY 121 SGTSTGLGVLGAGSYAVTPNVDDAGRYNYIGKVTYKVRSGELSGAGYRVK 174
 DB 121 SGTSTGLGVLGAGSYAVTPNVDDAGRYNYIGKVTYKVRSGELSGAGYRVK 174

RESULT 9
 O51124 PRELIMINARY; PRT: 256 AA.

ID O51124;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
 DE OPACITY OUTER MEMBRANE PROTEIN (FRAGMENT).
 GN OPA.
 OS Neisseria meningitidis.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_TaxID=487;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=24197;
 RX MEDLINE=98129089; PubMed=9467908;
 RA Hobbs M.M., Majorov B., Prasad P., Morelli G., Kusecek B.,
 RT "Recombinational reassortment among opa genes from ET-37 complex
 Neisseria meningitidis isolates of diverse geographical origins.";
 RL Microbiology 144:157-166(1998).
 DR EMBL: U37255; AAC46101.1; -;
 DR InterPro: IPR003394; Opacity.
 DR Pfam: PF02462; Opacity; 1.

FT NON TER 1 1
 SQ SEQUENCE 256 AA; 28335 MW; 9DA1C6079C6DD13F CRC64;

Query Match 28.3%; Score 246; DB 2; Length 256;
 Best Local Similarity 28.7%; Pred. No. 8.3e-13; Mismatches 65; Indels 78; Gaps 7;
 Matches 70; Conservative 31;

QY 8 LIALPAAALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 170
 DB 14 LFSSAQAQASRDSCHGPPYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 170

QY 48 PRISAGYRINDLRPAVDYTRYK-----NYKAPSTDFK-----LIS 82
 DB 74 PRVSGYDFGGMRIADYASRYKWKESNSTKKVTEADIANRYETKTEHQNGSFFHAAS 133

QY 83 IGASAIYDFQSPYKPYLIGARLSLN-----ASVDLG----- 116
 DB 134 LGLSAIYDFKINDKFKPYLIGARVAHYKQVHSEVETKTTVSKPATSPQGGPILQND 193

QY 117 -----SDPSFSGTSTGLGVLGAGSYAVTPNVDDAGRYNYIGKVTYKVRSGELSGAGY 170
 DB 194 PSKPPYHSHSSLSGLGVLGAGVFDTLPKLLDTGYRHNWGLEWTR-FKTHEVSLGM 252

QY 171 RYKF 174
 DB 253 RYRF 256

RESULT 10
 O9CM19 PRELIMINARY; PRT: 186 AA.

ID O9CM19;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE OPA.
 GN OPA OR PM1025.
 OS Pasteurella multocida.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Pasteurella.
 OX NCBI_TaxID=747;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PM70;
 RX MEDLINE=21145866; PubMed=11248100;
 RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
 RT "Complete genomic sequence of Pasteurella multocida pm70.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
 DR EMBL: AF006143; AAK03109.1; -;
 DR InterPro: IPR003394; Opacity.
 DR Pfam: PF02462; Opacity; 1.
 KW Complete proteome.
 SQ SEQUENCE 186 AA; 20512 MW; 1B17F044ACFC0157 CRC64;

Query Match 28.1%; Score 243.5; DB 16; Length 186;
 Best Local Similarity 32.3%; Pred. No. 9e-13; Mismatches 78; Indels 19; Gaps 5;
 Matches 61; Conservative 31;

QY 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRIN 57
 DB 2 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRIN 58

QY 58 DIRPAVDTRYKRYKAPSTDFKITYSGASAIYDFQSPYKPYLIGARLSLN 108
 DB 59 DIRPAVDTRYKRYKAPSTDFKITYSGASAIYDFQSPYKPYLIGARLSLN 118

QY 109 RASVDLGSDSF-----SGTSTGLGVLGAGSYAVTPNVDDAGRYNYIGKVTYKVRSGE 165
 DB 119 RASVDLGSDSF-----SGTSTGLGVLGAGSYAVTPNVDDAGRYNYIGKVTYKVRSGE 177

QY 166 LSAAGYRVK 174
 DB 178 AKYGLKRYDF 186

```

RESULT 11
ID 09AE80 PRELIMINARY; PRT; 241 AA.
AC 09AE80;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE OPACITY PROTEIN (FRAGMENT).
GN OPA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=29620;
RA MEDLINE=21221108; PubMed=11287631;
RA Zhu P., van der Ende A., Falush D., Brieske N., Morelli G., Bodo L.,
RA Popovic T., Schuurman I.G.A., Adegbola R.A., Zurth K., Gagneux S.,
RA Platonov A.E., Riou J.Y., Caugant D.A., Nicolas P., Achtman M.,
RT "Fit genotypes and escape variants of subgroup III Neisseria
RT meningitidis during three pandemics of epidemic meningitis.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:5234-5239(2001).
DR EMBL; AJ292238; CAC36361.1;
DR InterPro; IPR003394; Opacity.
DR Pfam; PF02462; Opacity; 1.
FT NON_TER
SQ SEQUENCE 241 AA; 26923 MW; 4923ACF9484BF183 CRC64;

Query Match 28.1%; Score 243.5; DB 2; Length 241;
Best Local Similarity 29.7%; Pred. No. 1.2e-12;
Matches 71; Conservative 33; Mismatches 54; Indels 81; Gaps 9;

QY 16 AALAEGA-SGFYVQADAAH-----KASSSLGS-----AKGSPRISAGY 54
DB 4 AASEDSGRSPYVQADLAVAAERITHDYPQATGANNSTVSDYFRNIRAHSHIPRVSVGY 63
QY 55 RINDLRFAVDYTRYK-----NYKAPSTDFK-----LYSIGASAI 88
DB 64 DFGDWRIADYASYRRKWKESNSYKKTVEFKHONGKQEDKTEHQNGSFHMTSLGISAI 123
QY 87 AAYDPTQSPYKPYLGARLSLN--RASVDL-----GSDS-FSQTST--- 125
DB 124 AYDFMTGSRFPYAGVAVGHVRSIDSTKTKTVLVPPNIPGCTPTITNOSTQDA 183
QY 126 -----GLGVLAGVSYAVTPNVDLAGRYNYIGKVNTRKVSSELGAGRVKF 174
DB 184 YHSHSIRRLGLGVAGVGFDTLPKLTLDYGRYHNMGRLENT-RKTHEVSLGKRYRF 241

RESULT 12
ID 09R719 PRELIMINARY; PRT; 234 AA.
AC 09R719;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE OPACITY PROTEIN (FRAGMENT).
GN OPA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=23906;
RA MEDLINE=98010345; PubMed=9350862;
RA Morelli G., Malorny B., Mueller K., Sella A., Wang J., del Valle J.,
RA Achtman M.,
RT "Clonal descent and microevolution of Neisseria meningitidis during 30
RT years of epidemic spread.";
RL Mol. Microbiol. 25:1047-1064(1997).
RN [2]

```

```

RP SEQUENCE FROM N.A.
RC STRAIN=3926;
RA Zhu P., van der Ende A., Falush D., Brieske N., Morelli G., Linz B.,
RA Popovic T., Schuurman I.G.A., Adegbola R.A., Zurth K., Gagneux S.,
RA Platonov A.E., Riou J.Y., Caugant D.A., Nicolas P., Achtman M.,
RT "Fit genotypes and escape variants of subgroup III Neisseria
RT meningitidis during three pandemics of epidemic meningitis.";
RL Submitted (JAN-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF001194; AAC32715.1;
DR EMBL; AJ292235; CAC36358.1;
DR InterPro; IPR003394; Opacity.
DR Pfam; PF02462; Opacity; 1.
FT NON_TER
SQ SEQUENCE 234 AA; 26161 MW; F97142F463136EC1 CRC64;

Query Match 28.0%; Score 243; DB 2; Length 234;
Best Local Similarity 29.3%; Pred. No. 1.3e-12;
Matches 68; Conservative 30; Mismatches 60; Indels 74; Gaps 8;

QY 16 AALAEGA-SGFYVQADAAH-----KASSSLGS-----AKGSPRISAGY 54
DB 4 AASEDSGRSPYVQADLAVAAERITHDYPQATGANNSTVSDYFRNIRAHSHIPRVSVGY 63
QY 55 RINDLRFAVDYTRYK-----NYKAPSTDFK-----LYSIGASAI 88
DB 64 DFGDWRIADYASYRRKWKESNSYKKTVEFKHONGKQEDKTEHQNGSFHMTSLGISAI 123
QY 89 YDPTQSPYKPYLGARLSLN-----ASVDLG-----SDSFQ 122
DB 124 YDFKLNDFKFPYIGVAVVAGHVKHOVHSEKTTVTNNCGPVPQGPFPAPVAVHSHI 183
QY 123 TSTGLGVLAGVSYAVTPNVDLAGRYNYIGKVNTRKVSSELGAGRVKF 174
DB 184 SSVGLGVLAGVGFDTLPKLTLDYGRYHNMGRLENT-RKTHEVSLGKRYRF 234

RESULT 13
ID 007280 PRELIMINARY; PRT; 234 AA.
AC 007280;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE OPACITY PROTEIN (FRAGMENT).
GN OPA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=23524;
RA MEDLINE=98010345; PubMed=9350862;
RA Morelli G., Malorny B., Muller K., Sella A., Wang J.F., del Valle J.,
RA Achtman M.,
RT "Clonal descent and microevolution of Neisseria meningitidis during 30
RT years of epidemic spread.";
RL Mol. Microbiol. 25:1047-1064(1997).
DR EMBL; AF001195; AAC32716.1;
DR InterPro; IPR003394; Opacity.
DR Pfam; PF02462; Opacity; 1.
FT NON_TER
SQ SEQUENCE 234 AA; 26134 MW; 005AD356E93BC50 CRC64;

Query Match 28.0%; Score 243; DB 2; Length 234;
Best Local Similarity 29.3%; Pred. No. 1.3e-12;
Matches 68; Conservative 30; Mismatches 60; Indels 74; Gaps 8;

QY 16 AALAEGA-SGFYVQADAAH-----KASSSLGS-----AKGSPRISAGY 54
DB 4 AASEDSGRSPYVQADLAVAAERITHDYPQATGANNSTVSDYFRNIRAHSHIPRVSVGY 63
QY 55 RINDLRFAVDYTRYK-----NYKAPSTDFK-----LYSIGASAI 88

```

```

DB 64 DFGDMRIADVSYRKWKESNTSKVTEPKHONGKOEDEKTEHOGNGSFHATSLGLSAI 123
QY 89 YDFDTGSPYKPYLGARLSLNR-----ASVDLGG-----SDSFSQ 122
DB 124 YDFKLSDKRKPKYIGVAVAGHVKHQHVSESKTITVTNNGGPVPQGPTRPKPAYHESH1 183
QY 123 TSTGLGVLAGVSYAVTPNVDLAGYRKYNTGKVNIVKNNRSGELSAGVRYKF 174
DB 184 SSVGLGVLAGVGEDITPKLTLDGYRYHNMGRLENTR-FKTHEVSLGMRYHF 234

RESULT 14
ID Q9R718 PRELIMINARY; PRT; 234 AA.
AC Q9R718;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE OPACITY PROTEIN (FRAGMENT).
GN OPA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN 11
RP SEQUENCE FROM N.A.
RC MEDLINE=98010345; PubMed=9350862;
RA Morelli G., Malorny B., Muller K., Seiler A., Wang J.F., del Valle J.,
RT "Clonal descent and microevolution of Neisseria meningitidis during 30
RT years of epidemic spread."
RL MOL. Microbiol. 25:1047-1064(1997).
DR EMBL; AF001196; AAC32717.1; -
DR InterPro; IPR003394; Opacity.
DR Pfam; PF02462; Opacity; 1.
FT NON_TER 1
SQ SEQUENCE 234 AA; 26191 MW; F01D3B9163066171 CRC64;

Query Match 27.7%; Score 240.5; DB 2; Length 232;
Best Local Similarity 30.9%; Pred. No. 2.1e-12;
Matches 71; Conservative 29; Mismatches 65; Indels 65; Gaps 8;

QY 16 AALAEGA-SGFYVOADAHA--KASSLSGAKG-----ESPRIAGY 54
DB 4 AASDGRSPYVQADLAAYARITHDYPOATGANNSTVSDYFRNIRTHSHIPRVSAGV 63
QY 55 RINDLRPAVDYTRYK-----NYKAPSTDEK-----LYSIGASAI 88
DB 64 DFGDMRIADVSYRKWKESNTSKVTEPKHONGKOEDEKTEHOGNGSFHATSLGLSAI 123
QY 89 YDFDTGSPYKPYLGARLSLNR-----ASVDLGG-----SDSFSQ 122
DB 124 YDFKLSDKRKPKYIGVAVAGHVKHQHVSESKTITVTNNGGPVPQGPTRPKPAYHESH1 183
QY 123 TSTGLGVLAGVSYAVTPNVDLAGYRKYNTGKVNIVKNNRSGELSAGVRYKF 174
DB 184 SSVGLGVLAGVGEDITPKLTLDGYRYHNMGRLENTR-FKTHEVSLGMRYHF 234

RESULT 15
ID Q9K4T9 PRELIMINARY; PRT; 232 AA.
AC Q9K4T9;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE OPA PROTEIN PRECURSOR (FRAGMENT).
GN OPA.
OS Neisseria lactamica.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=486;
RN 11
RP SEQUENCE FROM N.A.

```

```

RC SRRATN-G501;
RA Toleman M.A., Aho E., Virji M.;
RT "Antigenic relatedness of commensal and pathogenic neisserial adhesins
RT genetic and functional analyses of commensal Opa proteins."
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ288888; CAB93949.1; -
DR InterPro; IPR003394; Opacity.
DR Pfam; PF02462; Opacity; 1.
KW Signal.
FT NON_TER 1
FT SIGNAL <1 13 POTENTIAL.
FT CHAIN 14 >232 OPA A PROTEIN.
FT NON_TER 232
SQ SEQUENCE 232 AA; 26094 MW; 36FAAE60A3C014AF CRC64;

Query Match 27.7%; Score 240.5; DB 2; Length 232;
Best Local Similarity 30.9%; Pred. No. 2.1e-12;
Matches 71; Conservative 29; Mismatches 65; Indels 65; Gaps 8;

QY 6 ATLIALALPAALAEAGASGFYVQADAHAHAKASSSL-----GSAGKFS-----PRI 50
DB 3 SLEFSSAVQANEDNGRGPYVQADLYAVAEHTHDYPGNNAKLFDDYRDYKTRSTHPRL 62
QY 51 SAGYRINDLRPAVDYTRYK-----APSTD-----FKIYS-IG 84
DB 63 SVGYDFGNWRITALDYARVKNKHKHILTEQNKSVQNGTSVKLLADHTDGTGTFKAESNYG 122
QY 85 ASATYDFDTGSPYKPYLGARLSLNR-----ASVDLGG-----SDSFS 121
DB 123 ISATYDFDTGTRFRPKRYGARVGLGKIRHSTALEDKAEIIGNITSGGLKDAHPTIHSHS 182
QY 122 QSTGLGVLAGVSYAVTPNVDLAGYRKYNTGKVNIVKNNRSGELSAGV 171
DB 183 IRRVGFAGVAGVDITPNTLFDGYRYHNMGRLENTR-FKTHEASLGM 231

Search completed: October 28, 2002, 16:02:39
Job time : 20.9713 secs

```

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 28, 2002, 15:55:03 ; Search time 24.7145 Seconds
(without alignments)
782.004 Million cell updates/sec

Title: US-09-684-883-8

Sequence: 1 MKKALALALALPAAALAE.....VNFVKNVBSGELSACRVK 174

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
2: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
3: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
4: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
5: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
6: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
7: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*
8: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*
9: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
10: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*
11: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*
12: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
13: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
14: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
15: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
16: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*
17: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*
18: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
19: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
20: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
21: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	870	100.0	174	17	AAW04894
2	834	95.9	174	17	AAW04893
3	825	94.8	174	17	AAW04891
4	813.5	93.5	175	17	AAW04892
5	747	85.9	155	22	AA19895
6	733	15.3	25	17	AAW04912
7	125	14.4	170	16	AAW04911
8	106	12.2	353	22	AA19895
9	101	11.6	359	16	AAW04912
10	96	11.0	369	21	AA19895
11	96	11.0	369	21	AA19895

12	95.5	11.0	212	22	AAU34556
13	95	10.9	257	22	AAU38252
14	95	10.9	369	21	AA19895
15	94.5	10.9	797	20	AA19895
16	92	10.6	364	21	AA19895
17	92	10.6	364	21	AA19895
18	92	10.6	364	21	AA19895
19	90	10.3	500	22	AA19895
20	87.5	10.1	573	17	AA19895
21	87	10.0	16	17	AA19895
22	86.5	9.9	215	21	AA19895
23	86.5	9.9	215	21	AA19895
24	86	9.9	568	17	AA19895
25	83.5	9.6	339	21	AA19895
26	83.5	9.6	534	21	AA19895
27	83	9.5	610	19	AA19895
28	83	9.5	624	19	AA19895
29	83	9.5	889	19	AA19895
30	81.5	9.4	162	17	AA19895
31	81.5	9.4	708	19	AA19895
32	81.5	9.4	708	21	AA19895
33	81	9.3	279	17	AA19895
34	81	9.3	350	9	AA19895
35	81	9.3	350	22	AA19895
36	80	9.2	15	17	AA19895
37	80	9.2	259	21	AA19895
38	80	9.2	260	20	AA19895
39	80	9.2	266	20	AA19895
40	80	9.2	270	19	AA19895
41	80	9.2	270	19	AA19895
42	80	9.2	270	21	AA19895
43	80	9.2	270	22	AA19895
44	80	9.2	273	18	AA19895
45	80	9.2	273	18	AA19895

ALIGNMENTS

RESULT 1	AAW04894	standard; Protein: 174 AA.
ID	AAW04894	
XX	AAW04894	
AC	AAW04894	
XX	AAW04894	
DT	22-DEC-1996	(first entry)
XX	22-DEC-1996	
DE	Proteinase K resistant N. meningitidis 22 kd surface protein.	
XX	Proteinase K resistant; Neisseria meningitidis;	
KW	Neisseria gonorrhoeae; antibody; detection; probe; surface protein;.	
KW	Neisseria meningitidis strain b2.	
OS	Neisseria meningitidis strain b2.	
XX	Neisseria meningitidis strain b2.	
FT	key	location/Qualifiers
FT	Peptide	1..19
FT	Protein	/label= sig_peptide
FT		20..174
FT		/label= mat_protein
XX	WO9629412-A1.	
PN	WO9629412-A1.	
XX	26-SEP-1996.	
PD	26-SEP-1996.	
XX	15-MAR-1996;	96MO-CA00157.
PF	15-MAR-1996;	
XX	04-AUG-1995;	95US-0001983.
PR	17-MAR-1995;	95US-0406362.
XX	(IAFB-) IAF BIO VAC INC.	
PA	(IAFB-) IAF BIO VAC INC.	
XX	Brodeur BR, Hamel J, Martin D, Rioux C;	
PI	Brodeur BR, Hamel J, Martin D, Rioux C;	
XX	Brodeur BR, Hamel J, Martin D, Rioux C;	

DR WPI: 1996-443187/44.
 DR N-PSDB; AAT39042.
 XX Neisseria meningitidis antigen, highly conserved between different
 PT strains - useful for prodn. of antibodies for immunisation against,
 PT or diagnosis of, N. meningitidis infection
 XX
 PS Claim 7; Fig 10; 117pp; English.
 CC
 CC A proteinase K resistant surface protein has been isolated
 CC from 4 strains of N. meningitidis (AAT39039 to AAT39042). The isolated
 CC 22 kD antigen, antigenic fragments of antibodies can be used
 CC in a vaccine for the prevention of infection by N. meningitidis or
 CC by N. gonorrhoeae in humans. The antibodies may also be used
 CC diagnostically to detect N. meningitidis infection. The antigen
 CC may also be used to detect antibodies specific to N. meningitidis
 CC antigen.
 CC DNA sequences encoding the antigen, or their fragments, can be used
 CC as probes for the detection of pathogenic Neisseria bacteria.
 CC
 SQ Sequence 174 AA:
 Query Match 100.0%; Score 870; DB 17; Length 174;
 Best Local Similarity 100.0%; Pred. No. 3.8e-85;
 Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKKALALIALALPAAALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
 DB 1 MKKALALIALALPAAALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
 QY 61 FAVDYTRYKNYKAPSTDFKLYSIGASVITYDPTQSPVKPYFGARLSLNRAAHLGSDSF 120
 DB 61 FAVDYTRYKNYKAPSTDFKLYSIGASVITYDPTQSPVKPYFGARLSLNRAAHLGSDSF 120
 QY 121 SKTSAGLGLAGVSYAVTPNVDLDAGYRYNYGKNTVKNVRSGLSAGYRVKF 174
 DB 121 SKTSAGLGLAGVSYAVTPNVDLDAGYRYNYGKNTVKNVRSGLSAGYRVKF 174
 RESULT 2
 AAM04893
 ID AAM04893 standard; Protein; 174 AA.
 AC AAM04893;
 XX
 XX 22-DEC-1996 (first entry)
 DE Proteinase K resistant N. meningitidis 22 kD surface protein.
 XX
 KW Proteinase K resistant; Neisseria meningitidis;
 KW Neisseria gonorrhoeae; antibody; detection; probe; surface protein.
 XX
 OS Neisseria meningitidis strain Z4063.
 XX
 FH Key Location/Qualifiers
 FH Peptide 1..19
 FT /label= sig_peptide
 FT Protein 20..174
 FT /label= mat_protein
 PN WO9629412-A1.
 PD 26-SEP-1996.
 PF 15-MAR-1996; 96WO-CA00157.
 XX
 XX 04-AUG-1995; 95US-0001983.
 PR 17-MAR-1995; 95US-0406362.
 XX
 PA (IAFB-) IAF BIO VAC INC.
 PI Brodeur BR, Hamel J, Martin D, Rioux C;
 XX

DR WPI: 1996-443187/44.
 DR N-PSDB; AAT39041.
 XX Neisseria meningitidis antigen, highly conserved between different
 PT strains - useful for prodn. of antibodies for immunisation against,
 PT or diagnosis of, N. meningitidis infection
 XX
 PS Claim 7; Fig 9; 117pp; English.
 CC
 CC A proteinase K resistant surface protein has been isolated
 CC from 4 strains of N. meningitidis (AAT39039 to AAT39042). The isolated
 CC 22 kD antigen, antigenic fragments of antibodies can be used
 CC in a vaccine for the prevention of infection by N. meningitidis or
 CC by N. gonorrhoeae in humans. The antibodies may also be used
 CC diagnostically to detect N. meningitidis infection. The antigen
 CC may also be used to detect antibodies specific to N. meningitidis
 CC antigen.
 CC DNA sequences encoding the antigen, or their fragments, can be used
 CC as probes for the detection of pathogenic Neisseria bacteria.
 CC
 SQ Sequence 174 AA:
 Query Match 95.9%; Score 834; DB 17; Length 174;
 Best Local Similarity 95.4%; Pred. No. 2.7e-81;
 Matches 166; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
 QY 1 MKKALALIALALPAAALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
 DB 1 MKKALALIALALPAAALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
 QY 61 FAVDYTRYKNYKAPSTDFKLYSIGASVITYDPTQSPVKPYFGARLSLNRAAHLGSDSF 120
 DB 61 FAVDYTRYKNYKAPSTDFKLYSIGASVITYDPTQSPVKPYFGARLSLNRAAHLGSDSF 120
 QY 121 SKTSAGLGLAGVSYAVTPNVDLDAGYRYNYGKNTVKNVRSGLSAGYRVKF 174
 DB 121 SKTSAGLGLAGVSYAVTPNVDLDAGYRYNYGKNTVKNVRSGLSAGYRVKF 174
 RESULT 3
 AAM04891
 ID AAM04891 standard; Protein; 174 AA.
 AC AAM04891;
 XX
 XX 22-DEC-1996 (first entry)
 DE Proteinase K resistant N. meningitidis 22 kD surface protein.
 XX
 KW Proteinase K resistant; Neisseria meningitidis;
 KW Neisseria gonorrhoeae; antibody; detection; probe; surface protein.
 XX
 OS Neisseria meningitidis strain 608B.
 XX
 FH Key Location/Qualifiers
 FH Peptide 1..19
 FT /label= sig_peptide
 FT Protein 20..174
 FT /label= mat_protein
 PN WO9629412-A1.
 PD 26-SEP-1996.
 PF 15-MAR-1996; 96WO-CA00157.
 XX
 XX 04-AUG-1995; 95US-0001983.
 PR 17-MAR-1995; 95US-0406362.
 XX
 PA (IAFB-) IAF BIO VAC INC.
 PI Brodeur BR, Hamel J, Martin D, Rioux C;
 XX

DR WPI: 1996-443187/44.
 N-PSDB; AAT39039.
 XX
 PT Neisseria meningitidis antigen, highly conserved between different
 strains - useful for prodn. of antibodies for immunisation against,
 or diagnosis of, N. meningitidis infection
 XX
 PS Claim 7; Fig 1; 117pp; English.
 CC A proteinase K resistant surface protein has been isolated
 from 4 strains of N. meningitidis (AAT39039 to AAT39042). The isolated
 CC 22 kd antigen, antigenic fragments of antibodies can be used
 CC in a vaccine for the prevention of infection by N. meningitidis or
 CC by N. gonorrhoeae in humans. The antibodies may also be used
 CC diagnostically to detect N. meningitidis infection. The antigen
 CC may also be used to detect antibodies specific to N. meningitidis
 CC antigen.
 CC DNA sequences encoding the antigen, or their fragments, can be used
 CC as probes for the detection of pathogenic Neisseria bacteria.
 CC
 SQ Sequence 174 AA:

Query Match 94.8%; Score 825; DB 17; Length 174;
 Best Local Similarity 94.3%; Pred. No. 2,5e-80;
 Matches 164; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 MKKALALIALPALPAALAEAGSGFYQADAAHAKASSLSGKGFSPRISAGYRINDLR 60
 DB 1 MKKALATLIALPALPAALAEAGSGFYQADAAHAKASSLSGKGFSPRISAGYRINDLR 60
 QY 61 FAVDYTRKKNYKAPSTDFKLISGASVYIDPDTOSPVKPYGKARLSLNRAAHLCGSDS 120
 DB 61 FAVDYTRKKNYKAPSTDFKLISGASVYIDPDTOSPVKPYGKARLSLNRAAHLCGSDS 120
 QY 121 SKTSAGLGLAGSYAVTPNVDLAGRYRYNKGKNTYKNNVRSGLSAGRYK 174
 DB 121 SGTSTGLGLAGSYAVTPNVDLAGRYRYNKGKNTYKNNVRSGLSAGRYK 174

RESULT 4

AAW04892
 ID AAW04892 standard; Protein; 175 AA.

XX AC AAW04892;
 XX DT 22-DEC-1996 (first entry)
 XX DE Proteinase K resistant N. meningitidis 22 kd surface protein.
 XX KM Proteinase K resistant; Neisseria meningitidis;
 XX KM Neisseria gonorrhoeae; antibody; detection; probe; surface protein.
 XX OS Neisseria meningitidis strain MCH88.
 XX FH Key Location/Qualifiers
 FT Peptide 1..19
 FT /label= s1g-peptide
 FT Protein 20..175
 FT /label= mat_protein
 XX PN MO9629412-A1.
 PD 26-SEP-1996.
 XX PF 15-MAR-1996; 96WO-CA00157.
 XX PR 04-AUG-1995; 95US-0001983.
 XX PR 17-MAR-1995; 95US-0406362.
 XX PA (IAFB-) IAF BIO VAC INC.
 XX PI Brodeur BR, Hamel J, Martin D, Rioux C;
 XX

DR WPI: 1996-443187/44.
 N-PSDB; AAT39040.
 XX
 PT Neisseria meningitidis antigen, highly conserved between different
 strains - useful for prodn. of antibodies for immunisation against,
 or diagnosis of, N. meningitidis infection
 XX
 PS Claim 7; Fig 8; 117pp; English.
 CC A proteinase K resistant surface protein has been isolated
 from 4 strains of N. meningitidis (AAT39039 to AAT39042). The isolated
 CC 22 kd antigen, antigenic fragments of antibodies can be used
 CC in a vaccine for the prevention of infection by N. meningitidis or
 CC by N. gonorrhoeae in humans. The antibodies may also be used
 CC diagnostically to detect N. meningitidis infection. The antigen
 CC may also be used to detect antibodies specific to N. meningitidis
 CC antigen.
 CC DNA sequences encoding the antigen, or their fragments, can be used
 CC as probes for the detection of pathogenic Neisseria bacteria.
 CC
 SQ Sequence 175 AA:

Query Match 93.5%; Score 813.5; DB 17; Length 175;
 Best Local Similarity 93.7%; Pred. No. 4.3e-79;
 Matches 164; Conservative 2; Mismatches 8; Indels 1; Gaps 1;

QY 1 MKKALALIALPALPAALAEAGSGFYQADAAHAKASSLSGKGFSPRISAGYRINDLR 60
 DB 1 MKKALATLIALPALPAALAEAGSGFYQADAAHAKASSLSGKGFSPRISAGYRINDLR 60
 QY 61 FAVDYTRKKNYKAPSTDFKLISGASVYIDPDTOSPVKPYGKARLSLNRAAHLCGSDS 119
 DB 61 FAVDYTRKKNYKAPSTDFKLISGASVYIDPDTOSPVKPYGKARLSLNRAAHLCGSDS 120
 QY 120 FSKTSAGLGLAGSYAVTPNVDLAGRYRYNKGKNTYKNNVRSGLSAGRYK 174
 DB 121 FSKTSAGLGLAGSYAVTPNVDLAGRYRYNKGKNTYKNNVRSGLSAGRYK 175

RESULT 5

AAAB19895
 ID AAB19895 standard; Protein; 155 AA.

XX AC AAB19895;
 XX DT 19-MAR-2001 (first entry)
 XX DE Neisseria meningitidis NSPA protein.
 XX KM NSPA; infection; diagnosis; therapy; vaccine; meningococcal B.
 XX KM Neisseria meningitidis.
 XX OS Neisseria meningitidis.
 XX FH Key Location/Qualifiers
 FT Region 6..17
 FT /note= "transmembrane beta-strand"
 FT Region 18..26
 FT /note= "surface-exposed connecting loop"
 FT Region 27..37
 FT /note= "transmembrane beta-strand"
 FT Region 40..50
 FT /note= "transmembrane beta-strand"
 FT Region 51..62
 FT /note= "surface-exposed connecting loop"
 FT Region 63..74
 FT /note= "transmembrane beta-strand"
 FT Region 78..88
 FT /note= "transmembrane beta-strand"
 FT Region 89..104
 FT /note= "surface-exposed connecting loop"
 FT Region 105..114
 FT /note= "transmembrane beta-strand"
 FT Region 118..130

```

FT      /note= "transmembrane beta-strand"
FT      Region      131..145
FT      /note= "surface-exposed connecting loop"
FT      Region      146..155
FT      /note= "transmembrane beta-strand"
XX      WO200071725-A2.
XX      30-NOV-2000.
XX      19-MAY-2000; 2000MO-IB00828.
XX      19-MAY-1999; 99GB-0011692.
XX      19-AUG-1999; 99GB-0019705.
XX      09-MAR-2000; 2000GB-0005730.
XX      (CHIR-) CHIRON SPA.
XX      Giuliani MM, Pizsa M, Rappuoli R;
XX      WPI; 2001-025167/03.
XX      Novel composition comprising first and second biological molecules from
PT      a Neisseria bacterium, useful as vaccines or immunogenic compositions
PT      for treating Neisseria infections
XX      Example 12; Fig 32; 126pp; English.
XX      The present sequence is that of the Neisseria meningitidis NspA
CC      protein, which contains 8 transmembrane beta-strands and 4
CC      surface-exposed connected loops. Recombinant NspA is being
CC      developed as a vaccine for the prevention of meningococcal
CC      disease caused by all serotypes. The invention provides
CC      combination compositions comprising: (i) 2 or more Neisseria
CC      proteins, (ii) 2 or more different Neisseria nucleic acids; or
CC      (iii) mixtures of 1 or more Neisseria protein and 1 or more
CC      Neisseria nucleic acid. The proteins and nucleic acids are
CC      preferably from different Neisseria spp., especially Neisseria
CC      meningitidis and Neisseria gonorrhoeae, but may be from the same
CC      species. A claimed composition includes the NspA protein,
CC      preferably in a mature form. The compositions are used e.g. as
CC      immunogenic compositions, vaccines or diagnostic reagents. They
CC      are used to treat or prevent Neisseria infection, to detect the
CC      presence of Neisseria bacteria or of antibodies raised against
CC      Neisseria bacteria, and/or as reagents which can raise antibodies
CC      against Neisseria bacteria.
XX      Sequence      155 AA:
SQ
Query Match      85.9%; Score 747; DB 22; Length 155;
Best Local Similarity 94.2%; Pred. No. 4.8e-72;
Matches 146; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
XX      20 EGAGGFVVOADAHAHAKASSLSGAKGSPRISAGYRINDLRFADVTRYKNAKAPSTDPR 79
XX      1 EGAGGFVVOADAHAHAKASSLSGAKGSPRISAGYRINDLRFADVTRYKNAKAPSTDPR 60
XX      80 LYSIGASVYDFDTQSPVKKPYFCARLSLNRAHAGSGDSFSKTSAGLGVLAGVSYAVMP 139
XX      61 LYSIGASVYDFDTQSPVKKPYFCARLSLNRAHAGSGDSFSKTSAGLGVLAGVSYAVMP 120
XX      140 NVDDADAGRYRYGKVTYKNNVNSGELSGAVRYKF 174
XX      121 NVDDADAGRYRYGKVTYKNNVNSGELSGAVRYKF 155
XX      RESULT 6
XX      ID AAM04912 standard; Protein; 25 AA.
XX      AAM04912;
XX      22-DEC-1996 (first entry)

```

```

XX      N. meningitidis 608B peptide CS-857.
DE      Proteinase K resistant; Neisseria meningitidis; epitope; mapping;
XX      Neisseria gonorrhoeae; antibody; detection; probe; surface protein.
XX      Synthetic.
XX      WO9629412-A1.
XX      26-SEP-1996.
XX      15-MAR-1996; 96WO-CA00157.
XX      04-AUG-1995; 95US-0001983.
XX      17-MAR-1995; 95US-0406362.
XX      (IAFB-) IAF BIO VAC INC.
XX      Brodeur BR, Hamel J, Martin D, Rioux C;
XX      WPI; 1996-443187/44.
XX      Neisseria meningitidis antigen, highly conserved between different
PT      strains - useful for prodn. of antibodies for immunisation against,
PT      or diagnosis of, N. meningitidis infection
XX      Claim 24; Page 84; 117pp; English.
XX      Example 9 describes the epitope mapping of the 22 kD
CC      N. meningitidis protein. Identification was accomplished
CC      using 18 overlapping synthetic peptides (AAM04895 to AAM04912).
XX      Sequence      25 AA:
SQ
Query Match      15.3%; Score 133; DB 17; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.3e-07;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX      61 FAVDYTRYKNAKAPSTDPRKLYSIGA 85
XX      1 FAVDYTRYKNAKAPSTDPRKLYSIGA 25
XX      RESULT 7
XX      ID AAR73911 standard; protein; 170 AA.
XX      AAR73911;
XX      05-DEC-1995 (first entry)
XX      Neisseria meningitidis opacity related protein POPM3.
XX      Neisseria meningitidis; opacity related protein POPM3; vaccine;
XX      meningitis related homologous antigenic sequence; MRHA5; RV-1;
XX      immunosay; diagnosis; treatment; prophylactic; bacterial;
XX      viral.
XX      Neisseria meningitidis.
XX      WO9509232-A.
XX      06-APR-1995.
XX      28-SEP-1994; 94WO-CA00516.
XX      28-SEP-1993; 93US-0127499.
XX      (SHAR/) SHARMA L R.
XX      (VALS/) VAN ALSTYNE D.
XX      Sharma LR, Van Alstyne D;

```



```

FT XX /label= internal CNBR fragment
PN XX MO9426304-A.
XX XX
XX XX 24-NOV-1994.
XX XX
XX XX 12-MAY-1994; 94MO-US05477.
XX XX
XX XX 18-MAY-1993; 93US-0065442.
XX XX
XX XX (OHIO-) OHIO STATE RES FOUND.
XX XX
XX XX Bakaletz LO, Kolattukudy PE, Strakova T;
XX XX
XX XX WPI; 1995-006359/01.
XX XX
XX XX N-PSDB; AA078916.
XX XX
XX XX Vaccine comprising non-typable Haemophilus influenza fimbria
XX XX protein - useful in studying, preventing or reducing the
XX XX severity of otitis media, also fimbria protein and DNA.
XX XX
XX XX Disclosure; Fig 5; 45pp; English.
XX XX
XX XX The fimbria proteins from 15 randomly selected type b and non-
XX XX typable clinical isolates of Haemophilus influenza share common
XX XX epitopes. Thus fimbria isolated from non-typable Haemophilus
XX XX influenza 1128 strain is a particularly suitable immunogen to
XX XX protect against the different non-typable Hf. influenza that cause
XX XX otitis media. Fimbria protein is produced by culturing a transformed
XX XX microbial host, pref. E.coli, Sporodoptera frugiperda or a mucosal
XX XX pathogen. Fimbria protein (FP) produced by this process is claimed.
XX XX The FP protein migrates in polyacrylamide gels to a posn. equiv. to
XX XX a mol. wt. of 25.5 kD or 37.5 kD.
XX XX
XX XX Sequence 359 AA;
XX XX
XX XX Query Match 11.6%; Score 101; DB 16; Length 359;
XX XX Best Local Similarity 25.1%; Pred. No. 0.022;
XX XX Matches 57; Conservative 27; Mismatches 83; Indels 60; Gaps 12;

QY 1 MKKALALIALALPAAALAEGA---SGFYQADAA---HAKSSSLGSAKSPRISAG 53
DB 1 MKKTAIALVYAGLAAASVQAAPQENTFYAGVAGGSGHDGINNGAATKGLSS--NYG 59
QY 54 YRINDLFAVDYRKYRKAPSTDFKLYSIGASVIY-DF---DTQSPVP-----YFGAR 104
DB 60 YRNTFTYGV---FGYQILNOD--NFGLAELGYHDFGRALKRAGKPKKHTNHGAY 113
QY 105 LSLNRSAHLGSGDSFSKTSAGL-----GVLG-GVSYA 136
DB 114 LSLKSGYEVLGDLVYGKAGVALVRSDYKFEYEDANGTRDHKKGRHTARASGLFAVGALEYA 173
QY 137 VTPNVDLAGY-----RYNYGKVTYKVNYS--GELSAGVYKF 174
DB 174 VLPELAVREYQWLTVRGKTRPODKPENTAIINPMIGCINAGISTYRF 220

RESULT 10
AA97900
ID AA97900 standard; protein; 369 AA.
XX
XX AA97900;
XX
XX 19-DEC-2000 (first entry)
XX
XX Actinobacillus pleuropneumoniae OmpA2.
XX
XX Outer membrane protein; OmpA1; vaccine; pig; immunogen;
XX dual immune response; immunogen; pleuropneumonia.
XX
XX Actinobacillus pleuropneumoniae.
XX
XX EP105133-A2.

```

```

XX XX 13-SEP-2000.
XX XX
XX XX 14-FEB-2000; 2000EP-0301103.
XX XX
XX XX 17-FEB-1999; 99US-0120454.
XX XX
XX XX (Pfizer ) Pfizer PROD INC.
XX XX
XX XX Campos M, Martindale SR, Dutschi BA, Yule TD;
XX XX
XX XX WPI; 2000-566924/53.
XX XX
XX XX Novel fusion protein for producing a dual immune response comprises a
XX XX peptide analogous to an endogenous peptide which is to be inhibited
XX XX connected to a peptide analogous to an immunogen from a pathogen which
XX XX infects a vertebrate -
XX XX
XX XX Disclosure; Page 58-60; 93pp; English.
XX XX
XX XX The present sequence is that of outer membrane protein OmpA2 of
XX XX Actinobacillus pleuropneumoniae. OmpA2 can be utilized in fusion
XX XX proteins of the invention that are used as vaccines eliciting a
XX XX dual immune response. Such fusion proteins comprise: a first
XX XX protein that is endogenous to a vertebrate, and the activity of which
XX XX is to be inhibited within the vertebrate, and which is incapable by
XX XX itself of eliciting an effective immunoinhibitory response in the
XX XX vertebrate; and a second protein, which is an immunogen from a
XX XX pathogen capable of infecting the vertebrate, and which causes the
XX XX vertebrate's immune system to recognise the first protein,
XX XX producing a response that inhibits the activity of the first
XX XX protein, and also protecting the vertebrate from infection by the
XX XX pathogen when the vertebrate is vaccinated with the fusion protein.
XX XX In the present case, a fusion protein of cholestyrolin and OmpA2
XX XX is useful for encouraging appetite in swine while simultaneously
XX XX providing a protective immune response against porcine
XX XX pleuropneumonia.
XX XX
XX XX Sequence 369 AA;
XX XX
XX XX Query Match 11.0%; Score 96; DB 21; Length 369;
XX XX Best Local Similarity 23.6%; Pred. No. 0.078;
XX XX Matches 55; Conservative 29; Mismatches 81; Indels 68; Gaps 13;

QY 1 MKKALALIALALPAAALAEGA---SGFYQADAAHAKSSSLGSAK-GSPR----- 49
DB 1 MKKSLVLAVALS--AAVAQAAPQONTFYAGAKKGGSPFHGVNQLSGHDDRNDRKTR 58
QY 50 -----ISAGYRI--NDLFAVD--YTRYKRYKAPSTDFKLYSIGA----- 85
DB 59 YGINRNSVTYGVFGGYQILNQNNGLATLGYDYGVGRGNDGFRAMKHSAGLNFAIK 118
QY 86 ---SYIYFEDQSPVKKPFYFARLSLNRASAHLG-----SDSSKTSAGLGVYAGSYA 136
DB 119 PSYEVLPLDLYGKV---GVAVVRNDYKSY-GAENTNEPTEKFKKASTTIGAGVEYA 173
QY 137 VTPNVDLAGYRYNYGVKVTYKVN--VRSG-----ELSGAVYKF 174
DB 174 ILP--ELAAVREYQWLTVRGKTRPODKPENTAIINPMIGCINAGISTYRF 224

RESULT 11
AA97900
ID AA97900 standard; protein; 369 AA.
XX
XX AA97900;
XX
XX 11-SEP-2000 (first entry)
XX
XX Actinobacillus pleuropneumoniae outer membrane protein, OmpA2.
XX
XX OmpA2; outer membrane protein; APP; pneumonic pathogen; swine;
XX Sus scrofa; serotype; antigen; vaccine; cross-reactive immunity;

```

KM cross-protection; diagnosis.
 OS Actinobacillus pleuropneumoniae strain Pz420.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT Protein /note="Signal peptide"
 FT Protein /note="Mature OmpA2"
 XX
 PN EPI001025-A2.
 PD 17-MAY-2000.
 XX
 PF 20-OCT-1999; 99EP-0308262.
 XX
 PR 22-OCT-1998; 98US-0105285.
 XX
 PA (PEITZ) PEITZER PROD INC.
 XX
 PI Ankenbauer RG, Baarsch MJ, Campos M, Keich RL, Rosey EL;
 PI Warren-Stewart LM, Sulter BT;
 XX
 DR MPI; 2000-320438/28.
 DR N-PSDB; AAA38558.
 XX
 PT Low molecular weight Actinobacillus pleuropneumoniae proteins and DNA
 PT encoding them, for use as vaccines against the bacteria in swine -
 XX
 PS Claim 2; Fig 5; 81pp; English.
 XX
 CC This sequence represents a low molecular weight outer membrane
 CC protein, OmpA2, from Actinobacillus pleuropneumoniae (APP) strain
 CC Pz420 (ATCC 98930). The invention relates to the novel APP outer
 CC membrane proteins Omp20, Omp27, OmpA1 and OmpA2 (AAV97896-Y97900)
 CC and to nucleic acids encoding them (AAA38554-A38558). APP is a Gram
 CC negative coccobacillus which is one of the most important swine
 CC pneumonia pathogens. 12 different serotypes of APP have been recognised
 CC which vary in geographic distribution. Prior art attempts at vaccinating
 CC against APP have produced mainly serotype-specific immune responses. In
 CC contrast, natural immunity to any one serotype seems to confer
 CC significant protection from disease caused by other serotypes, suggesting
 CC that natural exposure induces cross-reactive immunity to shared antigens.
 CC The novel outer membrane proteins of the invention are present in all 12
 CC serotypes, and may provide a target for cross-protective immunisation.
 CC The novel outer membrane proteins and nucleic acids encoding them can be
 CC used as a vaccine against APP in swine. They can also be used as
 CC reagents for the diagnosis of APP infections.
 CC
 XX
 SQ Sequence 369 AA;
 Query Match 11.0%; Score 96; DB 21; Length 369;
 Best Local Similarity 23.6%; Pred. No. 0.078;
 Matches 53; Conservative 29; Mismatches 81; Indels 68; Gaps 13;
 OY 1 MKKALALIALALPAALAECA---SGFYVQADAAHAKASSISGSAK-GFSPR----- 49
 DB 1 MKKSLVALAVLS--AAVAQAAPQONTFTAGAKVGQSSHHGVNQLKSGHDKTRK 58
 OY 50 -----ISAGYRI--NDLRFAYD--YTRYKNKAPSTDPKLYSIGA----- 85
 DB 59 YGIRNSVTYGVFGGYOILNQNNGFLATELGYDYGRVNGNGFERAMKSHSHGLNPAFK 118
 OY 86 ---SVYDEPDQSPVKPYFGARLSLNRSAHLGG-----SSSEKTSAGLGVLAGVSTA 136
 DB 119 PSYEVLDPDLDVYGKY---GVAVVRNDYKSY-GAENTNEPTEKFKLKAASLTILGAGVEYA 173
 OY 137 VTPNDVLADGYRYNYGVKNYVKN--VRSQ-----EISAGYRVK 174
 DB 174 ILP--ELAAVREYQYLKNGKGNLKAALVRSRGTDVDYQYAPADLHSTYAGLSYRF 224
 RESULT 12

AAU34556
 ID AAU34556 standard; Protein; 212 AA.
 XX
 AC AAU34556;
 XX
 DT 14-FEB-2002 (first entry)
 DE
 XX E. coli cellular proliferation protein #137.
 XX
 KM Antisense; prokaryotic cellular proliferation protein;
 KM antibiotic; antibacterial; drug design.
 XX
 OS Escherichia coli.
 XX
 PN WO200170955-A2.
 PD 27-SEP-2001.
 XX
 PF 21-MAR-2001; 2001WO-US09180.
 XX
 PR 21-MAR-2000; 2000US-191078P.
 PR 23-MAY-2000; 2000US-206848P.
 PR 26-MAY-2000; 2000US-207727P.
 PR 23-OCT-2000; 2000US-242578P.
 PR 27-NOV-2000; 2000US-253625P.
 PR 22-DEC-2000; 2000US-257931P.
 PR 16-FEB-2001; 2001US-269308P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
 PI Yamamoto RT, Xu HH;
 XX
 DR MPI; 2001-611495/70.
 DR N-PSDB; AAS52415.
 XX
 PT New polynucleotides for the identification and development of
 PT antibiotics, comprise sequences of antisense nucleic acids -
 XX
 PS Example 3; Seq ID No 10149; 51pp; English.
 XX
 CC The invention relates to antisense inhibitors of genes essential to
 CC prokaryotic cellular proliferation, their use in identifying the
 CC genes, their use in the discovery of novel antibiotics, the essential
 CC genes themselves and the encoded proteins. The prokaryotes used are
 CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
 CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
 CC invention is also useful for the identification of potential new targets
 CC for antibiotic development. The antisense nucleic acids can also be used
 CC to identify proteins used in proliferation, to express these proteins,
 CC and to obtain antibodies capable of binding to the expressed proteins.
 CC The proteins can be used to screen compounds in rational drug discovery
 CC programmes. The antisense nucleic acid sequence is also useful to screen
 CC for homologous nucleic acids which are required for cell proliferation in
 CC a wide variety of organisms. The present sequence represents an
 CC essential prokaryotic cellular proliferation protein.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 CC
 XX
 SQ Sequence 212 AA;
 Query Match 11.0%; Score 95.5; DB 22; Length 212;
 Best Local Similarity 23.8%; Pred. No. 0.042;
 Matches 49; Conservative 26; Mismatches 72; Indels 59; Gaps 10;
 OY 1 MKKALALIALAL--LPAALAEAGSGFYVQADAAHAK---ASSISGSAKGFSPRISAGY 54
 DB 1 MKKLTVALAVTTLLSGSAFAHEAGFEFMRAGSATVPTREGAGTGLSGGFSY----- 54
 OY 55 RINDLRFAYDVTTRYKNKA-----PSTDPKLYSIGASVLYDF----- 91

Db 55 -TNNQGLGLET---YMATDNIGVELLAATPFR-HKIGTRATGDIATVHHLPTLMAQW 108
 Qy 92 ---DTQSPVKPFYFGARLS-----LNRAAHLGSDSFSKTSAGLGLAGSVAYTPN 140
 Db 109 YFGDASSKRPYGVAGINTTFFDNGFNHCKEAGLSDLSLDSWGAAGQGVYDLINRD 168
 Qy 141 --VDLDAGRYRNYGVKNTVKNVRSQ 164
 Db 169 WLVMNSVWYM-----DIDTTANYKLG 189

RESULT 13
 AAU38252
 ID AAU38252 standard; Protein; 257 AA.
 AC AAU38252;
 XX
 DT 14-FEB-2002 (first entry)
 XX
 DE Salmonella typhi cellular proliferation protein #143.
 XX
 KM Antisense; prokaryotic cellular proliferation protein;
 KM antidiotic; antibacterial; drug design.
 XX
 OS Salmonella typhi.
 XX
 PN W0200170955-A2.
 PD 27-SEP-2001.
 XX
 PE 21-MAR-2001; 2001WO-US09180.
 XX
 PR 21-MAR-2000; 2000US-191078P.
 PR 23-MAY-2000; 2000US-206848P.
 PR 26-MAY-2000; 2000US-207727P.
 PR 23-OCT-2000; 2000US-242578P.
 PR 27-NOV-2000; 2000US-253625P.
 PR 22-DEC-2000; 2000US-257931P.
 PR 16-FEB-2001; 2001US-269308P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr CJ;
 PI Yamamoto RT, Xu HH;
 XX
 DR MPI; 2001-611495/70.
 DR N-PSDB; AAS56111.
 XX
 PT New polynucleotides for the identification and development of
 PT antibiotics, comprise sequences of antisense nucleic acids -
 XX
 PS Example 3; seq ID No 13845; 511pp; English.
 XX
 CC The invention relates to antisense inhibitors of genes essential to
 CC prokaryotic cellular proliferation, their use in identifying the
 CC genes, their use in the discovery of novel antibiotics, the essential
 CC genes themselves and the encoded proteins. The prokaryotes used are
 CC Escherichia coli, staphylococcus aureus, Salmonella typhi, Klebsiella
 CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
 CC invention is also useful for the identification of potential new targets
 CC for antibiotic development. The antisense nucleic acids can also be used
 CC to identify proteins used in proliferation, to express these proteins,
 CC and to obtain antibodies capable of binding to the expressed proteins.
 CC The proteins can be used to screen compounds in rational drug discovery
 CC programmes. The antisense nucleic acid sequence is also useful to screen
 CC for homologous nucleic acids which are required for cell proliferation in
 CC a wide variety of organisms. The present sequence represents an
 CC essential prokaryotic cellular proliferation protein.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 257 AA;
 Query Match 10.9%; Score 95; DB 22; Length 257;
 Best Local Similarity 24.1%; Pred. No. 0.062;
 Matches 54; Conservative 26; Mismatches 78; Indels 66; Gaps 12;

Qy 1 MKKALALIALA--LPAALAEAGSGFYQADAHAH-----ASSISGSAKGFPRISAGT 54
 Db 27 MKKFTVALALTTLLSGSAFHEAGFEFFMRAGPATVPTGAGGTGLHNGFD--VS--- 81
 Qy 55 RINDRFVNDVTRYKNKYA-----PSTDFEYISIGASVYDF----- 91
 Db 82 --TQSPVKPFYFGARLS-----LNRAAHLGSDSFSKTSAGLGLAGSVAYTPN 134
 Qy 92 ---DTQSPVKPFYFGARLS-----LNRAAHLGSDSFSKTSAGLGLAGSVAYTPN 140
 Db 135 YFGDSSSKRPYGVAGINTTFFDNGFNHCKEAGLSDLSLDSWGAAGQGVYDLINRD 194
 Qy 141 -----VDLDAGRYRNYGVKNTVKNVRSQ-----LSAGVR 171
 Db 195 WLIGASVWYMDIDWTANYK-MGVQOHDVSRLDPWVEMFSKGR 237

RESULT 14
 AAB44589
 ID AAB44589 standard; Protein; 369 AA.
 AC AAB44589;
 XX
 DT 08-FEB-2001 (first entry)
 XX
 DE Virulence gene protein #69.
 XX
 KM Virulence gene; antibacterial; vaccine; bacterial infection;
 KM septicemia; bronchopneumonia; rhinitis; wound infection.
 XX
 OS Actinobacillus pleuropneumoniae.
 XX
 PN W0200061724-A2.
 PD 19-OCT-2000.
 XX
 PE 06-APR-2000; 2000WO-US09218.
 XX
 PR 09-APR-1999; 99US-0128689.
 PR 10-SEP-1999; 99US-0153453.
 XX
 PA (PHAA) PHARMACIA & UPJOHN INC.
 XX
 PI Lowery DE, Fuller TE, Kennedy MJ;
 PI
 XX
 DR MPI; 2000-647422/62.
 DR N-PSDB; AAC79664.
 XX
 PT Attenuated Pasteurellaceae bacteria comprising mutations in virulence
 PT genes, useful as a live attenuated vaccine against bacterial infections
 XX
 PS Claim 39; Pages 308-309; 322pp; English.
 XX
 CC The family Pasteurellaceae encompasses several pathogens that infect a
 CC wide variety of animals. The present invention relates to virulence genes
 CC from Pasteurellaceae. The present sequence is a protein encoded by one
 CC such virulence gene. The virulence genes of the present invention may be
 CC mutated in order to produce an inactive gene. The inactive virulence gene
 CC may in turn be used to produce a vaccine, which is useful for treating
 CC bacterial infections such as septicemias, bronchopneumonias, rhinitis and
 CC wound infections.
 CC
 SQ Sequence 369 AA;
 Query Match 10.9%; Score 95; DB 21; Length 369;
 Best Local Similarity 24.2%; Pred. No. 0.1;

Matches 57; Conservative 27; Mismatches 78; Indels 74; Gaps 14;

QY 1 MKRALALALALPAAALAGA---SGFYQADAAHAKASSLSGSAK-GFSPR----- 49
 DB 1 MKSLVALAVLS--AAVNAQAPQONTFYGAAGVGGSSFHGNGJLKGSDHEDYNDKTR 58
 QY 50 -----ISAGRI---NDLRAVD--YTRYKNYKAPSDFKLYSTGA----- 85
 DB 59 YGINRNSVTYGVFGYOILNQNNGELAAELGYDYGRVRGNVDEFRYKSHAGLNLALK 118
 QY 86 ---SVYDEPTQSPV-----KPYFGARLSLNRASAHLGSDSFSTSGAGLVAGV 133
 DB 119 PSYEVLPLDLVYGVKGLAVVRNDYKRY-GAE-NTNESTT-----KFKLKASTYLLGAGV 170
 QY 134 SYAVTEVVDLDAGRYNYGVKNTVRN--VRSG-----ELSGAVRVKF 174
 DB 171 EYALLP--ELAAVVEYOYLKAGNLKALVRSCTQVDVDFQYAPDIHSVTAGLSYRF 224

RESULT 15

AAV36955

ID AAV36955 standard; Protein; 797 AA.

XX AAY36955;

DT 07-OCT-1999 (first entry)

DE Chlamydia trachomatis surface exposed protein.

XX

KW Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
 KM paratrachoma; inclusion conjunctivitis; genital disease; perinephritis;
 KM nongonococcal urethritis; epididymitis; cervicitis; salpingitis;
 KM bartolinitis; pneumopathy; venereal lymphogranulomatosis.

XX

OS Chlamydia trachomatis.

XX WO9928475-A2.

XX 10-JUN-1999.

XX 27-NOV-1996; 98WO-IB01939.

XX 04-NOV-1996; 98US-0107077.

XX 28-NOV-1997; 97ER-0015041.

XX 17-DEC-1997; 97ER-0016034.

XX (GEST) GENSET.

XX Griffais R;

XX WPI; 1999-371125/31.

XX Genome sequence of Chlamydia trachomatis

XX Disclosure; Page 802; 1755pp; English.

AAV36754-Y37949 are encoded by open reading frames (ORFs) of the genome
 of Chlamydia trachomatis (see A4201425). The polypeptides can be used as
 vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences
 can also be used to control growth of the microorganism. Chlamydia
 trachomatis is responsible for a large number of diseases, e.g. eye
 diseases such as conventional trachoma, nonendemic trachoma,
 CC paratrachoma, and inclusion conjunctivitis; genital diseases such as
 CC nongonococcal urethritis, epididymitis, cervicitis, salpingitis,
 CC perinephritis, bartolinitis; pneumopathy in breast feeding infants;
 CC and venereal lymphogranulomatosis. The polypeptides of the invention
 may be of use in treating these diseases.

XX Sequence 797 AA;

Query Match 10.9%; Score 94.5; DB 20; Length 797;

Best Local Similarity 29.6%; Pred. No. 0.32;
 Matches 34; Conservative 16; Mismatches 48; Indels 17; Gaps 4;

QY 27 VQADAAHAKASSLSGSAKGFSPRISAGYRIND-LRFADV-----TRYKNYKA 73

DB 522 VELDKSINKALSKDYSDVTYGGNISTTYTLNDKLYGMYGSGQTSLSLRKTSSSNRLG 581

QY 74 PSTDFK--LVSIGASVIYDEPTQSPVKKPYFGARLSLNRASAHLGSDSFSTSGA 125

DB 582 PLDSNKGTFVSAAGLNLVD-SIDNPKRPTMGIRSFLLXKELSGLGTYQFTKLT 635

Search completed: October 28, 2002, 16:00:40
 Job time : 25.7145 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 28, 2002, 15:58:54 ; Search time 9.48637 seconds
(without alignments)
448.017 Million cell updates/sec

Title: US-09-684-883-8

Sequence: 1 MKKALALALALPAALAE.....VNTKVRSGELSGVRKF 174

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: /cgn2_Patents_AA:*
2: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/6C.COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	870	100.0	174 4	US-08-913-362-8
2	834	95.9	174 4	US-08-913-362-6
3	825	94.8	174 4	US-08-913-362-2
4	823.5	94.7	175 4	US-08-913-362-30
5	813.5	93.5	175 4	US-08-913-362-4
6	133	15.3	25 4	US-08-913-362-26
7	125	14.4	170 1	US-08-127-499A-20
8	125	14.4	170 1	US-08-482-847-20
9	104	12.0	359 1	US-08-457-997B-2
10	104	12.0	359 1	US-08-467-722A-2
11	87.5	10.1	573 4	US-09-336-447A-3
12	87	10.0	16 4	US-08-913-362-15
13	86	9.9	568 5	PCT-US95-13749-5
14	83	9.5	610 4	US-09-336-447A-11
15	83	9.5	624 4	US-09-336-447A-7
16	83	9.5	889 4	US-09-336-447A-15
17	80	9.2	15 4	US-08-913-362-23
18	80	9.2	409 4	US-09-066-046-31
19	80	9.2	409 4	US-09-066-047-19
20	78	9.0	15 4	US-08-913-362-14
21	78	9.0	15 4	US-08-913-362-16
22	77.5	8.9	560 3	US-08-926-842B-13
23	77	8.9	15 4	US-08-913-362-11
24	77	8.9	15 4	US-08-913-362-13
25	77	8.9	433 2	US-08-883-515-2
26	75	8.6	15 4	US-08-913-362-18
27	75	8.6	15 4	US-08-913-362-24

28	74.5	8.6	346 2	US-08-476-254-10	Sequence 10, Appl
29	74.5	8.6	346 6	5474933-2	Patent No. 5474933
30	74.5	8.6	346 6	5474933-7	Patent No. 5474933
31	74	8.5	264 1	US-08-482-271-3	Sequence 3, Appl1
32	74	8.5	264 1	US-08-482-271-4	Sequence 4, Appl1
33	74	8.5	264 2	US-08-854-811-45	Sequence 45, Appl
34	74	8.5	264 3	US-09-080-120A-2	Sequence 2, Appl1
35	74	8.5	264 3	US-09-080-120A-4	Sequence 4, Appl1
36	74	8.5	264 5	PCT-US95-08925-2	Sequence 2, Appl1
37	74	8.5	264 5	PCT-US95-08925-4	Sequence 4, Appl1
38	74	8.5	291 1	US-08-468-847B-19	Sequence 19, Appl
39	74	8.5	291 3	US-09-080-120A-7	Sequence 7, Appl1
40	74	8.5	291 5	PCT-US95-08925-7	Sequence 7, Appl1
41	74	8.5	291 6	5212074-5	Patent No. 5212074
42	74	8.5	346 2	US-08-476-254-2	Sequence 2, Appl1
43	74	8.5	866 2	US-08-483-101-4	Sequence 2, Appl1
44	73.5	8.4	1394 4	US-08-286-791-2	Sequence 2, Appl1
45	73.5	8.4	1394 5	PCT-US95-10661A-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-08-913-362-8
; Sequence 8, Application US/08913362
; Patent No. 6287574
; GENERAL INFORMATION:
; APPLICANT: Brodeur, Bernard R
; APPLICANT: Martin, Denis
; APPLICANT: Hamel, Josee
; APPLICANT: Rioux, Clement
; TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
; TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/913,362
; FILING DATE: 13-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406,362
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/001,983
; FILING DATE: 04-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 047998/0128
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 174 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-913-362-8
Query Match 100.0%; Score 870; DB 4; Length 174;

Best Local Similarity 100.0%; Pred. No. 3e-95;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKKALALIALPALPAALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
Db 1 MKKALALIALPALPAALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60

Qy 61 FAVDYTRYKNYKAPSTDFELKISIGASVITYDFTQSPVKPYFGARLSLNRAASHLGSDSF 120
Db 61 FAVDYTRYKNYKAPSTDFELKISIGASVITYDFTQSPVKPYFGARLSLNRAASHLGSDSF 120

Qy 121 SKTSAGLVLAGSVYAVTPNVDLDAGYRYNYGVKNTVKNVSGELSGAVRYKF 174
Db 121 SKTSAGLVLAGSVYAVTPNVDLDAGYRYNYGVKNTVKNVSGELSGAVRYKF 174

RESULT 2

US-08-913-362-6
; Sequence 6, Application US/08913362
; Patent No. 6287574

GENERAL INFORMATION:
APPLICANT: Brodeur, Bernard R
APPLICANT: Martin, Denis
APPLICANT: Hamel, Josee
APPLICANT: Rioux, Clement
TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/001,983
FILING DATE: 04-AUG-1995

ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 047998/0128
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-913-362-6

Query Match 95.9%; Score 834; DB 4; Length 174;
Best Local Similarity 95.4%; Pred. No. 5.5e-91;
Matches 166; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MKKALALIALPALPAALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
Db 1 MKKALALIALPALPAALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60

Qy 61 FAVDYTRYKNYKAPSTDFELKISIGASVITYDFTQSPVKPYFGARLSLNRAASHLGSDSF 120
Db 61 FAVDYTRYKNYKAPSTDFELKISIGASVITYDFTQSPVKPYFGARLSLNRAASHLGSDSF 120

Qy 121 SKTSAGLVLAGSVYAVTPNVDLDAGYRYNYGVKNTVKNVSGELSGAVRYKF 174
Db 121 SKTSAGLVLAGSVYAVTPNVDLDAGYRYNYGVKNTVKNVSGELSGAVRYKF 174

RESULT 3

US-08-913-362-2
; Sequence 2, Application US/08913362
; Patent No. 6287574

GENERAL INFORMATION:
APPLICANT: Brodeur, Bernard R
APPLICANT: Martin, Denis
APPLICANT: Hamel, Josee
APPLICANT: Rioux, Clement
TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/001,983
FILING DATE: 04-AUG-1995

ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 047998/0128
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-913-362-2

Query Match 94.8%; Score 825; DB 4; Length 174;
Best Local Similarity 94.3%; Pred. No. 6.4e-90;
Matches 164; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MKKALALIALPALPAALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
Db 1 MKKALALIALPALPAALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60

Qy 61 FAVDYTRYKNYKAPSTDFELKISIGASVITYDFTQSPVKPYFGARLSLNRAASHLGSDSF 120
Db 61 FAVDYTRYKNYKAPSTDFELKISIGASVITYDFTQSPVKPYFGARLSLNRAASHLGSDSF 120

Qy 121 SKTSAGLVLAGSVYAVTPNVDLDAGYRYNYGVKNTVKNVSGELSGAVRYKF 174
Db 121 SKTSAGLVLAGSVYAVTPNVDLDAGYRYNYGVKNTVKNVSGELSGAVRYKF 174

NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/001,983
FILING DATE: 04-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 047998/0128
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Neisseria meningitidis
STRAIN: 608B
US-08-913-362-26

Query Match 15.3%; Score 133; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 3e-09;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 61 FAVDYTRYKNYKAPSTDFKLYSIGA 85
DB 1 FAVDYTRYKNYKAPSTDFKLYSIGA 25

RESULT 7
US-08-127-499A-20
Sequence 20, Application US/08127499A
Patent No. 5510264
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/127,499A
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/102/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-127-499A-20

Query Match 14.4%; Score 125; DB 1; Length 170;
Best Local Similarity 25.2%; Pred. No. 4.8e-07;
Matches 37; Conservative 18; Mismatches 46; Indels 46; Gaps 3;

OY 6 AALIALPAAALAGCAGFYQADAAH-----AKASSLSG-----AKG 45
DB 15 SLFSSAAQAASEDRSPYQADLAVMERITHDYPQATGANNSTVSDFENRAHS 74
OY 46 FSPRISAGYRINDLRFADVTRYKNY-----KAPSTDFK 79
DB 75 IHPRVSVGIDEGGRRIADYASYRKNMNNKSVMTKELEKNNKKDKLTENQNGTFHA 134
OY 80 LYSIGASYIDFDGQSPVYFEGARLS 106
DB 135 ASLGLSAIYDFKLGKFKFYIGARVA 161

RESULT 8
US-08-482-847-20
Sequence 20, Application US/08482847
Patent No. 5556757
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THEREOF, AND USES THEREOF
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,847
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/104/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136

INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-467-720

Query Match 14.4%; Score 125; DB 1; Length 170;
Best Local Similarity 25.2%; Pred. No. 4.8e-07;
Matches 37; Conservative 18; Mismatches 46; Indels 46; Gaps 3;

QY 6 AALLALPAALALAGAGSGFYQADAA-----AKASSLG-----AKG 45
DB 15 SSLSSAAQAASEDRSPYYQADLAERITHDPQATGANNSTVSDYFRRIRAS 74
QY 46 FSPRISAGYRINDLRFADVTRYKNY-----KAPSTDFK 79
DB 75 IHPRTSVGDEGWRILADYASIRKNNKSVNTKELENKNNKKDLKTENQENGTFHA 134
QY 80 IYSIGASYIDFDTQSPVKPYFGARLS 106
DB 135 ASSLGISATYDFKLGKFKPYGARVA 161

RESULT 9
US-08-457-997B-2
Sequence 2, Application US/08457997B
Patent No. 5766608
GENERAL INFORMATION:
APPLICANT: Kolattukudy, P. E.
TITLE OF INVENTION: Otitis Media Vaccine
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Calfee, Halter and Griswold
STREET: Suite 1800 800 Superior Avenue
CITY: Cleveland
STATE: Ohio
COUNTRY: U.S.A.
ZIP: 44114-2688
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,997B
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Gollick, Mary E.
REGISTRATION NUMBER: 34,829
REFERENCE/DOCKET NUMBER: 22727/00102
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 622-8458
TELEFAX: (216) 241-0816
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-457-997B-2

Query Match 12.0%; Score 104; DB 1; Length 359;
Best Local Similarity 24.7%; Pred. No. 0.00046;
Matches 56; Conservative 29; Mismatches 82; Indels 60; Gaps 11;

QY 1 MKKALALIALALPAALALAGAGSGFYQADAA-----HAKASSLGASANGFSPRISAG 53
DB 1 MKKTAIALVAVAGLAASVAQAPOENTFYAGYKAGQGSFHDGINNGAIIKKGSSS-NYG 59
QY 54 YRINDLRFADVTRYKNYKAPSTDFKLYSIGASYIIDFDTQSPV-----KPFAR 104

DB 60 YRRNTFTYGV-----FGYQILNOD--NFGIAELGYDDGFRAKLREAGRPKAKHTNHGAY 113
QY 105 LSLNRSAGHLGSDSPSEKTSAGL-----GVLA-GVSYA 136
DB 114 LSLKGSYEVLDGDYIGKAGVALVRSDYKFEYDANGTRDHHKGRHTARASGLFPAVGAERYA 173
QY 137 VTPNVLDAGY-----RYNYGKVTYKAVRS--GELSAGYRVKF 174
DB 174 VLPELAVRLEYQWLTIRGKXRPQDKPWTALNYPWIGCINAGISYRF 220

RESULT 10
US-08-467-722A-2
Sequence 2, Application US/08467722A
Patent No. 6030626
GENERAL INFORMATION:
APPLICANT: Kolattukudy, P. E.
TITLE OF INVENTION: Otitis Media Vaccine
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Calfee, Halter and Griswold
STREET: Suite 1800 800 Superior Avenue
CITY: Cleveland
STATE: Ohio
COUNTRY: U.S.A.
ZIP: 44114-2688
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,722A
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Gollick, Mary E.
REGISTRATION NUMBER: 34,829
REFERENCE/DOCKET NUMBER: 22727/00102
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 622-8458
TELEFAX: (216) 241-0816
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-467-722A-2

Query Match 12.0%; Score 104; DB 3; Length 359;
Best Local Similarity 24.7%; Pred. No. 0.00046;
Matches 56; Conservative 29; Mismatches 82; Indels 60; Gaps 11;

QY 1 MKKALALIALALPAALALAGAGSGFYQADAA-----HAKASSLGASAKGFSRISAG 53
DB 1 MKKTAIALVAVAGLAASVAQAPOENTFYAGYKAGQGSFHDGINNGAIIKKGSSS-NYG 59
QY 54 YRINDLRFADVTRYKNYKAPSTDFKLYSIGASYIIDFDTQSPV-----KPFAR 104
DB 60 YRRNTFTYGV-----FGYQILNOD--NFGIAELGYDDGFRAKLREAGRPKAKHTNHGAY 113
QY 105 LSLNRSAGHLGSDSPSEKTSAGL-----GVLA-GVSYA 136
DB 114 LSLKGSYEVLDGDYIGKAGVALVRSDYKFEYDANGTRDHHKGRHTARASGLFPAVGAERYA 173
QY 137 VTPNVLDAGY-----RYNYGKVTYKAVRS--GELSAGYRVKF 174
DB 174 VLPELAVRLEYQWLTIRGKXRPQDKPWTALNYPWIGCINAGISYRF 220

RESULT 11

DB 509 GKVASV-FDESIASAKTSNAYG--AGVQPNPLPNEVIDASYEYS---KIDSIK-VGTWM 561
QY 166 LSAGVR 171
DB 562 LGAGVR 567

RESULT 14

US-09-336-447A-11
Sequence 11, Application US/09336447A
Patent No. 6310190
GENERAL INFORMATION:
APPLICANT: HANSEN, ERIC J.
APPLICANT: AEBI, CHRISTOPH
APPLICANT: COPE, LESLIE D.
APPLICANT: MACIVER, ISOBEL
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FREDENBURG, ROSS A.
TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
FILE REFERENCE: AMCY:024
CURRENT APPLICATION NUMBER: US/09/336,447A
CURRENT FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11
LENGTH: 610
TYPE: PRT
ORGANISM: Moraxella catarrhalis
US-09-336-447A-11

Query Match

Best Local Similarity 26.0%; Score 83; DB 4; Length 610;
Matches 45; Conservative 21; Mismatches 55; Indels 52; Gaps 9;

QY 19 AEGASGEVYQADA-----AHAKASSSIGG-AKGFSPRISA-GYRIN--DLRFADV 65
DB 473 ASADTKFAATADAITKNGNAITKNKASTIDLTGKVDGFGRTALDTKVNAFDGRITLAD 532
QY 66 TRYKN---YKAPSTDFKLYSIGASVIYDFDQSPVKPYFGARLSLNRSASHLGSDSFS 121
DB 533 SKVNGMAAQAALSGLFQPSYSGK-----NATAALGSGYSKS 570
QY 122 KTSAGLGVLAGVYAVTPVNDIDAGYRNVYGVKNTKRVNSGELSAGVRKF 174
DB 571 AVAIGAG-----YRVNPNLAFKAG-----AAINTSGN-KKGSYNIQVNYEF 610

RESULT 15

US-09-336-447A-7
Sequence 7, Application US/09336447A
Patent No. 6310190
GENERAL INFORMATION:
APPLICANT: HANSEN, ERIC J.
APPLICANT: AEBI, CHRISTOPH
APPLICANT: COPE, LESLIE D.
APPLICANT: MACIVER, ISOBEL
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FREDENBURG, ROSS A.
TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
FILE REFERENCE: AMCY:024
CURRENT APPLICATION NUMBER: US/09/336,447A
CURRENT FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 624
TYPE: PRT
ORGANISM: Moraxella catarrhalis
US-09-336-447A-7

Query Match 9.5%; Score 83; DB 4; Length 624;
Best Local Similarity 26.0%; Pred. No. 0.32;

Matches 45; Conservative 21; Mismatches 55; Indels 52; Gaps 9;
QY 19 AEGASGEVYQADA-----AHAKASSSIGG-AKGFSPRISA-GYRIN--DLRFADV 65
DB 487 ASADTKFAATADAITKNGNAITKNKASTIDLTGKVDGFGRTALDTKVNAFDGRITLAD 546
QY 66 TRYKN---YKAPSTDFKLYSIGASVIYDFDQSPVKPYFGARLSLNRSASHLGSDSFS 121
DB 547 SKVNGMAAQAALSGLFQPSYSGK-----NATAALGSGYSKS 584
QY 122 KTSAGLGVLAGVYAVTPVNDIDAGYRNVYGVKNTKRVNSGELSAGVRKF 174
DB 585 AVAIGAG-----YRVNPNLAFKAG-----AAINTSGN-KKGSYNIQVNYEF 624

Search completed: October 28, 2002, 16:04:21
Job time : 10.4864 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 28, 2002, 15:58:04 ; Search time 12.4821 Seconds

(without alignments)
1339.485 Million cell updates/sec

Title: US-09-684-883-8

Perfect score: 870
Sequence: 1 MKKALALIALALPAAALAE.....VNTVKNRSGELSGAVRVKF 174

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	834	95.9	174	2	B81932
2	829	95.3	174	2	G81174
3	237.5	27.3	261	2	S16610
4	236	27.1	270	2	S04380
5	235	27.0	260	2	S16611
6	235	27.0	266	2	S16616
7	234.5	27.0	338	2	S16612
8	234	26.9	258	2	S16612
9	233.5	26.8	237	2	S36343
10	233.5	26.8	257	2	S16614
11	233.5	26.8	268	1	KONH2C
12	231	26.6	258	1	S08514
13	231	26.6	260	1	KONH0
14	231	26.6	283	2	S72343
15	228.5	26.3	282	2	S16617
16	226	26.0	233	2	S36350
17	225.5	25.9	234	2	S36342
18	225	25.9	234	2	S36342
19	225	25.9	234	2	S36341
20	224	25.7	254	2	S20043
21	222	25.5	261	2	S16619
22	221	25.4	234	2	S36348
23	220.5	25.3	243	2	S36346
24	219	25.2	234	1	KONH8
25	219	25.2	238	2	S36349
26	216	24.8	248	2	PL0038
27	210	24.1	178	2	F64124
28	209	24.0	238	2	S36344
29	206.5	23.7	247	2	S28627

30	206	23.7	239	2	S28630	opacity protein op
31	194.5	22.4	214	2	S44706	opacity protein op
32	184.5	21.2	235	2	S44707	opacity protein op
33	176.5	20.3	121	2	I64187	opacity protein op
34	144.5	16.6	210	2	S77737	opacity protein ho
35	134	15.4	187	2	S20044	opacity protein op
36	129	14.8	239	2	S08513	opacity protein op
37	125	14.4	168	2	AH0541	probable outer mem
38	125	14.4	170	2	T10256	opacity protein-re
39	124.5	14.3	281	2	AH3012	opacity protein-re
40	124.5	14.3	284	2	G98271	outer surface prot
41	122.5	14.1	70	2	F64066	hypothetical prote
42	120.5	13.9	201	2	S16286	probable outer mem
43	120	13.8	192	2	S44712	opacity protein op
44	116.5	13.4	264	2	I54668	opacity protein op
45	114	13.1	182	2	A10353	heat resistant agg
						attachment invasio

ALIGNMENTS

RESULT 1

B81932

outer membrane protein NMA0862 [imported] - Neisseria meningitidis (strain z2491 sero

C:Species: Neisseria meningitidis

C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001

C:Accession: B81932

R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mo

Nature 404, 502-506, 2000

A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis z2491

A:Reference number: A81775; MUID:20222556

A:Accession: B81932

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-174 <PAR>

A:Cross-references: GB:AL162754; GB:AL157959; MID:97379424; PIDN:CAB84143.1; PID:9737

A:Experimental source: serogroup A, strain z2491

C:Genetics:

A:Gene: nspa; NMA0862

Query Match

Best Local Similarity 95.9%; Score 834; DB 2; Length 174;

Matches 166; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY

1 MKKALALIALALPAAALAEAGSGFYQADAAHAKASSISGAKGFSRISAGYRINDLR 60

1 MKKALATIALALPAAALAEAGSGFYQADAAHAKASSISGAKGFSRISAGYRINDLR 60

61 FAVDYTRKKNYKAPSTDFKLYSIGASVYDFDQSPVKKPYFGARLSINRAAHILGSGDSF 120

61 FAVDYTRKKNYKAPSTDFKLYSIGASVYDFDQSPVKKPYFGARLSINRAAHILGSGDSF 120

DB

121 SKTSGAGVLAGVSYAVTPNVDLAGYRVNKGVRNKNVRSSELGAGRVKF 174

121 SKTSGAGVLAGVSYAVTPNVDLAGYRVNKGVRNKNVRSSELGAGRVKF 174

RESULT 2

G81174

outer membrane protein NsgA NMB0663 [imported] - Neisseria meningitidis (strain MC58

C:Species: Neisseria meningitidis

C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001

C:Accession: G81174

R:Telletlin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen,

Hickey, E.K.; Haft, D.H.; Salberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.

Science 287, 1809-1815, 2000

A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.;

A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.

A:Accession: G81174

A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-174 <ENT>
A:Cross-references: GB:AE002420; GB:AE002098; NID:97225876; PTDN:AAFA1081.1; PID:9722588
A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB0663

Query Match 95.3%; Score 829; DB 2; Length 174;
Best Local Similarity 94.8%; Pred. No. 9, 2e-67;
Matches 165; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Db 1 MKKALALALALPAALAEAGAGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
1 MKKALALALALPAALAEAGAGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
Db 61 FAVDYTRKRYKAPSTDFKLYSGASVYDFQSPYKRYFFGARLSLNRASAHLGSDSF 120
61 FAVDYTRKRYKAPSTDFKLYSGASVYDFQSPYKRYFFGARLSLNRASAHLGSDSF 120
Db 121 SKTSAGVLAGVSYAVTPNVDLAGYRNYGVKNTVKNVRSGLSAGVRKF 174
121 SKTSAGVLAGVSYAVTPNVDLAGYRNYGVKNTVKNVRSGLSAGVRKF 174
Db 121 SGTSLGLVLTGVSIVATPNVDLAGYRNYGVKNTVKNVRSGLSAGVRKF 174

RESULT 3

opacity protein opak precursor - Neisseria gonorrhoeae (strain MS11) (fragments)
N:Alternate names: outer membrane protein opak
C:Species: Neisseria gonorrhoeae
A:Variety: strain MS11
C:Date: 13-Jan-1995 #sequence_revision 17-Oct-1997 #text_change 17-Oct-1997
C:Accession: S16610
R:Bhat, K.S.; Glibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsch, M.L. Microbiol. 5, 1989-1991, 1991
A:Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a family of repeats place the start codon in frame with the rest of the protein
A:Reference number: S16610; MUID:92114767
A:Accession: S16610
A:Molecule type: DNA
A:Residues: 1-261 <BHA>
A:Cross-references: EMBL:X52364
A:Experimental source: strain MS11, variant 4.8
A:Note: the authors did not translate the sequence for the signal peptide
A:Note: expression of opacity proteins is regulated by the number of translated repeat of repeats place the start codon in frame with the rest of the protein
C:Genetics:
A:Gene: opak
C:Superfamily: opacity protein
C:Keywords: cell surface component; transmembrane protein
F:1-10,11-23/Domain: signal sequence (fragments) #status predicted <SIG>
F:24-261/Product: opacity protein opak #status predicted <MAT>
F:34-42/Domain: transmembrane #status predicted <TM1>
F:43-75/Domain: extracellular #status predicted <EXT1>
F:51-61/Region: semivariable region
F:76-84/Domain: transmembrane #status predicted <TM2>
F:89-95/Domain: transmembrane #status predicted <TM3>
F:96-134/Domain: extracellular #status predicted <EXT2>
F:102-129/Region: hypervariable region HV1
F:135-149/Domain: transmembrane #status predicted <TM4>
F:155-165/Domain: transmembrane #status predicted <TM5>
F:166-212/Domain: extracellular #status predicted <EXT3>
F:171-218/Region: hypervariable region HV2
F:213-225/Domain: transmembrane #status predicted <TM6>
F:229-237/Domain: transmembrane #status predicted <TM7>
F:238-252/Domain: extracellular #status predicted <EXT4>
F:253-261/Domain: transmembrane #status predicted <TM8>

Query Match 27.3%; Score 237.5; DB 2; Length 261;
Best Local Similarity 29.3%; Pred. No. 8e-14;
Matches 72; Conservative 22; Mismatches 61; Indels 91; Gaps 9;

Db 15 AAALAEAG-ASGEVQADAAHAKA-----SSLSGAKG-----FSPRI 50
21 AQAASEGNGRGPVQADLAAERITHDYPTPTGAKKGTITISYSDYFRNIRHSHPRV 80

Op 51 SAGYRINDLRFAVDYTRKRY-----KAPSTDFK-----LYS 82
81 SVGDPEGMRIRADYATYRRKNNKYSVSIKELLRNKNNRDLAKRNGENGTFAVSS 140
Op 83 IGASVYDFQSPYKRYFFGARLSLNRASAHLGSS-DSFKTS-----124
141 LGLSAVYDFKINDKFKPYIGARV----AYCHVRSIDSTFKTTEVTILHGPTTPTVY 196
Op 125 -----AGVLAGVSYAVTPNVDLAGYRNYGVKNTVKNVRSGLSAGV 168
197 GKNTQNAHRESDSIRRVGLAVAGVGDITPNLTLDGGRYHWRGLNTR-FKTHPSL 255
Db 169 GVRVRF 174
Op 256 GVRVRF 261

RESULT 4

opacity protein P.II precursor - Neisseria gonorrhoeae (strain F62-SF and others) (fr
S04380
C:Species: Neisseria gonorrhoeae
A:Variety: strain F62-SF
C:Date: 30-Jun-1991 #sequence_revision 17-Oct-1997 #text_change 13-Nov-1998
C:Accession: S04380; S16504
R:Palmer, L.; Brooks, G.F.; Falkow, S.
Mol. Microbiol. 3, 663-671, 1989
A:Title: Expression of gonococcal protein II in Escherichia coli by translational fus
A:Reference number: S04380; MUID:89343653
A:Accession: S04380
A:Molecule type: DNA
A:Residues: 1-270 <PAL>
A:Cross-references: EMBL:X15780
A:Experimental source: strain F62-SF, serogroup IB-3; clone F62-SF61
A:Note: the authors did not translate the sequence of the signal peptide
A:Note: expression of opacity proteins is regulated by the number of translated repeat of repeats place the start codon in frame with the rest of the protein
R:Tana, M.K.; So, M.; Seifert, H.S.; Bilyard, E.; Marchal, C.
EMBO J. 7, 4367-4378, 1988
A:Title: Pili expression in Neisseria gonorrhoeae is under both positive and negative
A:Reference number: S02017; MUID:89210824
A:Accession: S16504
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 259-270 <TAB>
A:Cross-references: EMBL:X13965
A:Experimental source: strain MS11A
A:Note: expression of opacity proteins is regulated by the number of translated repeat of repeats place the start codon in frame with the rest of the protein
C:Genetics:
A:Gene: opak
C:Superfamily: opacity protein
C:Keywords: cell surface component; transmembrane protein
F:1-10,11-23/Domain: signal sequence (fragments) #status predicted <SIG>
F:24-270/Product: opacity protein opak #status predicted <MAT>
F:34-42/Domain: transmembrane #status predicted <TM1>
F:43-75/Domain: extracellular #status predicted <EXT1>
F:51-61/Region: semivariable region
F:76-84/Domain: transmembrane #status predicted <TM2>
F:89-95/Domain: transmembrane #status predicted <TM3>
F:96-141/Domain: extracellular #status predicted <EXT2>
F:102-136/Region: hypervariable region HV1
F:142-156/Domain: transmembrane #status predicted <TM4>
F:162-172/Domain: transmembrane #status predicted <EXT3>
F:173-221/Domain: extracellular #status predicted <EXT5>
F:178-227/Region: hypervariable region HV2
F:222-234/Domain: transmembrane #status predicted <TM6>
F:238-246/Domain: transmembrane #status predicted <TM7>
F:247-261/Domain: extracellular #status predicted <EXT4>
F:262-270/Domain: transmembrane #status predicted <TM8>

Query Match 27.1%; Score 236; DB 2; Length 270;
Best Local Similarity 27.4%; Pred. No. 1.1e-13;

Db 182 LAGPPTPTVYPKNTQAHRESDSIRRVGLGAVGVIDITPMLTLDAGYRHYWGRL 241
QY 157 TVKNVRSGLSAGVRYKF 174
Db 242 NTR-FKTHEASLGAVRYF 258

RESULT 9

Opacity protein opa57 - Neisseria gonorrhoeae (strain MS11) (fragment)
N:Alternate names: outer membrane protein opa57
C:Species: Neisseria gonorrhoeae
A:Variety: strain MS11
C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 26-Aug-1999
C:Accession: S36343; S28626
R:Kupsch, E.M.; Knepper, B.; Kuroki, T.; Heuer, I.; Meyer, T.F.
EMBO J. 12, 641-650, 1993
A:Title: Variable opacity (Opa) outer membrane proteins account for the cell tropisms of
A:Reference number: S36328; MUID:93178439
A:Accession: S36343
A:Molecule type: DNA
A:Residues: 1-237 <NUP>
A:Cross-references: EMBL:Z18935; NID:949331; PIDN:CAA79368.1; PID:940797
A:Experimental source: strain MS11, variant F3
A:Note: expression of opacity proteins is regulated by the number of translated repeat
of repeats place the start codon in frame with the rest of the protein
C:Genetics:
A:Gene: opa57
C:Superfamily: opacity protein
C:Keywords: cell surface component; transmembrane protein
F:1-237/Product: opacity protein opa57 #status predicted <MAT>
F:1-19/Domain: transmembrane #status predicted <TM1>
F:20-51/Domain: extracellular #status predicted <EXT1>
F:28-37/Region: semivariable region
F:53-60/Domain: transmembrane #status predicted <TM2>
F:65-71/Domain: transmembrane #status predicted <TM3>
F:72-110/Domain: extracellular #status predicted <EXT2>
F:78-105/Region: hypervariable region HV1
F:111-125/Domain: transmembrane #status predicted <TM4>
F:131-141/Domain: transmembrane #status predicted <TM5>
F:142-188/Domain: extracellular #status predicted <EXT3>
F:147-194/Region: hypervariable region HV2
F:189-201/Domain: transmembrane #status predicted <TM6>
F:205-213/Domain: transmembrane #status predicted <TM7>
F:214-228/Domain: extracellular #status predicted <EXT4>
F:229-237/Domain: transmembrane #status predicted <TM8>

Query Match 26.8%; Score 233.5; DB 2; Length 237;
Best Local Similarity 28.9%; Pred. No. 1.6e-13;
Matches 70; Conservative 22; Mismatches 61; Indels 89; Gaps 8;

QY 17 ALAEGSGFYVQADAAH-----KASSLSGS-----AKGFSPRISAGY 54
Db 1 ASDEGGGPGFYVQADLAAYAEHTHDYPEPTAPKNKISTVSYFNRIRRSVHPRVSVG 60
QY 55 RINDLRFVADYTYRKY-----KAPSTDFK-----LVSIGS 86
Db 61 DEFGWRLADYARYRRKNNKYSVSIKELRNKGNRDLDAENOENCTFHAVALSGLS 120
QY 87 VIYDPTQSPVRYFGARLSLNRASAHLSGS--DSFSKTS----- 124
Db 121 AYVDFLNDKFRYIGARV---AYGHRHSIDSTFKTTEVTTLHGPTPTVYPKNFT 176
QY 125 -----AGLGLVAGSYAVTPNDLDAGYRYNVGVNRYKVRSELSAGVRY 172
Db 177 QQAHRSDSIRRVGLGAVGVIDITPMLTLDAGYRHYWGRL 241

QY 173 KF 174
Db 236 RF 237

RESULT 10

S16614
Opacity protein opaF precursor - Neisseria gonorrhoeae (strain MS11) (fragments)
C:Species: Neisseria gonorrhoeae
A:Variety: strain MS11
C:Date: 04-Jun-1997 #sequence_revision 17-Oct-1997 #text_change 17-Oct-1997
C:Accession: S16614
R:Bhat, K.S.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehmig, F.; Stern, A.; Kupsc
Mol. Microbiol. 5, 1889-1901, 1991
A:Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a f
A:Reference number: S16610; MUID:92114767
A:Accession: S16614
A:Molecule type: DNA
A:Residues: 1-257 <BHA>
A:Cross-references: EMBL:X52368
A:Experimental source: strain MS11, variant 4.8
A:Note: the authors translated the codon ACC for residue 206 as Ala and TAT for resid
A:Note: the authors did not translate the sequence for the signal peptide
A:Note: expression of opacity proteins is regulated by the number of translated repea
of repeats place the start codon in frame with the rest of the protein
C:Genetics:
A:Gene: opaF
C:Superfamily: opacity protein
C:Keywords: cell surface component; transmembrane protein
F:1-10,11-23/Domain: signal sequence (fragments) #status predicted <SIG>
F:24-257/Product: opacity protein opaF #status predicted <MAT>
F:101-126/Region: hypervariable region HV1
F:132-146/Domain: transmembrane #status predicted <TM1>
F:152-162/Domain: transmembrane #status predicted <TM2>
F:163-208/Domain: extracellular #status predicted <EXT1>
F:51-60/Region: semivariable region
F:75-83/Domain: transmembrane #status predicted <TM2>
F:88-94/Domain: transmembrane #status predicted <TM3>
F:95-131/Domain: extracellular #status predicted <EXT2>
F:101-126/Region: hypervariable region HV1
F:132-146/Domain: transmembrane #status predicted <TM1>
F:152-162/Domain: transmembrane #status predicted <TM2>
F:163-208/Domain: extracellular #status predicted <EXT1>
F:168-214/Region: hypervariable region HV2
F:209-221/Domain: transmembrane #status predicted <TM6>
F:225-233/Domain: transmembrane #status predicted <TM7>
F:234-248/Domain: extracellular #status predicted <EXT4>
F:249-257/Domain: transmembrane #status predicted <TM8>

Query Match 26.8%; Score 233.5; DB 2; Length 257;
Best Local Similarity 28.8%; Pred. No. 1.8e-13;
Matches 74; Conservative 23; Mismatches 71; Indels 89; Gaps 9;

QY 2 KKAALALALPAALEGG---ASGFYVQADAAH-----KASSLSGSK----- 44
Db 6 KKPRLFFSLLFSSAAQAGEDEHGRPGFYVQADLAAYAEHTHDYPEPTGKKKISTVSD 65
QY 45 -----GFSPRISAGYRINDLRFVADYTYRKY---NKAPSTDFK----- 79
Db 66 YFRNIRTHSHPRVSVGDFGWRRLADYARYRRKNNKYSVVDIKELKNKNNKRDLTE 125
QY 80 -----LVSIGASVYDPTQSPVRYFGARLSLNRASAHLSGS--DSFSKTS----- 124
Db 126 NOENCTFHAVALSGLSAVYDFKLNDKFRYIGARV---AYGHRHSIDSTFKTTEVTLS 161
QY 125 -----AGLGLVAGSYAVTPNDLDAGYRYNVGVNRYKVRSELSAGVRY 157
Db 182 SYGGLNPTVYTEENTQNAHNSNSIRRVGLGAVGVIDITPMLTLDAGYRHYWGRL 241
QY 158 VKNVRSGLSAGVRYKF 174
Db 242 TR-FKTHEASLGAVRYF 257

RESULT 11

KONH2C
Opacity protein P.IIC precursor - Neisseria gonorrhoeae (strain JS3) (fragments)
N:Alternate names: outer membrane protein P.IIC
C:Species: Neisseria gonorrhoeae
A:Variety: strain JS3
C:Date: 31-Mar-1992 #sequence_revision 17-Oct-1997 #text_change 08-May-1998

C:Accession: S03095; S16360
 R:van der Ley, P.
 Mol. Microbiol. 2, 797-806, 1988
 A:Title: Three copies of a single protein II-encoding sequence in the genome of *Neisseria meningitidis*.
 A:Reference number: S03095; MUID:89096501
 A:Accession: S03095
 A:Molecule type: DNA
 A:Residues: 1-268 <YAN>
 A:Cross-references: EMBL:X12625
 A:Experimental source: strain JS3
 A:Note: 241-Val was also found
 A:Note: expression of opacity proteins is regulated by the number of translated repeat of repeats place the start codon in frame with the rest of the protein
 R:partly, D.S.; Schwalbe, R.S.; Klapper, D.G.; Cannon, J.G.
 Infect. Immun. 55, 2026-2031, 1987
 A:Title: Antigenic and structural differences among six proteins II expressed by a single
 A:Reference number: S16360; MUID:87306843
 A:Accession: S16360
 A:Molecule type: protein
 A:Residues: 24-34 <BAR>
 C:Genetics:
 A:Gene: PiliC
 C:Superfamily: Opacity protein
 C:Keywords: cell surface component; transmembrane protein
 F:1-10,11-23/Domain: signal sequence (fragments) #status predicted <SIG>
 F:24-268/Product: opacity protein P.IIC #status experimental <MAT>
 F:34-42/Domain: transmembrane #status predicted <EXT1>
 F:43-74/Domain: extracellular #status predicted <EXT1>
 F:51-60/Region: semivariable region
 F:75-83/Domain: transmembrane #status predicted <TM2>
 F:88-94/Domain: transmembrane #status predicted <TM3>
 F:95-140/Domain: extracellular #status predicted <EXT2>
 F:101-135/Region: hypervariable region HV1
 F:141-155/Domain: transmembrane #status predicted <TM4>
 F:161-171/Domain: transmembrane #status predicted <TM5>
 F:172-219/Domain: extracellular #status predicted <EXT3>
 F:177-225/Region: hypervariable region HV2
 F:220-232/Domain: transmembrane #status predicted <TM6>
 F:236-244/Domain: transmembrane #status predicted <TM7>
 F:245-259/Domain: extracellular #status predicted <EXT4>
 F:260-268/Domain: transmembrane #status predicted <TM8>

Query Match 26.8%; Score 233.5; DB 1; Length 268;
 Best Local Similarity 26.5%; Pred. No. 1,9e-13;
 Matches 68; Conservative 29; Mismatches 71; Indels 89; Gaps 7;

QY 6 AALTAALPAAALAEAGSGFYVOADAHAKA-----SSSLGSAK----- 44
 DB 13 SLLFSSAARASDEGSRGPRYQADLVAERITHYPRFTGTGKKNISTVSDYFNIRIR 72
 QY 45 -GFSRISAGYRINDLRPAVDYTRYK-----NTRKAPS 75
 DB 73 HSHVPRVSVGYDEGSMRIADYARFKMNNKYSVSIKELLRNDNSASGVRLHNIQTOK 132
 QY 76 TDFK-----LYSIGASVIYDFPTQSPVKPYFGARLSLRASAHL----- 114
 DB 133 TEHENGTFHVAVSSIGLSTIYDFPTGSRFRPYIGMRAVAGHVRHQVSVDETEIITTP 192
 QY 115 ---GGSDSFSK-----TSAGLGVLAVGSYAVTPNVLDAGRYRYNKGKVT 157
 DB 193 SNGGKYSLSKMPKSHHOSNSIRVGLGVINGVGFDTITPNTLDGTGRYHNGRLN 252

QY 158 VKNVRSGLSAGVRYKF 174
 DB 253 TR-FRTHEASLGMYRF 268

RESULT 12
 S08514
 opacity protein-related protein OPM1 precursor - *Neisseria meningitidis* (strain C1938)
 N:Alternate names: outer membrane protein class 5
 C:Species: *Neisseria meningitidis*

A:Variety: strain C1938
 C:Date: 19-Mar-1997 #sequence_revision 17-Oct-1997 #text_change 20-Jun-2000
 C:Accession: S08514
 R:Stern, A.; Meyer, T.F.
 Mol. Microbiol. 1, 5-12, 1987
 A:Title: Common mechanism controlling phase and antigenic variation in pathogenic *nei*
 A:Reference number: S08513; MUID:88260884
 A:Accession: S08514
 A:Molecule type: DNA
 A:Residues: 1-258 <STP>
 A:Cross-references: EMBL:X06445; NID:g44906; PTD:g1333787
 A:Experimental source: strain C1938
 A:Note: expression of opacity proteins is regulated by the number of translated repeat of repeats place the start codon in frame with the rest of the protein
 C:Genetics:
 A:Gene: opm1
 C:Superfamily: opacity protein
 C:Keywords: cell surface component; transmembrane protein
 F:1-13,14-21/Domain: signal sequence (fragments) #status predicted <SIG>
 F:22-258/Product: opacity protein-related protein OPM1 #status predicted <MAT>
 F:33-41/Domain: transmembrane #status predicted <EXT1>
 F:42-73/Domain: extracellular #status predicted <EXT1>
 F:50-59/Region: semivariable region
 F:74-82/Domain: transmembrane #status predicted <TM2>
 F:87-93/Domain: transmembrane #status predicted <TM3>
 F:94-129/Domain: extracellular #status predicted <EXT2>
 F:100-124/Region: hypervariable region HV1
 F:130-144/Domain: transmembrane #status predicted <TM4>
 F:150-160/Domain: transmembrane #status predicted <TM5>
 F:161-209/Domain: extracellular #status predicted <EXT3>
 F:168-215/Region: hypervariable region HV2
 F:210-222/Domain: transmembrane #status predicted <TM6>
 F:226-234/Domain: transmembrane #status predicted <TM7>
 F:235-249/Domain: extracellular #status predicted <EXT4>
 F:250-258/Domain: transmembrane #status predicted <TM8>

Query Match 26.6%; Score 231; DB 1; Length 258;
 Best Local Similarity 26.5%; Pred. No. 3e-13;
 Matches 70; Conservative 26; Mismatches 70; Indels 80; Gaps 7;

QY 8 LIALPAAALAEAGSGFYVOADAHAKA-----KASSISGS-----AKG 45
 DB 14 LFSSAQAASDEGSRSPRYQADLVAERITHYPRFTGADKOKISTVSDYFNIRIR 73
 QY 46 EFSRISAGYRINDLRPAVDYTRYK-----NTRKAPSTDK-----L 80
 DB 74 IHRVSVGYDEGSMRIADYASVRKKNESNFTKVKTEIKDKTEHOGNGSFHAT 133
 QY 81 YSIGASVIYDFPTQSPVKPYFGARLSLR-----ASAHIGS----- 117
 DB 134 SLLGLSAIYDFPLNKKFRPYIGARAVAGHVRHQVSVETKTTVTSKPKGCTPAGGPYIK 193
 QY 118 -----DSFSKTSAGLGVLAVGSYAVTPNVLDAGRYRYNKGKVTVKNVRSGLISA 168
 DB 194 TDPKRPYHSHSISLIGVINGVGFDTITPRLTLDGTGRYHNGRLNTR-FRTHEASL 252

QY 169 GYRVKF 174
 DB 253 GMYRF 258

RESULT 13
 K0NH0
 opacity protein opac precursor - *Neisseria gonorrhoeae* (strain MS11) (fragments)
 N:Alternate names: opacity protein V0; triosephosphate dehydrogenase
 C:Species: *Neisseria gonorrhoeae*
 A:Variety: strain MS11
 C:Date: 31-Mar-1989 #sequence_revision 17-Oct-1997 #text_change 16-Jul-1999
 C:Accession: S16618; A24429; S36328; S28621
 R:Bhat, K.S.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsc
 Mol. Microbiol. 5, 1889-1901, 1991
 A:Title: The opacity proteins of *Neisseria gonorrhoeae* strain MS11 are encoded by a f
 A:Reference number: S16610; MUID:92114767

A:Accession: S16618
 A:Molecule type: DNA
 A:Residues: 1-260 <BNA>
 A:Cross-references: EMBL:X52370
 A:Experimental source: strain MS11, variant 4.8
 A>Note: the authors translated the codon CCA for residue 32 as Thr
 A>Note: expression of opacity proteins is regulated by the number of translated repeat
 of repeats place the start codon in frame with the rest of the protein
 R:Stern, A.; Brown, M.; Nickel, P.; Meyer, T.F.
 Cell 47, 61-71, 1986
 A:Title: Opacity genes in *Neisseria gonorrhoeae*: control of phase and antigenic variation
 A:Reference number: A90887; MUID:87002493
 A:Accession: A24429
 A:Molecule type: DNA
 A:Residues: 25-260 <STE>
 A>Note: this protein is synthesized as a precursor; however, the authors are uncertain
 of the exact position of the start codon
 R:Kupsch, E.M.; Krepper, B.; Kuroki, T.; Heuer, I.; Meyer, T.F.
 EMBO J. 12, 641-650, 1993
 A:Title: Variable opacity (Opa) outer membrane proteins account for the cell tropisms of
Neisseria gonorrhoeae
 A:Reference number: S36328; MUID:93178439
 A:Accession: S36328
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 25-260 <KUP>
 A:Cross-references: EMBL:Z18927; NID:949323; PIDN:CAA79360.1; PID:940789
 R:Meyer, T.F.
 submitted to the EMBL Data Library, November 1992
 A:Reference number: S28617
 A:Accession: S28617
 A:Molecule type: DNA
 A:Residues: 25-260 <MEY>
 A:Cross-references: EMBL:Z18927; NID:949323; PIDN:CAA79360.1; PID:940789
 C:Genetics:
 A:Gene: opaC
 C:Superfamily: opacity protein
 C:Keywords: cell surface component; transmembrane protein
 F:1-11,12-24/Domain: signal sequence (fragments) #status predicted <SIG>
 F:25-260/Product: opacity protein opaC #status predicted <MAT>
 F:35-43/Domain: transmembrane #status predicted <TM1>
 F:44-75/Domain: extracellular #status predicted <EXT1>
 F:52-61/Region: semivariable region
 F:76-84/Domain: transmembrane #status predicted <TM2>
 F:89-95/Domain: transmembrane #status predicted <TM3>
 F:96-134/Domain: extracellular #status predicted <EXT2>
 F:102-129/Region: hypervariable region HV1
 F:135-149/Domain: transmembrane #status predicted <TM4>
 F:155-165/Domain: transmembrane #status predicted <TM5>
 F:166-211/Domain: extracellular #status predicted <EXT3>
 F:171-217/Region: hypervariable region HV2
 F:212-224/Domain: transmembrane #status predicted <TM6>
 F:228-236/Domain: transmembrane #status predicted <TM7>
 F:237-251/Domain: extracellular #status predicted <EXT4>
 F:252-260/Domain: transmembrane #status predicted <TM8>

Query Match 26.6%; Score 231; DB 1; Length 260;
 Best Local Similarity 27.9%; Pred. No. 3e-13;
 Matches 70; Conservative 25; Mismatches 70; Indels 86; Gaps 7;

QY 6 AALIALPALAEAGSCFYQADAAHA-----KASSLSGASGFS----- 47
 DB 14 SLLFSSAQAASEDEGRPYQADLAAYEHITHDYPRPTDSKGIKTSVSDYFNINFT 73
 QY 48 -----PRISAGYRINDLEAVDYTRY-----KTKKAPSTD-- 77
 DB 74 HSTHPRVSVYDDEGGRRLADYARVKKMSDNKYSVSKNMRVHKNSNRKLNKTEQENG 133
 QY 78 --FKLYSIGASVYIDFTQSPVKKPYFGARLS----- 106
 DB 134 SFRAVSSLSGLSALYDFQINDKFKPYIGARVAGVHRSIDSTKTKITGLTTSTPGMSGV 193
 QY 107 ---LNRASAHLGSDSFSKTSAGLVAGVSTAATPNDLDAGYRYNKGKVVYKKNRS 163

DB 194 YKVLRTGGAH---RESSTIRVGLVAGVGFITPKLTIDAGRYHNMGRLENTFR-FRT 249
 QY 164 GEISAGVYRKF 174
 DB 250 HEASLGVYRKF 260

RESULT 14
 S72343
 Opa2343
 N:Alternate names: cell invasion protein opaH
 C:Species: *Neisseria gonorrhoeae*
 A:Variety: isolate 15063G
 C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 26-Aug-1999
 C:Accession: S72343
 R:Waldeser, L.S.; Ajlaka, R.S.; Metz, A.J.; Puaoli, D.; Lhn, L.; Thomas, M.; So, M.
 Mol. Microbiol. 13, 919-928, 1994
 A:Title: The opaH locus of *Neisseria gonorrhoeae* MS11A is involved in epithelial cell
 A:Reference number: S72343; MUID:95115561
 A:Accession: S72343
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-283 <WAL>
 A:Cross-references: EMBL:U13708; NID:9535357; PIDN:AA74082.1; PID:9535358
 A:Experimental source: isolate 15063G
 A>Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
 A>Note: expression of opacity proteins is regulated by the number of translated repeat
 of repeats place the start codon in frame with the rest of the protein
 C:Superfamily: opacity protein
 C:Keywords: cell surface component; transmembrane protein
 F:1-48/Domain: signal sequence #status predicted <SIG>
 F:49-283/Product: opacity protein opaH #status predicted <MAT>
 F:58-66/Domain: transmembrane #status predicted <TM1>
 F:67-88/Domain: extracellular #status predicted <EXT1>
 F:75-84/Region: semivariable region
 F:99-107/Domain: transmembrane #status predicted <TM2>
 F:112-118/Domain: transmembrane #status predicted <TM3>
 F:119-155/Domain: extracellular #status predicted <EXT2>
 F:125-150/Region: hypervariable region HV1
 F:156-170/Domain: transmembrane #status predicted <TM4>
 F:176-186/Domain: transmembrane #status predicted <TM5>
 F:187-234/Domain: extracellular #status predicted <EXT3>
 F:192-240/Region: hypervariable region HV2
 F:235-247/Domain: transmembrane #status predicted <TM6>
 F:251-259/Domain: transmembrane #status predicted <TM7>
 F:260-274/Domain: extracellular #status predicted <EXT4>
 F:275-283/Domain: transmembrane #status predicted <TM8>

Query Match 26.6%; Score 231; DB 2; Length 283;
 Best Local Similarity 28.2%; Pred. No. 3.3e-13;
 Matches 70; Conservative 25; Mismatches 65; Indels 88; Gaps 8;

QY 10 AALPALAEAGSCFYQADAAHA-----SSLSGASG-----FS 47
 DB 41 SLLSQAQAASEEMRPPYQADLAFAERITHDYDEPTGKTKITSTVSDYRNIRTHSVH 100
 QY 48 PRISAGYRINDLEAVDYTRYKNY-----TAPS-----TDRKLY 81
 DB 101 PRVSVYDDEGGRRLADYARVKKMNKNKYSVNIERVQEAHSNRIDLAENQENGTHAVS 160
 QY 82 SIGASVYIDFTQSPVKKPYFGARLSLNRASAHLGGS-DSFSKTS----- 124
 DB 161 SLGSAVYDFKLNDFKPYIGARV---AYGHVRSIDSTKTKITLISFYGVATKPTTY 216
 QY 125 -----AGLGVLAGVYATPNDLDAGRYRYNKGKVVYKKNRS 166
 DB 217 DIGPKTQAHOESNSIRVGLVAGVGFITPKLTIDAGRYHNMGRLENTFR-FKTHFA 275
 QY 167 SAGVYRKF 174
 DB 276 SLGMYRKF 283

RESULT 15

S16617

opacity protein opa1 precursor - Neisseria gonorrhoeae (strain MS11) (fragments)

N:Alternate names: outer membrane protein opa54

C:Species: Neisseria gonorrhoeae

A:Variety: strain MS11

C:Date: 13-Jan-1995 #sequence revision 17-Oct-1997 #text change 26-Aug-1999

C:Accession: S16617; S36332; S28618; S28622; S36333

R:Bhat, K.S.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehmig, F.; Stern, A.; Kupsch, M.L. Microbiol. 5, 1889-1901, 1991

A:Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a family of repeats place the start codon in frame with the rest of the protein

A:Reference number: S16610; MID:92114767

A:Accession: S16617

A:Molecule type: DNA

A:Residues: 1-282 <BHA>

A:Cross-references: EMBL:X52365

A:Experimental source: strain MS11, variant 4.8

A:Note: the authors did not translate the sequence for the signal peptide

A:Note: expression of opacity proteins is regulated by the number of translated repeat e

of repeats place the start codon in frame with the rest of the protein

R:Kupsch, E.M.; Knepper, B.; Kuroki, T.; Heuer, I.; Meyer, T.F.

EMBO J. 12, 641-650, 1993

A:Title: Variable opacity (Opa) outer membrane proteins account for the cell tropisms di

A:Reference number: S36328; MID:93178439

A:Accession: S36332

A:Molecule type: DNA

A:Residues: 39-248, 'N', 250-282 <KUP>

A:Cross-references: EMBL:Z18931; NID:g49327; PID:CAA79364.1; PID:g940793; EMBL:Z18932;

A:Experimental source: strain MS11, variant F3

A:Note: expression of opacity proteins is regulated by the number of translated repeat e

of repeats place the start codon in frame with the rest of the protein

C:Superfamily: opacity protein

C:Keywords: cell surface component; transmembrane protein

F:1-15,16-38/Domain: signal sequence (fragments) #status predicted <SIG>

F:39-282/Product: opacity protein opa1 #status predicted <MAT>

F:49-57/Domain: transmembrane #status predicted <TM1>

F:58-89/Domain: extracellular #status predicted <EXT1>

F:66-75/Region: semivariable region

F:90-98/Domain: transmembrane #status predicted <TM2>

F:103-109/Domain: transmembrane #status predicted <TM3>

F:110-155/Domain: extracellular #status predicted <EXT2>

F:133-150/Region: hypervariable region HV1

F:156-170/Domain: transmembrane #status predicted <TM4>

F:176-186/Domain: transmembrane #status predicted <TM5>

F:187-233/Domain: extracellular #status predicted <EXT3>

F:192-239/Region: hypervariable region HV2

F:234-246/Domain: transmembrane #status predicted <TM6>

F:250-258/Domain: transmembrane #status predicted <TM7>

F:259-273/Domain: extracellular #status predicted <EXT4>

F:274-282/Domain: transmembrane #status predicted <TM8>

Query Match

Best Local Similarity 26.3%; Score 228.5; DB 2; Length 282;

Matches 72; Conservative 25; Mismatches 67; Indels 91; Gaps 8;

OY 10 ALALPAALAEAG--ASGFYQADAAH-----KASSSLGSAK----- 44

DB 29 SLRPSAQAAGBEGNGRPYQADLAVAYETHDYPEPTGKTKKISTVSDYFRNIRTH 88

OY 45 GSPRISAGYRINDIRFVNDYTRK-----NYKAPST 76

DB 89 SIHPRSVGVDFGGRYADARYRKNNNNKYSVNIKELRNDNANGGNKHLNIRKRT 148

OY 77 DFK-----LYSIGASYTDFDQSPKPYEGARLSL----- 107

DB 149 EHRENGTTHAASSLGLNAVYDFDGSRKRYIGARVAAGHVRHQRVRSVQETIAVTTPQ 208

OY 108 NKASA-----HLGSDSFSKTSAGLGLAGVSYAVTPNVLDAGYRNYVGVKNTVK 159

DB 209 NAASVVTNAPIRKLPHHESRSISLGGAVAGVGDITPKLTLDAGYRHHMGRLENT 268

OY 160 NVKSGELSNAGVVKF 174

DB 269 -FKTHEASLGVRVRF 282

Search completed: October 28, 2002, 16:03:37
Job time : 13.4821 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 28, 2002, 15:55:44 ; Search time 6.98996 Seconds
(without alignments)
963.840 Million cell updates/sec

Title: US-09-684-883-8
Perfect score: 870
Sequence: 1 MKKALALALALPAAALAE.....VNTYKVRSGELSGVRVRF 174

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	233.5	26.8	237	1	OPAK_NEIGO	Q04880 neisseria g
2	233.5	26.8	270	1	OMPC_NEIGO	P09888 neisseria g
3	232	26.7	260	1	OPRL_NEIGO	P10170 neisseria m
4	226	26.0	233	1	OP67_NEIGO	O05034 neisseria g
5	225.5	25.9	234	1	OPAB_NEIGO	Q04874 neisseria g
6	225.5	25.9	237	1	OPAD_NEIGO	Q04882 neisseria g
7	225	25.9	234	1	OPAE_NEIGO	Q04878 neisseria g
8	225	25.9	236	1	OPAF_NEIGO	Q04879 neisseria g
9	225	25.9	236	1	OPAG_NEIGO	P11296 neisseria g
10	222	25.5	238	1	OPAH_NEIGO	Q04884 neisseria g
11	221	25.4	234	1	OP65_NEIGO	Q04885 neisseria g
12	220.5	25.3	243	1	OPAD_NEIGO	Q04883 neisseria g
13	220	25.3	244	1	OPAL_NEIGO	Q04877 neisseria g
14	219	25.2	234	1	OP28_NEIGO	P11297 neisseria g
15	219	25.2	238	1	OP66_NEIGO	O05033 neisseria g
16	210	24.1	178	1	YES7_HAEIN	O57201 haemophilus
17	209	24.0	238	1	OP68_NEIGO	Q04881 neisseria g
18	206.5	23.7	247	1	OPAG_NEIGO	Q04875 neisseria g
19	206	23.7	239	1	OPAE_NEIGO	Q04876 neisseria g
20	176.5	20.3	121	1	OPRA_HAEIN	P05088 haemophilus
21	125	14.1	170	1	OPR3_NEIMC	P10171 neisseria m
22	122.5	14.1	70	1	YA14_HAEIN	O57392 haemophilus
23	115	13.2	182	1	ATL_YERPS	O56957 yersinia ps
24	107	12.3	353	1	OM52_HAEIN	P38366 haemophilus
25	106	12.2	353	1	OM51_HAEIN	P38340 haemophilus
26	104	12.0	359	1	OM53_HAEIN	O44664 haemophilus
27	101	11.6	341	1	OM45_BRUBA	O44664 bruceella ab
28	98.5	11.3	349	1	OMPU_VIBCH	P57085 vibrio chol
29	95.5	11.0	312	1	OMPA_BUCOI	P57414 bruchera ap
30	93.5	10.7	350	1	OMPW_ECOLI	P21366 escherichia
31	93.5	10.7	350	1	OMPA_SALTY	P02938 salmonella
32	93	10.7	213	1	OM25_BRUSU	O45689 bruceella su
33	93	10.7	521	1	TSAS_RICHS	P37917 rickettsia

34	91	10.5	213	1	OM25_BRUME	O45321 bruceella me
35	87.5	10.1	240	1	OM31_BRUME	O45322 bruceella me
36	87	10.0	178	1	ATL_YEREN	P16454 yersinia me
37	87	10.0	201	1	OM25_BRUV	O45335 bruceella ov
38	87	10.0	213	1	OM25_BRUCA	O45110 bruceella ca
39	86.5	9.9	346	1	OMPA_ECOLI	P02934 escherichia
40	86.5	9.9	428	1	OM47_PASMU	P06003 pasteurella
41	85	9.8	213	1	OM25_BRUME	O45326 bruceella ne
42	85	9.8	351	1	OM32_COMAC	P24305 comamonas a
43	84	9.7	172	1	OMPX_ENTCL	P25253 enterobacte
44	81.5	9.4	995	1	Y109_YEAST	P40442 saccharomyc
45	81	9.3	350	1	PORF_PSEAE	P13794 pseudomonas

ALIGNMENTS

RESULT 1	OPAK_NEIGO	STANDARD;	PRT;	237 AA.
ID	OPAK_NEIGO			
AC	Q04880:			
DT	01-OCT-1993 (Rel. 27, Created)			
DT	01-OCT-1993 (Rel. 32, Last sequence update)			
DT	01-NOV-1995 (Rel. 32, Last annotation update)			
DE	Opacity protein OPA57 precursor (Fragment).			
GN	OPAK.			
OS	Neisseria gonorrhoeae.			
CC	Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.			
OX	NCBI_TaxID=485;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=MS11 / F3;			
RA	MEDLINE=93178439; PubMed=8440254;			
RX	Kusch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;			
RT	"Variable opacity (Opa) outer membrane proteins account for the cell			
RT	tropisms displayed by Neisseria gonorrhoeae for human leukocytes and			
RT	epithelial cells."			
RL	EMBO J. 12:641-650(1993).			
CC	-1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA			
CC	PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE			
CC	VARIATION.			
CC	-1- SUBCELLULAR LOCATION: Outer membrane.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL: Z18935; CAA79368.1; -			
DR	PIR: S28626; S28626.			
DR	InterPro: IPR003394; Opacity.			
DR	Pfam: PF02462; Opacity; 1.			
KW	Outer membrane; Multigene family; Signal.			
FT	NON_TER			
FT	SIGNAL			
FT	CHAIN			
FT	NON_TER			
SO	SEQUENCE			
Query Match	26.8%; Score 233.5; DB 1; Length 237;			
Best Local Similarity	28.9%; Pred. No. 3e-14;			
Matches	70; Conservative 22; Mismatches 61; Indels 89; Gaps 8;			
QY	17 ALAAGAGFVQDAHA-----KASSLSGS-----AKGSPRISAGY 54			
DB	1 ASDEGGGPTVQDLATAYEHITHDPEPTAPKNKISTVSDYFRNIRRSVHPRVSGY 60			
QY	55 RINDLRFAVDYTRYKNY-----KAPSTDFK-----LYSIGAS 86			
DB	61 DFGWMRIADYARYRRKNNKNSVSIKELLRNKGNGNRDLDKAEQNDGTFHAAVSLGSL 120			

```

QY 87 VIYDFDTQSPVRYKPGARLSINRASHLGS--DSFSEKTS----- 124
DB 121 AVYDFKLNDEKFKPYIGARY---AYGHVRSIDSTIKTTEVTTLHGPGITPPVYPGKPT 176
QY 125 -----AGLVLAGVSYAATPNVDLDAGYRNTYGVKYNVKNVSGELSGAGVRY 172
DB 177 QDAHRESDSIRRYGLGAVAGVGIDITPNTLDAGYRYHWGRLENNR-FKTHEASLGAVRY 235
QY 173 KF 174
DB 236 RF 237

RESULT 2
OMPC_NEIGO STANDARD; PRT; 270 AA.
ID OMPC_NEIGO
AC P09888;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE Outer membrane protein P. IIC precursor (Protein IIC).
GN P.IIC.
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=485;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-JS3;
RX MEDLINE=89096501; PubMed=3145386;
RA van der Ley P.;
RT "Three copies of a single protein II-encoding sequence in the genome
RT of Neisseria gonorrhoeae JS3: evidence for gene conversion and gene
RT duplication."
RL Mol. Microbiol. 2:797-806(1988).
CC -I- FUNCTION: THIS PROTEIN SERVES AS A PORIN.
CC -I- SUBUNIT: HOMOTRIMER.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
CC CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X12625; CA31144.1;
CC DR PIR: S03095; KONHZC.
CC DR InterPro: IPR003394; Opacity.
CC KW Outer membrane; Porin; Transmembrane; Antigen; Signal.
FT SIGNAL 1 25
FT CHAIN 26 270 OUTER MEMBRANE PROTEIN P. IIC.
FT TRANSMEM 36 44 POTENTIAL.
FT TRANSMEM 77 85 POTENTIAL.
FT TRANSMEM 90 96 POTENTIAL.
FT TRANSMEM 143 157 POTENTIAL.
FT TRANSMEM 163 173 POTENTIAL.
FT TRANSMEM 222 234 POTENTIAL.
FT TRANSMEM 238 246 POTENTIAL.
FT TRANSMEM 262 270 POTENTIAL.
SQ SEQUENCE 270 AA; 30269 MW; F6B448373830A50D CRC64;

Query Match 26.8%; Score 233.5; DB 1; Length 270;
Best Local Similarity 26.5%; Pred. No. 3.4e-14;
Matches 66; Conservative 29; Mismatches 71; Indels 89; Gaps 7;
QY 6 AALIALALPAALALAGASGVYQADAHAHA-----SSLSGSAK----- 44
DB 15 SSLFSSAARAAASDGGGPGYQADLAVAAERITHDYKPKTGCKNKISTVSDYFRNIRT 74
QY 45 -GSPRISAGYRINDLPAVDYTRYK-----NYAPS 75

```

```

DB 75 HSYHPRVSVGYDFGSMRIADYARYRKWNKNSYSIKELLRDNDSASVGHNLIOFQK 134
QY 76 TDFK-----LYSIGAVTYDFDTQSPVRYKPGARLSINRASHL----- 114
DB 135 TEHENGTFHVAVSSLGISTYDFDTQSPVRYKPGARLSINRASHL----- 194
QY 115 ---GSDSEFSK-----TSAGLVLAGVSYAATPNVDLDAGYRNTYGVKYNVKNVSGELSGAGVRY 157
DB 195 SNGGKAVSLSSKMPKSAHHOSNSIRRYGLGAVAGVGIDITPNTLDGTGRYHNMGRLEN 254
QY 158 VKNVSGELSGAGVRYKE 174
DB 255 TR-FKTHEASLGMYRYF 270

RESULT 3
OPRI_NEIMC STANDARD; PRT; 260 AA.
ID OPRI_NEIMC
AC P10170;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Opacity-related protein POPM1.
GN OPRI.
OS Neisseria meningitidis (serogroup C).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=135720;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C1938 / SEROGROUP C;
RX MEDLINE=88260884; PubMed=2455211;
RA Stern A., Meyer T.F.;
RT "Common mechanism controlling phase and antigenic variation in
RT pathogenic neisseriae."
RL Mol. Microbiol. 1:5-12(1987).
CC -I- SUBCELLULAR LOCATION: Outer membrane.
CC -I- SIMILARITY: STRONG TO THE OPACITY-RELATED PROTEIN POPM3 AND
CC REGIONS OF HOMOLOGY WITH N.GONORRHOEA (STRAIN MS11) OPA GENE
CC PRODUCTS.
CC CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X06445; CA829748.1; ALT_SEQ.
CC DR PIR: S08514; S08514.
CC DR InterPro: IPR003394; Opacity.
CC KW Outer membrane.
SQ SEQUENCE 260 AA; 28936 MW; EB47A2843BF037B CRC64;

Query Match 26.7%; Score 232; DB 1; Length 260;
Best Local Similarity 27.6%; Pred. No. 4.5e-14;
Matches 71; Conservative 31; Mismatches 69; Indels 86; Gaps 8;
QY 3 KALAIALIALALPAALALAGASGVYQADAHAHA-----KASSLSG 41
DB 5 KTFSSLLFSSLLFSSAAQAASDGSRSPPYQADLAVAAERITHNYPPPTGADDKSTIV 64
QY 42 S-----AKGSPRISAGYRINDLPAVDYTRYK-----NYKAPST 76
DB 65 SDYFRIRARHSHIPKVSQYDGGRIADYASYSKKMESNSTKTYTEIKDKNKTKKT 124
QY 77 DFK-----LYSIGAVTYDFDTQSPVRYKPGARLSINR-----ASGHL 114
DB 125 EHQQNGSFHATSLGISAIDYDKLNDKFKPYIGAVAAVGHVHQVSEYETRTTYTSRKP 184
QY 115 GGS-----DSFSEKTSAGLVLAGVSYAATPNVDLDAGYRNTYGVKYNV 157

```

Db 185 GGTACGAGVATKTDSPYHSHSISLGLGVIAGVGFDITPKLTLDGTGRHYHNGRLN 244
 QY 158 VKNVRSGLSAGVRKF 174
 Db 245 TR-FKTHASLGVRKF 260

RESULT 4

OP67_NEIGO
 ID OP67_NEIGO STANDARD: PRT: 233 AA.
 AC 005034;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Opacity protein OPA67 precursor (Fragment).
 OS Neisseria gonorrhoeae.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_TaxID=485;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VPI;
 RA MEDLINE=93178439; PubMed=8440254;
 RT Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
 RT "Variable opacity (Opa) outer membrane proteins account for the cell
 tropisms displayed by Neisseria gonorrhoeae for human leukocytes and
 epithelial cells.";
 RT EMBO J. 12:641-650(1993).
 CC -!- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
 CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
 CC VARIATION.
 CC -!- SUBCELLULAR LOCATION: Outer membrane.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sdb.ch/announce/>
 CC or send an email to license@isb-sdb.ch).
 CC
 DR EMBL: Z18942; CAA79375.1;
 DR PIR: S28625; S28625.
 DR InterPro: IPR003394; Opacity.
 DR Pfam: PF02462; Opacity; 1.
 KW Outer membrane; Multigene family; Signal.
 FT NON_TER 1 1
 FT SIGNAL <1 1
 FT CHAIN 2 >233 POTENTIAL.
 FT NON_TER 233 233 OPACITY PROTEIN OPA67.
 SQ SEQUENCE 233 AA; 26039 MW; 6C13AA6AB163C67F CRC64;

Query Match 26.0%; Score 226; DB 1; Length 233;
 Best Local Similarity 27.8%; Pred. No. 1.4e-13;
 Matches 66; Conservative 27; Mismatches 58; Indels 86; Gaps 8;

QY 19 AEG-ASGFYVQADAHA-----KASSISGSAGF-----SPRISAGY 54
 Db 2 SEGNGRGYVQADLAAYEAHITHDYPQGTGKKNKISTVSDYFNIRTHSHRVSAGYD 61
 QY 55 RINDLRANDYTRYK--NYKASTDFK-----LYSIGASVY 89
 Db 62 DFGWMLADYARVYKMDNKSVDIKELKNKONKRDJKTENQENGTFHVAVSSLSGASVY 121
 QY 93 TOSPYKPYFGARLSLNRASAHLGGS-DSFKTS-----LVSIGASVY 174
 Db 122 DFKLNGKFKPYIGARV---AYGHVRHSIDSTYKTTFTFLSSISGGLNLPYTYTEENQMAH 177
 QY 125 -----AGLGVLAGSVYAVTPVNDLDAGYRYNYGVKNTVKNVRSGLSAGVRKF 174
 Db 178 ESNISIRRVGLGIAGVGFDITPKLTLDGTGRHYHNGRLNTR-FKTHASLGVRKF 233

RESULT 5

OPAB_NEIGO
 ID OPAB_NEIGO STANDARD: PRT: 234 AA.
 AC 004874;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Opacity protein OPA51 precursor (Fragment).
 OS Neisseria gonorrhoeae.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_TaxID=485;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MS11 / F3;
 RA MEDLINE=93178439; PubMed=8440254;
 RT Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
 RT "Variable opacity (Opa) outer membrane proteins account for the cell
 tropisms displayed by Neisseria gonorrhoeae for human leukocytes and
 epithelial cells.";
 RT EMBO J. 12:641-650(1993).
 CC -!- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
 CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
 CC VARIATION.
 CC -!- SUBCELLULAR LOCATION: Outer membrane.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sdb.ch/announce/>
 CC or send an email to license@isb-sdb.ch).
 CC
 DR EMBL: Z18928; CAA79361.1;
 DR PIR: S28628; S28628.
 DR InterPro: IPR003394; Opacity.
 DR Pfam: PF02462; Opacity; 1.
 KW Outer membrane; Multigene family; Signal.
 FT NON_TER 1 1
 FT SIGNAL <1 1
 FT CHAIN 2 >234 POTENTIAL.
 FT NON_TER 234 234 OPACITY PROTEIN OPA51.
 SQ SEQUENCE 234 AA; 26772 MW; 9FE5B5DABBA96CA CRC64;

Query Match 25.9%; Score 225.5; DB 1; Length 234;
 Best Local Similarity 29.0%; Pred. No. 1.0e-13;
 Matches 69; Conservative 22; Mismatches 60; Indels 87; Gaps 9;

QY 19 AEG-ASGFYVQADAHA-----KASSISGSAGF-----GSPRISAGY 55
 Db 2 SEGNGRGYVQADLAAYEAHITHDYPQGTGKKNKISTVSDYFNIRTHSHRVSAGYD 61
 QY 56 INDLRFANDYTRYK--NYKASTDFK-----LYSIGASVY 89
 Db 62 DFGWMLADYARVYKMDNKSVDIKELKNKONKRDJKTENQENGTFHVAVSSLSGASVY 121
 QY 90 DEDTOSPYKPYFGARLSLNRASAHLGGS-DSFKTS-----LVSIGASVY 174
 Db 122 DFKLNGKFKPYIGARV---AYGHVRHSIDSTYKTTFTFLSSISGGLNLPYTYTEENQMAH 177
 QY 125 -----AGLGVLAGSVYAVTPVNDLDAGYRYNYGVKNTVKNVRSGLSAGVRKF 174
 Db 178 HOSNSIRRVGLGIAGVGFDITPKLTLDGTGRHYHNGRLNTR-FKTHASLGVRKF 234

RESULT 6

OPAL_NEIGO
 ID OPAL_NEIGO STANDARD: PRT: 237 AA.
 AC 004882;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)

DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Opacity protein OPA58 precursor (Fragment).
 GN OPA58
 OS Neisseria gonorrhoeae.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_TaxID=485;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MS11 / F3;
 RX MEDLINE=93178439; PubMed=8440254;
 RA Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
 RT "Variable opacity (Opa) outer membrane proteins account for the cell
 tropisms displayed by Neisseria gonorrhoeae for human leukocytes and
 epithelial cells."
 RL EMBO J. 12:641-650(1993).
 CC CC
 CC -1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
 CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
 CC VARIATION.
 CC -1- SUBCELLULAR LOCATION: Outer membrane.
 CC CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; Z18937; CAA79370.1; -
 DR PIR; S28624; S28624.
 DR InterPro; IPR003394; Opacity.
 DR Pfam; PF02462; Opacity; 1.
 KW Outer membrane; Multigene family; Signal.
 FT NON_TER 1 1
 FT SIGNAL <1 1 POTENTIAL.
 FT CHAIN 2 >237 OPACITY PROTEIN OPA58.
 FT NON_TER 237 237
 SQ SEQUENCE 237 AA; 26855 MW; B165033B2C8D6A53 CRC64;
 Query Match 25.9%; Score 225.5; DB 1; Length 237;
 Best Local Similarity 28.9%; Pred. No. 1.6e-13;
 Matches 68; Conservative 21; Mismatches 57; Indels 89; Gaps 8;
 QY 24 GRYVQADLAHA-----KASSSLGSAK-----PRISAGYRINDLRF 61
 DB 8 GRYVQADLAHAHEITHDYPEQTPSKGLISTVSDYFRNIRTHSHIPRVSVGYDFGGMRI 67
 QY 62 AVDYTRYK-----KAPSTDFK-----LYSGASVIYDFDT 93
 DB 68 AADYARRKMNKNKYSVSIKELLNKNYNGMKTDRKTENQENGTFHVAVSSGLSAVYDFKL 127
 QY 94 QSPKPFEGARLSNRSASHLGGS-DSFSKTS-----124
 DB 128 NDKRPYIGARV-----AYGVRHSIDSTKTKTETITLHGPGTTPPYVPEKNTQDAHRES 183
 QY 125 -----AGLGVLAGSVAVTPNDLDAGRYNYGVKNVKNVSGELSAGYRYKF 174
 DB 184 DSIRRVGAGVAVGIDITPMLTLDAGRYHYWGLNTR-FKTHASLGYRYKF 237
 RESULT 7
 OPAE_NEIGO STANDARD; PRT; 234 AA.
 ID OPAE_NEIGO
 AC Q04878;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Opacity protein OPA55 precursor (Fragment).
 GN OPAE.
 OS Neisseria gonorrhoeae.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_TaxID=485;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=MS11 / F3;
 RX MEDLINE=93178439; PubMed=8440254;
 RA Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
 RT "Variable opacity (Opa) outer membrane proteins account for the cell
 tropisms displayed by Neisseria gonorrhoeae for human leukocytes and
 epithelial cells."
 RL EMBO J. 12:641-650(1993).
 CC CC
 CC -1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
 CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
 CC VARIATION.
 CC -1- SUBCELLULAR LOCATION: Outer membrane.
 CC CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; Z18933; CAA79366.1; -
 DR PIR; S28632; S28632.
 DR InterPro; IPR003394; Opacity.
 DR Pfam; PF02462; Opacity; 1.
 KW Outer membrane; Multigene family; Signal.
 FT NON_TER 1 1
 FT SIGNAL <1 1 POTENTIAL.
 FT CHAIN 2 >234 OPACITY PROTEIN OPA55.
 FT NON_TER 234 234
 SQ SEQUENCE 234 AA; 26881 MW; 8EBB30B3A774C766 CRC64;
 Query Match 25.9%; Score 225; DB 1; Length 234;
 Best Local Similarity 28.9%; Pred. No. 1.7e-13;
 Matches 67; Conservative 21; Mismatches 58; Indels 86; Gaps 8;
 QY 24 GRYVQADLAHA-----KASSSLGSAK-----GFSPRISAGYRINDLRF 61
 DB 8 GRYVQADLAHAHEITHDYPEQTPSKGLISTVSDYFRNIRTHSHIPRVSVGYDFGGMRI 67
 QY 62 AVDYTRYK-----KAPSTDFK-----LYSGASVIYDFDT 95
 DB 68 AADYARRKMNKNKYSVSIKELLNKNYNGMKTDRKTENQENGTFHVAVSSGLSAVYDFKL 127
 QY 96 PVKPFEGARLSNRSASHLGGS-DSFSKTS-----124
 DB 128 KRPYIGARV-----AYGVRHSIDSTKTKTETITLHGPGTTPPYVPEKNTQDAHRES 183
 QY 125 -----AGLGVLAGSVAVTPNDLDAGRYNYGVKNVKNVSGELSAGYRYKF 174
 DB 184 RNVGLGVLAGVGFDTIPKLLDTGIRHYWGLNTR-FKTHASLGYRYKF 234
 RESULT 8
 OPAE_NEIGO STANDARD; PRT; 234 AA.
 ID OPAE_NEIGO
 AC Q04879;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Opacity protein OPA56 precursor (Fragment).
 GN OPAE.
 OS Neisseria gonorrhoeae.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_TaxID=485;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MS11 / F3;
 RX MEDLINE=93178439; PubMed=8440254;
 RA Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
 RT "Variable opacity (Opa) outer membrane proteins account for the cell
 tropisms displayed by Neisseria gonorrhoeae for human leukocytes and
 epithelial cells."
 RL EMBO J. 12:641-650(1993).
 CC CC
 CC -1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
 CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
 CC VARIATION.
 CC -1- SUBCELLULAR LOCATION: Outer membrane.
 CC CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; Z18933; CAA79366.1; -
 DR PIR; S28632; S28632.
 DR InterPro; IPR003394; Opacity.
 DR Pfam; PF02462; Opacity; 1.
 KW Outer membrane; Multigene family; Signal.
 FT NON_TER 1 1
 FT SIGNAL <1 1 POTENTIAL.
 FT CHAIN 2 >234 OPACITY PROTEIN OPA55.
 FT NON_TER 234 234
 SQ SEQUENCE 234 AA; 26881 MW; 8EBB30B3A774C766 CRC64;

```

RL EMO J. 12:641-650(1993).
CC -1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
CC VARIATION.
CC -1- SUBCELLULAR LOCATION: Outer membrane.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL, Z18934; CAA79367.1; -.
DR PIR, S28620; S28620.
DR InterPro: IPR003394; Opacity.
DR Pfam: PF02462; Opacity: 1.
DR Outer membrane; Multigene family; Signal.
FT SIGNAL 1 1
FT NON_TER 1 1
FT CHAIN 2 >234 POTENTIAL.
FT NON_TER 234 234 OPACITY PROTEIN OPA56.
SQ SEQUENCE 234 AA; 26868 MW; 5175C6606839EFB CRC64;

Query Match 25.9%; Score 225; DB 1; Length 234;
Best Local Similarity 28.4%; Pred. No. 1.7e-13;
Matches 66; Conservative 22; Mismatches 58; Indels 86; Gaps 8;

QY 24 GFVYQADAAHA-----KASSSLGSAK-----GFSPRISAGYRINDLR 61
DB 8 GPFYQADAAVAHEITHDPEQGTGKDKISTVSDYFRNRTSHIPRSVSGTDFGGMH 67
QY 62 AVDTYRKNTKAP--STDFK-----LYSIGAVYDEDTOS 95
DB 68 AADYARRKNDKYSYDIKELENKQNKRDLEKQENGTFFAVSSLSGSAVYDKLMD 127
QY 96 PVPYFGARSLNRASHAGGS--DSFSKTS----- 124
DB 128 KRPYIGARV---AYGHVHSHIDSTKTKYKFLTSSYGGINPTVTEONTNAAHQSNSI 183
QY 125 --AGLIVAGSYAVTPNDLDAGYRNYGKNTVKNVRSGLSAGVYKF 174
DB 184 RRVGLGVIAGVGFDTIPKLTLDGGRYHMGRLNTR-EKTHASLGAVYRF 234

RESULT 9
OPAC_NEIGO STANDARD; PRT; 236 AA.
AC P11296;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Opacity protein OPA50 precursor (OPA50) (V0) (Fragment).
GN OPAC.
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=485;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=MS11 / V0; PubMed=3093085;
RX MEDLINE=87002493; PubMed=3093085;
RA Stern A., Brown M., Nickel P., Meyer T.F.;
RT "Opacity genes in Neisseria gonorrhoeae: control of phase and
RT antigenic variation.";
RL Cell 47:61-71(1986).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MS11 / F3;
RX MEDLINE=93178439; PubMed=8440254;
RA Kusch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
RT "Variable opacity (Opa) outer membrane proteins account for the cell
RT tropisms displayed by Neisseria gonorrhoeae for human leukocytes and
```

```

RT epithelial cells.";
RL EMO J. 12:641-650(1993).
CC -1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
CC VARIATION.
CC -1- SUBCELLULAR LOCATION: Outer membrane.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL, M14746; -; NOT_ANNOTATED_CDS.
DR PIR, A24429; KONH0.
DR PIR, S28621; S28621.
DR PIR, S36328; S36328.
DR InterPro: IPR003394; Opacity.
DR Pfam: PF02462; Opacity: 1.
DR Outer membrane; Multigene family; Signal.
FT SIGNAL 1 1
FT NON_TER 1 1
FT CHAIN 2 >236 POTENTIAL.
FT NON_TER 236 236 OPACITY PROTEIN OPA50.
SQ SEQUENCE 236 AA; 26685 MW; 68DC237692183398 CRC64;

Query Match 25.9%; Score 225; DB 1; Length 236;
Best Local Similarity 28.3%; Pred. No. 1.7e-13;
Matches 68; Conservative 21; Mismatches 65; Indels 86; Gaps 7;

QY 17 ALAEGASGFYQADAAHA-----KASSSLGSAAGFS-----PRISAGY 54
DB 1 ASEDGGRGPFYQADAAVAHEITHDYPKPTDPSKGIKISTVSDYFRNRTSHIPRSVSGY 60
QY 55 RINDRFAVDYTRY-----KNKAPSTD-----FKLISGAS 86
DB 61 DCGGRIRIADYARVKKMSDNKYSVSIKMRVYKHNKSNKLNKTEQNGSFHAAVSLGLS 120
QY 87 VIYDEDTOSPVKPYFGARLS-----LNRAASHL 114
DB 121 AIVDFQINDKRPYIGARVAGVHSHIDSTKTKITGLTSTPGIMSGYVVLTPPAH- 179
QY 115 GGSDFSEKTSAGLIVAGSYAVTPNDLDAGYRNYGKNTVKNVRSGLSAGVYKF 174
DB 180 --RESDSIRRVGLGVIAGVGFDTIPKLTLDGGRYHMGRLNTR-EKTHASLGAVYRF 236

RESULT 10
OPAH_NEIGO STANDARD; PRT; 238 AA.
AC O04884;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Opacity protein OPA60 precursor (Fragment).
GN OPAH.
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=485;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MS11 / F3;
RX MEDLINE=93178439; PubMed=8440254;
RA Kusch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
RT "Variable opacity (Opa) outer membrane proteins account for the cell
RT tropisms displayed by Neisseria gonorrhoeae for human leukocytes and
RT EMO J. 12:641-650(1993).
RN [2]
RP SEQUENCE FROM N.A.
```

RC STRAIN-MS11 / V18;
 RX MEDLINE=92114767; PubMed=1815562;
 RA Bat K.S., Gibbs C.P., Barrera O., Morrison S.G., Jaehnis F.,
 RA Stern A., Kupsch E.-M., Meyer T.F., Swanson J.;
 RT "The opacity proteins of *Neisseria gonorrhoeae* strain MS11 are
 RT encoded by a family of 11 complete genes.";
 RL Mol. Microbiol. 5:1889-1901(1991).
 RN [1].
 RP ERRATUM.
 RX MEDLINE=92261333; PubMed=1584024;
 RA Bat K.S., Gibbs C.P., Barrera O., Morrison S.G., Jaehnis F.,
 RA Stern S., Kupsch E.-M., Meyer T.F., Swanson J.;
 RL Mol. Microbiol. 6:1073-1076(1992).
 CC -1- FUNCTION: ARE IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
 CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
 CC VARIATION.
 CC -1- SUBCELLULAR LOCATION: Outer membrane.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: Z18939; CAA79372.1; -;
 DR EMBL: X60711; CAA43121.1; -;
 DR PIR: S28631; S28631.
 DR InterPro: IPR003394; Opacity.
 DR Pfam: PF02462; Opacity; 1.
 KW Outer membrane; Multigene family; Signal.
 FT NON_TER 1
 FT SIGNAL <1 1 POTENTIAL.
 FT CHAIN 2 >238 OPACITY PROTEIN OPA60.
 FT VARIANT 2 234 SED -> MLKA (IN MS11 / V18).
 FT VARIANT 234 234 V -> M (IN MS11 / V18).
 FT NON_TER 238
 SQ SEQUENCE 238 AA; 27073 MW; 883A3560C2DF1B9F CRC64;
 Query Match 25.5%; Score 222; DB 1; Length 238;
 Best Local Similarity 28.0%; Pred. No. 3.3e-13;
 Matches 68; Conservative 22; Mismatches 63; Indels 90; Gaps 7;
 QY 17 ALAEGASGVYQADAAHA-----KASSSLGS-----AKGSEPRISAGY 54
 DB 1 ASEGGRRPPYQADLAAYEHITHDYEPPTAPKNKISTVSDYFRNIRTSVHPRVSGY 60
 QY 55 RINDLRFAVDYTRYKNY-----KAPSDFKLYSGAS 86
 DB 61 DFGGRRIRADYARFKRNKNRYSVNIENVRIRKNGIRIDRKTENQNGTFHVAVSLGLS 120
 QY 87 VIYDFDTQSPYKPYFGARLSNRASAHLGSG-DSFSKT-----123
 DB 121 AIYDPQINDKRPYIGANV-----AYGHRHSIDSTKTKTIEVTTPSNAPNCAVTTYNDP 176
 QY 124 -----SAGLVLAGVSYAVTPNVDLAGYRNYGVKNTVKNVRSGLSAGVR 171
 DB 177 KTQNDYQNSIRVGLGIYAGVGEDITPKLTLDAGYRHYHNGRLENTNR-FETHBASLGVR 235
 QY 172 VKF 174
 DB 236 YRF 238
 RESULT 11
 OP65_NEIGO STANDARD; PRT; 234 AA.
 AC Q04885;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Opacity protein OPA65 precursor (Fragment).

OS *Neisseria gonorrhoeae*.
 CC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; *Neisseria*.
 OX NCBI_TaxID=485;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN-VPI;
 RX MEDLINE=93178439; PubMed=8440254;
 RA Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
 RT "Variable opacity (Opa) outer membrane proteins account for the cell
 RT tropisms displayed by *Neisseria gonorrhoeae* for human leukocytes and
 RT epithelial cells";
 RL EMBD J. 12:641-650(1993).
 CC -1- FUNCTION: ARE IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
 CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
 CC VARIATION.
 CC -1- SUBCELLULAR LOCATION: Outer membrane.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: Z18940; CAA79373.1; -;
 DR PIR: S28617; S28617.
 DR InterPro: IPR003394; Opacity.
 DR Pfam: PF02462; Opacity; 1.
 KW Outer membrane; Multigene family; Signal.
 FT NON_TER 1
 FT SIGNAL <1 1 POTENTIAL.
 FT CHAIN 2 >234 OPACITY PROTEIN OPA65.
 FT NON_TER 234
 SQ SEQUENCE 234 AA; 26242 MW; D66A0BA6424C2F1 CRC64;
 Query Match 25.4%; Score 221; DB 1; Length 234;
 Best Local Similarity 28.1%; Pred. No. 4e-13;
 Matches 64; Conservative 21; Mismatches 65; Indels 78; Gaps 7;
 QY 24 GRYVQADAAHA-----KASSSLGS-----AKGSPRISAGYRINDLR 61
 DB 8 GRYVQADLAAYAEIRITHDYEPPTGAKKQLSVSDYFRNIRTSVHPRVSGYDFGGR 67
 QY 62 ANDYTRYK-----NKAPSTDK-----LSTGASVYDFDTQSP 96
 DB 68 AADYARFRKWKESNSSIKKVTEDIKDNYKETKTEHQENGFHVAVSLGLSTIYDFQISDK 127
 QY 97 VKPYFGARLSNRASAHL-----GG-----SDSFKTSAG 126
 DB 128 IKYIGVRYGVGHVHQVSVGCEITTYTPKRNKTQSGPVPKSTPIAYHENSRLG 187
 QY 127 LGVLAVSYAVTPNVDLAGYRNYGVKNTVKNVRSGLSAGVRKF 174
 DB 188 FGAMAGVGIDVAPGLTLDAGYRHYHNGRLENTNR-FETHBASLGVR 234
 RESULT 12
 OPAD_NEIGO STANDARD; PRT; 243 AA.
 AC Q04883;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Opacity protein OPA59 precursor (Fragment).
 GN OPAD.
 OS *Neisseria gonorrhoeae*.
 CC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; *Neisseria*.
 OX NCBI_TaxID=485;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN-MS11 / F3;
 RX MEDLINE=93178439; PubMed=8440254;

RA Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
 CT "Variable opacity (Opa) outer membrane proteins account for the cell
 RT tropisms displayed by Neisseria gonorrhoeae for human leukocytes and
 RL epithelial cells."
 CC EMBL J. 12:641-650(1993).
 CC -1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
 CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
 CC VARIATION.
 CC -1- SUBCELLULAR LOCATION: Outer membrane.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: Z18938; CAA79371.1; -
 CC PIR: S28629; S28629.
 CC InterPro: IPR003394; Opacity.
 CC Pfam: PF02462; Opacity; 1.
 CC Outer membrane; Multigene family; Signal.
 CC NON_TER 1
 CC SIGNAL <1 1 POTENTIAL.
 CC CHAIN 2 >243 OPACITY PROTEIN OPA59.
 CC NON_TER 243 243
 CC SEQUENCE 243 AA; 27414 MW; 5930C73917436041 CRC64;
 SO
 Query Match 25.3%; Score 220.5; DB 1; Length 243;
 Best Local Similarity 28.3%; Pred. No. 4,6e-13;
 Matches 67; Conservative 23; Mismatches 60; Indels 87; Gaps 7;
 QY 24 GFYQADLAHNA-----KASSLSGSAK-----GSPRISAGYRINDLR 61
 DB 8 GFYQADLAHNAVEHITHDYPEPTGKDKISTVSDYRNIRTHSIHPRVSGYDFGWMRI 67
 QY 62 AVDYTRYK-----NYKAPSTDFK-----LYSIGASV 87
 DB 68 AADYARAKRMNNKYSVNIKELRLNDNANGSGSHNITKRTKEHRENGTFHAASSLGSLA 127
 QY 88 YVDFTQSPVKPYFGARLSL-----NRASA-----HLGGS 117
 DB 128 YVDFTQSPVKPYFGARLSL-----NRASA-----HLGGS 117
 QY 118 DSFSKTSAGLGAGSYAVTPNVDLDAGRYNYGKNTVKNVNSGELSGAVRYKF 174
 DB 188 HESRSISLGFAGVAGVGDITPNTLDAGRYHNMGRLENTF-KTHASLGVRYRF 243
 RESULT 13
 OP28_NEIGO STANDARD; PRT; 244 AA.
 AC 004877;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Opacity protein OPA54 precursor (Fragment).
 GN OPA1.
 OS Neisseria gonorrhoeae.
 CC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 CC NCBI_TaxID=485;
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=MS11 / F3;
 RX MEDLINE=93178439; PubMed=8440254.
 RA Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
 RT "Variable opacity (Opa) outer membrane proteins account for the cell
 RT tropisms displayed by Neisseria gonorrhoeae for human leukocytes and
 RT epithelial cells."
 RL EMBL J. 12:641-650(1993).
 CC -1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
 CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE

CC VARIATION.
 CC -1- SUBCELLULAR LOCATION: Outer membrane.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: Z18931; CAA79364.1; -
 CC PIR: S28622; S28622.
 CC PIR: S28618; S28618.
 CC PIR: S36332; S36332.
 CC InterPro: IPR003394; Opacity.
 CC Pfam: PF02462; Opacity; 1.
 CC Outer membrane; Multigene family; Signal.
 CC NON_TER 1
 CC SIGNAL <1 1 POTENTIAL.
 CC CHAIN 2 >244 OPACITY PROTEIN OPA54.
 CC NON_TER 244 244
 CC SEQUENCE 244 AA; 27488 MW; 968AB8603D961DD8 CRC64;
 SO
 Query Match 25.3%; Score 220; DB 1; Length 244;
 Best Local Similarity 28.2%; Pred. No. 5,2e-13;
 Matches 67; Conservative 23; Mismatches 60; Indels 88; Gaps 7;
 QY 24 GFYQADLAHNA-----KASSLSGSAK-----GSPRISAGYRINDLR 61
 DB 8 GFYQADLAHNAVEHITHDYPEPTGKDKISTVSDYRNIRTHSIHPRVSGYDFGWMRI 67
 QY 62 AVDYTRYK-----NYKAPSTDFK-----LYSIGASV 86
 DB 68 AADYARAKRMNNKYSVNIKELRLNDNANGSGSHNITKRTKEHRENGTFHAASSLGSLA 127
 QY 87 YVDFTQSPVKPYFGARLSL-----NRASA-----HLGGS 116
 DB 128 YVDFTQSPVKPYFGARLSL-----NRASA-----HLGGS 116
 QY 117 DSFSKTSAGLGAGSYAVTPNVDLDAGRYNYGKNTVKNVNSGELSGAVRYKF 174
 DB 188 HESRSISLGFAGVAGVGDITPNTLDAGRYHNMGRLENTF-KTHASLGVRYRF 244
 RESULT 14
 OP28_NEIGO STANDARD; PRT; 234 AA.
 AC P11297;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Opacity protein V28 precursor (Fragment).
 OS Neisseria gonorrhoeae.
 CC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 CC NCBI_TaxID=485;
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87002493; PubMed=3093085;
 RA Stern A., Brown M., Nickel P., Meyer T.F.;
 RT "Opacity genes in Neisseria gonorrhoeae: control of phase and
 RT antigenic variation."
 RL Cell 47:61-71(1986).
 CC -1- FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
 CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
 CC VARIATION.
 CC -1- SUBCELLULAR LOCATION: Outer membrane.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

DR EMBL; M14747; -; NOT_ANNOTATED_CDS.
 DR PIR; B24429; K0N8.
 DR InterPro: IPR003394; Opacity.
 DR Pfam; PF02462; Opacity; 1.
 KW Outer membrane; Multigene family; Signal.
 FT NON_TER 1 1
 FT SIGNAL <1 1 POTENTIAL.
 FT CHAIN 2 >234 OPACITY PROTEIN V28.
 FT NON_TER 234 234
 SQ SEQUENCE 234 AA; 26770 MW; 339AEB09C2FE75E4 CRC64;

Query Match 25.2%; Score 219; DB 1; Length 234;
 Best Local Similarity 28.9%; Pred. No. 6.1e-13;
 Matches 67; Conservative 21; Mismatches 38; Indels 86; Gaps 8;

QY 24 GFYVQADAAHA-----KASSISGSAAK-----GFSRISAGYRINDLRF 61
 DB 8 GPVQADLAAYAEHTHDYPRPTDPSKGLSTVSDYFRNIRTHSIHPRVSGYDFGGMRI 67
 QY 62 AVDYTRK--NYKAPSTDFK-----LYSIGAVIYDFDTQS 95
 DB 68 AADYARIRKNDKSYSDIKELNKNQNRDLKTENQENGTFHAVSLGLSAVYDFKIND 127
 QY 96 PVPKPYFGARLSLRASAHLGGS--DSFSKTS----- 124
 DB 128 KFKPYIGARV---AYGHVHSHIDSTKKTTEFLTAGARGTDPVSSPKNTODAHQE 183
 QY 125 --AGLGLAGVSYAVTPNVLDAGYRNYGKNTVKNVRSGLSAGVRYKF 174
 DB 184 RRYGLGLAGVAGVDFITPNTLDAGYRHYHNMGRLENTR-FKTHBASLGVRIRF 234

RESULT 15
 OP66_NEIGO STANDARD; PRT; 238 AA.
 ID 005033;
 AC 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Opacity protein OPA66 precursor (Fragment).
 OS Neisseria gonorrhoeae.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_TaxID:485;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VPI;
 RC MEDLINE=93178439; PubMed=8440254;
 RA Kupsch E.-M., Knepper B., Kuroki T., Heuer I., Meyer T.F.;
 RT "Variable opacity (Opa) outer membrane proteins account for the cell
 RT tropisms displayed by Neisseria gonorrhoeae for human leukocytes and
 RT epithelial cells.";
 RL EMBO J. 12:641-650(1993).
 CC - FUNCTION: IMPLICATED IN A NUMBER OF ADHERENCE FUNCTIONS. OPA
 CC PROTEINS ARE IMPLICATED IN PATHOGENESIS AND ARE SUBJECT TO PHASE
 CC VARIATION.
 CC - SUBCELLULAR LOCATION: Outer membrane.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

DR EMBL; Z18941; CAA79374.1; -.
 DR PIR; S28619; S28619.
 DR InterPro: IPR003394; Opacity.
 DR Pfam; PF02462; Opacity; 1.

KW Outer membrane; Multigene family; Signal.
 FT NON_TER 1 1
 FT SIGNAL <1 1 POTENTIAL.
 FT CHAIN 2 >238 OPACITY PROTEIN OPA66.
 FT NON_TER 238 238
 SQ SEQUENCE 238 AA; 26888 MW; B6E38AF1585263AA CRC64;

Query Match 25.2%; Score 219; DB 1; Length 238;
 Best Local Similarity 28.0%; Pred. No. 6.2e-13;
 Matches 66; Conservative 23; Mismatches 57; Indels 90; Gaps 8;

QY 24 GFYVQADAAHA-----KASSISGSAAK-----SPRISAGYRINDLRF 61
 DB 8 GPVQADLAAYAEHTHDYPRPTDPSKGLSTVSDYFRNIRTHSIHPRVSGYDFGGMRI 67
 QY 62 AVDYTRK--NYKAPSTDFK-----LYSIGAVIYDFDTQS 93
 DB 68 AADYARIRKNDKSYSDIKELNKNQNRDLKTENQENGTFHAVSLGLSAVYDFKIND 127
 QY 94 QSPKPYFGARLSLRASAHLGGS--DSFSKTS----- 124
 DB 128 NDKFKPYIGARV---AYGHVHSHIDSTKKTTEFLTAGARGTDPVSSPKNTODAHQE 183
 QY 125 -----AGLGLAGVSYAVTPNVLDAGYRNYGKNTVKNVRSGLSAGVRYKF 174
 DB 184 SNSIRRVGLAGVAGVDFITPNTLDAGYRHYHNMGRLENTR-FKTHBASLGVRIRF 238

Search completed: October 28, 2002, 16:01:13
 Job time : 7.98996 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd

OM protein - protein search, using sw model

```
Run on:      October 28, 2002, 15:56:04 ; Search time 19,9713 Seconds
              (without alignments)
              1507.218 Million cell updates/sec
```

Title: US-09-684-883-8
Perfect score: 870
Sequence: 1 MKKALALIALALPAAALAE.....VNTVKNVRSGLSAGYRVKF 174

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 5622222

```
Minimum DB seq length: 0
Maximum DB seq length: 20000000000
```

```

Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

```

```
Database :
1:  sp.archaea:*
2:  sp.bacteria:*
3:  sp.fungi:*
4:  sp.human:*
5:  sp.invertebrate:*
6:  sp.mammal:*
7:  sp.mhc:*
8:  sp.organella:*
9:  sp.phage:*
10: sp.plant:*
11: sp.podent:*
12: sp.virus:*
13: sp.vertebrate:*
14: sp.unclassified
15: sp.virus:*
16: sp.bacteriap:*
17: sp.archaeap:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	Match	Length	DB	ID	Description
No.	Score					
1	870	100.0	174	2	P95343	P95343 neisseria g
2	835	96.0	174	2	Q9Rp18	Q9Rp18 neisseria m
3	834	95.9	174	16	P95372	P95372 neisseria
4	832	95.6	174	2	Q9Rp16	Q9Rp16 neisseria m
5	829	95.3	174	16	Q9Rp17	Q9Rp17 neisseria
6	828	95.2	174	2	Q9R2R1	Q9R2R1 neisseria m
7	825	94.8	174	2	P96943	P96943 neisseria r
8	813.5	93.5	175	2	P95371	P95371 neisseria m
9	242	27.8	256	2	O51124	O51124 neisseria m
10	237	27.2	234	2	Q9R719	Q9R719 neisseria m
11	237	27.2	234	2	O07280	O07280 neisseria m
12	236	27.1	234	2	Q9R718	Q9R718 neisseria m
13	235	27.0	234	2	O07287	O07287 neisseria m
14	235	27.0	259	2	O51125	O51125 neisseria r
15	233.5	26.8	230	2	Q9R947	Q9R947 neisseria m
16	233.5	26.8	232	2	Q9K479	Q9K479 neisseria l

17	233	26.8	272	2	051013	051013	neisseria	m
18	232.5	26.7	272	2	09R3P5	09R3P5	neisseria	m
19	231.5	26.6	241	2	09AE80	09AE80	neisseria	m
20	231	26.6	283	3	050943	050943	neisseria	m
21	230.5	26.5	186	16	09CMJ9	09cmj9	pasteurella	m
22	230.5	26.5	253	2	051303	051303	neisseria	s
23	230.5	26.5	257	2	050929	050929	neisseria	f
24	230	26.4	256	2	051126	051126	neisseria	m
25	228	26.2	233	2	09K4T5	09K4T5	neisseria	l
26	228	26.2	237	2	031176	031176	neisseria	m
27	227	26.2	241	2	09K4T4	09K4T4	neisseria	l
28	227	26.1	240	2	007925	007925	neisseria	m
29	227	26.1	262	2	033388	033388	neisseria	m
30	226	26.0	235	2	030753	030753	neisseria	m
31	226	26.0	270	2	09RQV4	09rqv4	neisseria	m
32	225.5	25.9	232	2	09R9A9	09r9a9	neisseria	m
33	225.5	25.9	232	2	09R9A8	09r9a8	neisseria	m
34	225.5	25.9	235	2	09K4T3	09K4T3	neisseria	s
35	225	25.9	232	2	030752	030752	neisseria	m
36	224.5	25.8	241	2	007274	007274	neisseria	m
37	223.5	25.7	241	2	007912	007912	neisseria	m
38	223	25.6	237	2	09K4T6	09K4t6	neisseria	l
39	222	25.5	260	2	033389	033389	neisseria	m
40	221.5	25.5	234	2	030759	030759	neisseria	m
41	221.5	25.5	242	2	007279	007279	neisseria	m
42	220.5	25.3	243	2	007278	007278	neisseria	m
43	219.5	25.2	232	2	09K4T7	09K4t7	neisseria	l
44	219	25.2	242	2	09K4T8	09K4t8	neisseria	l
45	218.5	25.1	238	2	031172	031172	neisseria	m

ALIGNMENTS

Query Match	Best Local Similarity	Matches 174; Conservative	100.0%; Score 870; DB 2; Length 174;
1 MKKLAALILALPAALALEGASGFVQADAAHAKASSLSGAGFSPTISAGYRINDLR 60	100.0%; Pred. No. 9.7e-64;	0; Mismatches 0; Indels 0; Gaps 0;	
1 MKKLAALILALPAALALEGASGFVQADAAHAKASSLSGAGFSPTISAGYRINDLR 60			
61 FAVDYTRYKNYKAPSTDFFKLYSIGASVIYDFDTQSPVKPYFGARLSINRAASHLGSDSF 120			
61 FAVDYTRYKNYKAPSTDFFKLYSIGASVIYDFDTQSPVKPYFGARLSINRAASHLGSDSF 120			
121 SKTSAGCAGVYAGSYAVTPEVDDACGYRINYGKATNYKKNVRSGSELSAGRYKVF 174			

```

Db 121 SKTSAGLVLAGVSYAVTPNVDDAGYRNYGVKNTVKNVRSGLSAGYRVKF 174
|||||
RESULT 2
ID Q9RP18 PRELIMINARY; PRT; 174 AA.
AC Q9RP18;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE SURFACE PROTEIN A.
GN NSPA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=8047;
RA Moe G.R., Tan S., Granoff D.M.;
RT "Differences in Surface Expression of Neisserial Surface Protein A
among Neisseria meningitidis Group B strains.";
RL Infect. Immun. 0:0-0(1999).
DR EMBL: AF175676; AAD53279.1;
DR InterPro: IPR003394; Opacity.
DR Pfam: PF02462; Opacity.
DR SIGNAL: Complete proteome.
SQ SEQUENCE 174 AA; 18357 MM; 0205AALDA1B7F005 CRC64;

Query Match 96.0%; Score 835; DB 2; Length 174;
Best Local Similarity 95.4%; Pred. No. 7e-61;
Matches 166; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 MKKALALIALALPAALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
| | | | |
DB 1 MKKALALIALALPAALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
| | | | |
QY 61 FAVDYTRYKNKAPSTDFKLYSIGASVLYDPTQSPVKPYFGARLSLNRAASVLDGSDSF 120
| | | | |
DB 61 FAVDYTRYKNKAPSTDFKLYSIGASVLYDPTQSPVKPYFGARLSLNRAASVLDGSDSF 120
| | | | |
QY 121 SKTSAGLVLAGVSYAVTPNVDDAGYRNYGVKNTVKNVRSGLSAGYRVKF 174
| | | | |
DB 121 SKTSAGLVLAGVSYAVTPNVDDAGYRNYGVKNTVKNVRSGLSAGYRVKF 174
| | | | |

RESULT 3
ID P95372 PRELIMINARY; PRT; 174 AA.
AC P95372;
DT 01-MAY-1997 (TREMblrel. 03, Created)
DT 01-MAY-1997 (TREMblrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE OUTER MEMBRANE PROTEIN PRECURSOR.
GN NSPA OR NMA0862.
OS Neisseria meningitidis, and
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487; 65699;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=24063;
RA Martin D., Cadieux N., Hamel J., Rioux C., Brodeur B.R.;
RL Submitted (MAR-1996) to the EMBL/Genbank/DBD databases.
RN 121
DE SEQUENCE FROM N.A.
RC STRAIN=24491 / SEROGROUP A / SEROTYPE 4A;
RC MEDLINE=20222556; PubMed=10761919;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies K.M., Davis P., Devlin K., Felwell T., Hamlin N., Holroyd S.,
RA Jagers K., Leather S., Moute S., Mungall K., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrell B.G.;

```

```

RT "Complete DNA sequence of a serogroup A strain of Neisseria
meningitidis 22491".
RL Nature 404:502-506(2000).
DR EMBL: U52068; AAB41580.1;
DR EMBL: AL162754; CAB84143.1;
DR InterPro: IPR003394; Opacity.
DR Pfam: PF02462; Opacity.
DR SIGNAL: Complete proteome.
FT SIGNAL 1 19
SQ SEQUENCE 174 AA; 18355 MM; EBA4A1ADA4FEF009 CRC64;

Query Match 95.9%; Score 834; DB 16; Length 174;
Best Local Similarity 95.4%; Pred. No. 8.5e-61;
Matches 166; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 MKKALALIALALPAALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
| | | | |
DB 1 MKKALALIALALPAALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
| | | | |
QY 61 FAVDYTRYKNKAPSTDFKLYSIGASVLYDPTQSPVKPYFGARLSLNRAASVLDGSDSF 120
| | | | |
DB 61 FAVDYTRYKNKAPSTDFKLYSIGASVLYDPTQSPVKPYFGARLSLNRAASVLDGSDSF 120
| | | | |
QY 121 SKTSAGLVLAGVSYAVTPNVDDAGYRNYGVKNTVKNVRSGLSAGYRVKF 174
| | | | |
DB 121 SKTSAGLVLAGVSYAVTPNVDDAGYRNYGVKNTVKNVRSGLSAGYRVKF 174
| | | | |

```

```

RESULT 4
ID Q9RP16 PRELIMINARY; PRT; 174 AA.
AC Q9RP16;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE SURFACE PROTEIN A.
GN NSPA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=NG3/88;
RA Moe G.R., Tan S., Granoff D.M.;
RT "Differences in Surface Expression of Neisserial Surface Protein A
among Neisseria meningitidis Group B strains.";
RL Infect. Immun. 0:0-0(1999).
DR EMBL: AF175681; AAD53284.1;
DR InterPro: IPR003394; Opacity.
DR Pfam: PF02462; Opacity.
DR SIGNAL: Complete proteome.
SQ SEQUENCE 174 AA; 18355 MM; ECF6F3B89286800E CRC64;

Query Match 95.6%; Score 832; DB 2; Length 174;
Best Local Similarity 94.8%; Pred. No. 1.2e-60;
Matches 165; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 MKKALALIALALPAALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
| | | | |
DB 1 MKKALALIALALPAALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
| | | | |
QY 61 FAVDYTRYKNKAPSTDFKLYSIGASVLYDPTQSPVKPYFGARLSLNRAASVLDGSDSF 120
| | | | |
DB 61 FAVDYTRYKNKAPSTDFKLYSIGASVLYDPTQSPVKPYFGARLSLNRAASVLDGSDSF 120
| | | | |
QY 121 SKTSAGLVLAGVSYAVTPNVDDAGYRNYGVKNTVKNVRSGLSAGYRVKF 174
| | | | |
DB 121 SKTSAGLVLAGVSYAVTPNVDDAGYRNYGVKNTVKNVRSGLSAGYRVKF 174
| | | | |

RESULT 5
ID Q9RP17 PRELIMINARY; PRT; 174 AA.
AC Q9RP17;

```

DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE SURFACE PROTEIN A (OUTER MEMBRANE PROTEIN NSGA).
 GN NSPA OR NMB0663.
 OS Neisseria meningitidis, and
 OS Neisseria meningitidis (serogroup B).
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 ON NCB1_Taxid=487, 491;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP STRAIN-CU385;
 RA Moe G.R., Tan S., Granoff D.M.;
 RT "Differences in Surface Expression of Neisserial Surface Protein A
 among Neisseria meningitidis group B strains.";
 RL Infect. Immun. 0:0-0(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MC58 / SEROGROUP B;
 RX MEDLINE=20175755; PubMed=10710307;
 RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
 Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
 Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
 Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
 Mason T., Ciecko A., Parksey D.S., Blair E., Cifton H., Clark E.B.,
 Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,
 Gill J., Scarlato V., Maignani V., Pizza M., Grandi G., Sun L.,
 Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
 RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
 MC58.";
 RL Science 287:1809-1815(2000).
 DR EMBL: AF175678; AAD53281.1; -;
 DR EMBL: AE002420; AAF41081.1; -;
 DR TIGR: NMB0663; -;
 DR InterPro: IPR003394; Opacity.
 DR Pfam: PF02462; Opacity; 1.
 DR Complete proteome.
 SQ SEQUENCE 174 AA; 18397 MW; EBB02767DDCE109 CRC64;

Query Match 95.3%; Score 829; DB 16; Length 174;
 Best Local Similarity 94.8%; Pred. No. 2.2e-60;
 Matches 165; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 MKKALALIALPAALAEAGSGFYQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 DB 1 MKKALATLIALPAALAEAGSGFYQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 QY 61 FAVDYTRYKNYKAPSTDFKLYSIGASYVDPTQSPVKPYFGARLSLNRAAHLGSSDSF 120
 DB 61 FAVDYTRYKNYKAPSTDFKLYSIGASYVDPTQSPVKPYFGARLSLNRAAHLGSSDSF 120
 QY 121 SKTSAGLGLVAGSYAVTPNVDDLDAAGRYNYGKNTVKNVRSGLSAGYRVKF 174
 DB 121 SKTSAGLGLVAGSYAVTPNVDDLDAAGRYNYGKNTVKNVRSGLSAGYRVKF 174
 DB 121 SQTSTGLGLVAGSYAVTPNVDDLDAAGRYNYGKNTVKNVRSGLSAGYRVKF 174

RESULT 6
 Q9R2R1 PRELIMINARY; PRT; 174 AA.
 AC Q9R2R1;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE SURFACE PROTEIN A.
 GN NSPA.
 OS Neisseria meningitidis.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 ON NCB1_Taxid=487;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP STRAIN-M136, AND B232;
 RA Moe G.R., Tan S., Granoff D.M.;
 RT "Differences in Surface Expression of Neisserial Surface Protein A

RT among Neisseria meningitidis Group B strains.";
 RL Infect. Immun. 0:0-0(1999).
 DR EMBL: AF175679; AAD53282.1; -;
 DR EMBL: AF175677; AAD53280.1; -;
 DR InterPro: IPR003394; Opacity.
 DR Pfam: PF02462; Opacity; 1.
 SQ SEQUENCE 174 AA; 18385 MW; ECF6F39A9286910E CRC64;

Query Match 95.2%; Score 828; DB 2; Length 174;
 Best Local Similarity 94.3%; Pred. No. 2.6e-60;
 Matches 164; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 MKKALALIALPAALAEAGSGFYQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 DB 1 MKKALATLIALPAALAEAGSGFYQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 QY 61 FAVDYTRYKNYKAPSTDFKLYSIGASYVDPTQSPVKPYFGARLSLNRAAHLGSSDSF 120
 DB 61 FAVDYTRYKNYKAPSTDFKLYSIGASYVDPTQSPVKPYFGARLSLNRAAHLGSSDSF 120
 QY 121 SKTSAGLGLVAGSYAVTPNVDDLDAAGRYNYGKNTVKNVRSGLSAGYRVKF 174
 DB 121 SQTSTGLGLVAGSYAVTPNVDDLDAAGRYNYGKNTVKNVRSGLSAGYRVKF 174

RESULT 7
 P96943 PRELIMINARY; PRT; 174 AA.
 AC P96943;
 DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE OUTER MEMBRANE PROTEIN PRECURSOR.
 GN NSPA.
 OS Neisseria meningitidis.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 ON NCB1_Taxid=487;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP STRAIN=608B;
 RX MEDLINE=97149429; PubMed=8996237;
 RA Martin D., Cadieux N., Hamel J., Brodeur B.R.;
 RT "Costimulation of T cell activation by integrin-associated protein
 (CD47) is an adhesion-dependent, CD28-independent signaling pathway.";
 RL J. Exp. Med. 185:1-11(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NGP165, M986, AND NG6/88;
 RA Moe G.R., Tan S., Granoff D.M.;
 RT "Differences in Surface Expression of Neisserial Surface Protein A
 among Neisseria meningitidis Group B strains.";
 RL Infect. Immun. 0:0-0(1999).
 DR EMBL: U52066; AAC36000.1; -;
 DR EMBL: AF175683; AAD53286.1; -;
 DR EMBL: AF175680; AAD53283.1; -;
 DR EMBL: AF175682; AAD53285.1; -;
 DR InterPro: IPR003394; Opacity.
 DR Pfam: PF02462; Opacity; 1.
 DR Signal.
 FT SIGNAL.
 SQ SEQUENCE 174 AA; 18425 MW; EBB02767DDCE109 CRC64;

Query Match 94.8%; Score 825; DB 2; Length 174;
 Best Local Similarity 94.3%; Pred. No. 4.6e-60;
 Matches 164; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 MKKALALIALPAALAEAGSGFYQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 DB 1 MKKALATLIALPAALAEAGSGFYQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 QY 61 FAVDYTRYKNYKAPSTDFKLYSIGASYVDPTQSPVKPYFGARLSLNRAAHLGSSDSF 120
 DB 61 FAVDYTRYKNYKAPSTDFKLYSIGASYVDPTQSPVKPYFGARLSLNRAAHLGSSDSF 120

QY 121 SKTSAGLVAGVSYAVTPNVLDAGYRKYNGKVTYKKNVSGELSGAGYVKF 174
 Db 121 SQTSGVLGVAGVSYAVTPNVLDAGYRKYNGKVTYKKNVSGELSGAGYVKF 174

RESULT 8

P95371 PRELIMINARY; PRT; 175 AA.
 AC P95371;
 DT 01-MAY-1997 (TREMblrel. 03, Created)
 DT 01-MAY-1997 (TREMblrel. 03, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE OUTER MEMBRANE PROTEIN PRECURSOR.
 OS Neisseria meningitidis.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 NCBI_TaxID=487;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MCH 88;
 RX MEDLINE=9386904; PubMed=10456958;
 RA Cadieux N., Plante M., Rioux C.R., Brodeur B.R., Martin D.;
 RT "Bactericidal and cross-protective activities of a monoclonal antibody
 directed against Neisseria meningitidis NSP4 outer membrane protein.";
 RL Infect. Immun. 67:4955-4959(1999).
 DR EMBL; U52067; AAB41579.1; -;
 DR InterPro; IPR003394; Opacity.
 DR Pfam; PF02462; Opacity; 1.
 KW Signal.
 FT SIGNAL.
 SQ SEQUENCE 175 AA; 18572 MW; DIEAF2FF5CC2FEA CRC64;

Query Match 93.5%; Score 813.5; DB 2; Length 175;
 Best Local Similarity 93.7%; Pred. No. 4e-59;
 Matches 164; Conservative 2; Mismatches 8; Indels 1; Gaps 1;

QY 1 MKKALAIALALPAALAEAGSGFYVQADAAHAKKASSISGASGEPSPRISAGYRINDLR 60
 Db 1 MKKALAIALALPAALAEAGSGFYVQADAAHAKKASSISGASGEPSPRISAGYRINDLR 60
 QY 61 FAVDYTRKKNYK-APSTDFKLYSGASYVDFDQSPVKPFYFARLSLNRSASHLGSSDS 119
 Db 61 FAVDYTRKKNYKQYPSDFKLYSGASYVDFDQSPVKPFYFARLSLNRSASVDFPNSDS 120
 QY 120 FSKTSAGLVAGVSYAVTPNVLDAGYRKYNGKVTYKKNVSGELSGAGYVKF 174
 Db 121 FSKTSGVLGVAGVSYAVTPNVLDAGYRKYNGKVTYKKNVSGELSGAGYVKF 175

RESULT 9

Q51124 PRELIMINARY; PRT; 256 AA.
 ID Q51124;
 AC Q51124;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-MAY-1997 (TREMblrel. 03, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE OPACITY OUTER MEMBRANE PROTEIN (FRAGMENT).
 GN OPA.
 OS Neisseria meningitidis.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 NCBI_TaxID=487;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-24197;
 RX MEDLINE=98129089; PubMed=9467908;
 RA Hobbs M.M., Malorny B., Prasad P., Morelli G., Kusecek B.,
 RA Heckels J.E., Cannon J.G., Achtman M.;
 RT "Recombinational reassortment among opa genes from ET-37 complex
 Neisseria meningitidis isolates of diverse geographical origins.";
 RL Microbiology 144:157-166(1998).
 DR EMBL; U37255; AAC46101.1; -;
 DR InterPro; IPR003394; Opacity.
 DR Pfam; PF02462; Opacity; 1.

FT NON_TER 1
 SQ SEQUENCE 256 AA; 28335 MW; 9D41C6079C6DD13F CRC64;

Query Match 27.8%; Score 242; DB 2; Length 256;
 Best Local Similarity 28.3%; Pred. No. 3.2e-12;
 Matches 69; Conservative 31; Mismatches 66; Indels 78; Gaps 7;

QY 8 LIALPALPAALAEAGSGFYVQADAAHAKKASSISGASGEPSPRISAGYRINDLR 47
 Db 14 LFSSAQAASSESGHGPYVQADLAVALMERITHDPKATGANNITVSDYFNNITASHIH 73
 QY 48 PRISAGYRINDLRFAVDYTRYK-----NYKADSTDFK-----LYS 82
 Db 74 PRYSVGYDFGGRKADYASRYKWKESNSTKKYEDIANRYKFKETHEQNGSFFHAAS 133
 QY 83 IGASVYDFDQSPVKPFYFARLSLNRSASHLGSSDS-----ASAHIG----- 116
 Db 134 LGLSALYDFKLDKREKPYTGARVAIGHVKHGVSEFTKTTVTSKPTATSPGCGPIQTD 193
 QY 117 -----SDSFKTSAGLVAGVSYAVTPNVLDAGYRKYNGKVTYKKNVSGELSGAGY 170
 Db 194 PSKPRYHESHSSISGLGVAGVDFDIPKLLDGYRHHMGRLENR-FKTHEVSLGM 252
 QY 171 RYKF 174
 Db 253 RYKF 256

RESULT 10

O9R719 PRELIMINARY; PRT; 234 AA.
 ID O9R719;
 AC O9R719;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE OPACITY PROTEIN (FRAGMENT).
 GN OPA.
 OS Neisseria meningitidis.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 NCBI_TaxID=487;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=23906;
 RX MEDLINE=98010345; PubMed=9350862;
 RA Morelli G., Malorny B., Mueller K., Sellar A., Wang J., del Valle J.,
 RA Achtman M.;
 RT "Clonal descent and microevolution of Neisseria meningitidis during 30
 years of epidemic spread.";
 RL Mol. Microbiol. 25:1047-1064(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=3926;
 RA Zhu P., van der Ende A., Falush D., Brieske N., Morelli G., Linn B.,
 RA Popovic T., Schuurman I.G.A., Adegbola R.A., Zurch K., Gagneux S.,
 RA Platonov A.E., Riou J.Y., Caugant D.A., Nicotol P., Achtman M.;
 RT "Fit genotypes and escape variants of subgroup III Neisseria
 meningitidis during three pandemics of epidemic meningitis.";
 RL Submitted (JAN-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF001194; AAC32715.1; -;
 DR EMBL; AJ292235; CAC36358.1; -;
 DR InterPro; IPR003394; Opacity.
 DR Pfam; PF02462; Opacity; 1.
 FT NON_TER 1
 SQ SEQUENCE 234 AA; 26161 MW; F97142F463136EC1 CRC64;

Query Match 27.2%; Score 237; DB 2; Length 234;
 Best Local Similarity 28.9%; Pred. No. 7.3e-12;
 Matches 67; Conservative 29; Mismatches 62; Indels 74; Gaps 8;

QY 16 AALAEAG-SGFYVQADAAH-----AKASSISGASGEPSPRISAGY 54
 Db 4 AASEGSRSPYVQADLAVALMERITHDPQATGANNITVSDYFNNITASHIHPRVSVGY 63

OY 55 RINDRFAVDYTRYK-----NYKAPSTDFK-----LYSIGASVI 88
 DB 64 DFGDMRIADYASYRKWKESNSKVTETKQNGKOEKTEHOGNGSFHATSSLSLSAI 123
 OY 89 YDFDQSPVKPYFGARLSLNR-----ASHLGG-----SDSFSK 122
 DB 124 YDFKLNKFKPYIGVRAVGHVGHVSVESKTTVTNNNGVPPOGPTPKPAYHSHSI 183
 OY 123 TSAGLGVLAGVSYAVTPNVDLAGRYNYGVKNTVKNVSGELSGAGVRYKF 174
 DB 184 SSVGLGVLAGVGFDTLPKLTLDGTGRYHNMGRLENTR-FKTHEVSLGMRHYF 234

RESULT 11

ID 007280 PRELIMINARY: PRT: 234 AA.

AC 007280;
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE OPACITY PROTEIN (FRAGMENT).
 GN OPA.
 OS Neisseria meningitidis.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_TaxId=487;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=23324;
 RX MEDLINE=98010345; PubMed=9350862;
 RA Morelli G., Malorny B., Muller K., Sella A., Wang J.F., del Valle J., Achtmann M.;
 RT "Clonal descent and microevolution of Neisseria meningitidis during 30 years of epidemic spread."
 RL Mol. Microbiol. 25:1047-1064(1997).
 DR EMBL: AF001195; AAC32716.1; -
 DR InterPro: IPR003394; Opacity.
 DR Pfam: PF02462; Opacity; 1.
 FT NON_TER 1
 SQ SEQUENCE 234 AA; 26134 MW; 005AD356E93BCC50 CRC64;

Query Match 27.2%; Score 237; DB 2; Length 234;
 Best Local Similarity 28.9%; Pred. No. 7.3e-12;

Matches 67; Conservative 29; Mismatches 62; Indels 74; Gaps 8;

OY 16 AALAECA-SGEYVQADAAH-----AKSSSLGS-----AKGSPRISAGY 54
 DB 4 AASEDSRSPTVQADLAVERITHDYQATGANNSTVSDYFRNIRAHSHIPRVSVGY 63
 OY 55 RINDRFAVDYTRYK-----NYKAPSTDFK-----LYSIGASVI 88
 DB 64 DFGDMRIADYASYRKWKESNSKVTETKQNGKOEKTEHOGNGSFHATSSLSLSAI 123
 OY 89 YDFDQSPVKPYFGARLSLNR-----ASHLGG-----SDSFSK 122
 DB 124 YDFKLNKFKPYIGVRAVGHVGHVSVESKTTVTNNNGVPPOGPTPKPAYHSHSI 183
 OY 123 TSAGLGVLAGVSYAVTPNVDLAGRYNYGVKNTVKNVSGELSGAGVRYKF 174
 DB 184 SSVGLGVLAGVGFDTLPKLTLDGTGRYHNMGRLENTR-FKTHEVSLGMRHYF 234

RESULT 12

ID 09R718 PRELIMINARY: PRT: 234 AA.

AC 09R718;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE OPACITY PROTEIN (FRAGMENT).
 GN OPA.
 OS Neisseria meningitidis.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_TaxId=487;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-B1;
 RX MEDLINE=98010345; PubMed=9350862;
 RA Morelli G., Malorny B., Muller K., Sella A., Wang J.F., del Valle J., Achtmann M.;
 RT "Clonal descent and microevolution of Neisseria meningitidis during 30 years of epidemic spread."
 RL Mol. Microbiol. 25:1047-1064(1997).
 DR EMBL: AF001195; AAC32717.1; -
 DR InterPro: IPR003394; Opacity.
 DR Pfam: PF02462; Opacity; 1.
 FT NON_TER 1
 SQ SEQUENCE 234 AA; 26191 MW; F01D3B9163066171 CRC64;

Query Match 27.1%; Score 236; DB 2; Length 234;
 Best Local Similarity 28.9%; Pred. No. 8.8e-12;

Matches 67; Conservative 28; Mismatches 63; Indels 74; Gaps 8;

OY 16 AALAECA-SGEYVQADAAH-----AKSSSLGS-----AKGSPRISAGY 54
 DB 4 AASEDSRSPTVQADLAVERITHDYQATGANNSTVSDYFRNIRAHSHIPRVSVGY 63
 OY 55 RINDRFAVDYTRYK-----NYKAPSTDFK-----LYSIGASVI 88
 DB 64 DFGDMRIADYASYRKWKESNSKVTETKQNGKOEKTEHOGNGSFHATSSLSLSAI 123
 OY 89 YDFDQSPVKPYFGARLSLNR-----ASHLGG-----SDSFSK 122
 DB 124 YDFKLNKFKPYIGVRAVGHVGHVSVESKTTVTNNNGVPPOGPTPKPAYHSHSI 183
 OY 123 TSAGLGVLAGVSYAVTPNVDLAGRYNYGVKNTVKNVSGELSGAGVRYKF 174
 DB 184 SSVGLGVLAGVGFDTLPKLTLDGTGRYHNMGRLENTR-FKTHEVSLGMRHYF 234

RESULT 13

ID 007287 PRELIMINARY: PRT: 234 AA.

AC 007287;
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE OPACITY PROTEIN (FRAGMENT).
 GN OPA OR OPA.
 OS Neisseria meningitidis.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_TaxId=487;

RN [1]
 RP SEQUENCE FROM N.A.
 RA Achtmann M., Malorny B., Muller K., Sella A., Wang J.F., del Valle J., Achtmann M.;
 RT "Clonal descent and microevolution of Neisseria meningitidis during 30 years of epidemic spread."
 RL Mol. Microbiol. 25:1047-1064(1997).
 DR EMBL: AF001204; AAC32725.1; -
 DR EMBL: AF004823; AAC32684.1; -
 DR InterPro: IPR003394; Opacity.
 DR Pfam: PF02462; Opacity; 1.
 FT NON_TER 1
 SQ SEQUENCE 234 AA; 25933 MW; 61E3755DDE82AF22 CRC64;

Query Match 27.0%; Score 235; DB 2; Length 234;
 Best Local Similarity 28.0%; Pred. No. 1.1e-11;

Matches 65; Conservative 29; Mismatches 64; Indels 74; Gaps 6;

OY 16 AALAECA-SGEYVQADAAH-----AKSSSLGS-----AKGSPRISAGY 54

```

DB 4 AASEDSGRSPYVOADLAAERITHDYPKATGANNSTVSDYFRNIRAHSHIPRVSGY 63
QY 55 RINDLRADVTRYKKNKAPSTD-----FKVSGASVLY 89
DB 64 DFDGWRADYASYRKWKESNSTENTONRIKIETGHOGNSFLNASSLGLSALT 123
QY 90 DFDTSFVKPFYFGLRLSLNRSASHLGSDSFSKT----- 123
DB 124 DFLNKDFKRYIGARAVYGVKKHGVSVESKTKTVTSKPNCGPVKGGPTPKPAYHESNSI 183
QY 124 -SAGLGVLAIVSAVTPNVLDAGRYNYGKNTVKNRSGLSAGVRYKF 174
DB 184 SSIGLGVIAVGFDPITPKLTDGYRYHNMGRLENTR-FKTHEVSLGVRHYF 234

RESULT 14
ID 051125 PRELIMINARY; PRT; 259 AA.
AC 051125;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-MAY-1997 (T-EMBLrel. 03, last sequence update)
DT 01-JUN-2001 (T-EMBLrel. 17, last annotation update)
DE OPACITY OUTERMEMBRANE PROTEIN (FRAGMENT).
GN OPA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=24197;
RX MEDLINE=98129089; PubMed=9467908;
RA Hobbs M.M., Malorny B., Prasad P., Morelli G., Kusecek B.,
  Heckels J.E., Cannon J.G., Achtman M.;
RT "Recombinational reassortment among opa genes from ET-37 complex
  Neisseria meningitidis isolates of diverse geographical origins.";
RL Microbiol. 144:157-166(1998).
DR EMBL; U37256; AAC46102.1; -.
DR InterPro; IPR003394; Opacity.
DR Pfam; PF02462; Opacity; 1.
FT NON_TER 1
SQ SEQUENCE 259 AA; 28856 MW; 8E19050D51157DE3 CRC64;

Query Match 27.0%; Score 235; DB 2; Length 259;
Best Local Similarity 28.5%; Pred. No. 1.2e-11;
Matches 70; Conservative 29; Mismatches 67; Indels 80; Gaps 7;

```

```

DT 01-MAY-2000 (T-EMBLrel. 13, last sequence update)
DT 01-DEC-2001 (T-EMBLrel. 19, last annotation update)
DE OPACITY PROTEIN (FRAGMENT).
GN OPA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98010345; PubMed=9350862;
RA Morelli G., Malorny B., Muller K., Sella A., Wang J.F., del Valle J.,
  Achtman M.;
RT "Clonal descent and microevolution of Neisseria meningitidis during 30
  years of epidemic spread.";
RL Mol. Microbiol. 25:1047-1064(1997).
DR EMBL; AF031337; AAC45980.1; -.
DR InterPro; IPR003394; Opacity.
DR Pfam; PF02462; Opacity; 1.
FT NON_TER 1
SQ SEQUENCE 230 AA; 23819 MW; 970DC4570B57A697 CRC64;

Query Match 26.8%; Score 233.5; DB 2; Length 230;
Best Local Similarity 28.6%; Pred. No. 1.4e-11;
Matches 64; Conservative 27; Mismatches 60; Indels 73; Gaps 7;

```

Search completed: October 28, 2002, 16:02:40
 Job time : 20.9713 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 28, 2002, 16:00:44 ; Search time 103.601 Seconds

(without alignments)
591.158 Million cell updates/sec

Title: US-09-684-883-2

Perfect score: 1 MKKALVTLLALPAALAE.....VTVKNVNSGLSVGRVRF 174

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Pending_Patents_AA_Main:*
1: /cgn2_6/ptodata/1/paa/US086_COMB.pep.*
2: /cgn2_6/ptodata/1/paa/US086_COMB.pep.*
3: /cgn2_6/ptodata/1/paa/US087_COMB.pep.*
4: /cgn2_6/ptodata/1/paa/US088_COMB.pep.*
5: /cgn2_6/ptodata/1/paa/US089_COMB.pep.*
6: /cgn2_6/ptodata/1/paa/US090_COMB.pep.*
7: /cgn2_6/ptodata/1/paa/US091_COMB.pep.*
8: /cgn2_6/ptodata/1/paa/US092_COMB.pep.*
9: /cgn2_6/ptodata/1/paa/US093_COMB.pep.*
10: /cgn2_6/ptodata/1/paa/US094_COMB.pep.*
11: /cgn2_6/ptodata/1/paa/US095_COMB.pep.*
12: /cgn2_6/ptodata/1/paa/US096_COMB.pep.*
13: /cgn2_6/ptodata/1/paa/US097_COMB.pep.*
14: /cgn2_6/ptodata/1/paa/US098_COMB.pep.*
15: /cgn2_6/ptodata/1/paa/US099_COMB.pep.*
16: /cgn2_6/ptodata/1/paa/US100_COMB.pep.*
17: /cgn2_6/ptodata/1/paa/US101_COMB.pep.*
18: /cgn2_6/ptodata/1/paa/US102_COMB.pep.*
19: /cgn2_6/ptodata/1/paa/US103_COMB.pep.*
20: /cgn2_6/ptodata/1/paa/US104_COMB.pep.*
21: /cgn2_6/ptodata/1/paa/US105_COMB.pep.*
22: /cgn2_6/ptodata/1/paa/US106_COMB.pep.*
23: /cgn2_6/ptodata/1/paa/US107_COMB.pep.*
24: /cgn2_6/ptodata/1/paa/US108_COMB.pep.*
25: /cgn2_6/ptodata/1/paa/US109_COMB.pep.*
26: /cgn2_6/ptodata/1/paa/US110_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	868	100.0	174	8	US-08-406-362-2
2	868	100.0	174	22	US-09-870-759-36
3	135	15.6	170	8	US-08-479-520-20
4	135	15.6	170	8	US-08-486-050-20
5	135	15.6	170	8	US-08-486-050A-20
6	135	15.6	170	13	US-08-988-444-20
7	135	15.6	170	16	US-09-217-849-20

8	135	15.6	170	18	US-09-489-850-20	Sequence 20, Appl
9	129.5	14.9	281	21	US-09-739-449-11638	Sequence 11638, A
10	129.5	14.9	281	22	US-09-803-110-11638	Sequence 11638, A
11	113.5	13.1	98	19	US-09-540-236-2245	Sequence 2245, Ap
12	109.5	12.6	187	18	US-09-489-039A-13699	Sequence 13699, Ap
13	104.5	12.0	384	19	US-09-543-681A-7922	Sequence 7922, Ap
14	101	11.6	21	24	US-10-082-014-124	Sequence 124, App
15	101	11.6	21	26	US-60-358-618-48	Sequence 48, Appl
16	99	11.4	217	16	US-09-252-691-9162	Sequence 9162, Ap
17	99	11.4	217	16	US-09-252-691C-9162	Sequence 9162, Ap
18	97	11.2	21	24	US-10-082-014-123	Sequence 123, App
19	97	11.2	21	26	US-60-358-618-47	Sequence 47, Appl
20	94.5	10.9	212	1	PCT-US02-03987-10149	Sequence 10149, A
21	94.5	10.9	212	22	US-09-815-242-10149	Sequence 10149, A
22	94.5	10.9	212	24	US-10-072-851-10149	Sequence 10149, A
23	93	10.7	190	19	US-09-543-681A-7922	Sequence 7922, Ap
24	92.5	10.7	261	16	US-09-252-991A-19759	Sequence 19759, A
25	92	10.6	225	24	US-10-015-127-13821	Sequence 13821, Ap
26	89.5	10.3	186	19	US-09-540-236-2792	Sequence 2792, Ap
27	89.5	10.3	186	26	US-60-128-476-4082	Sequence 4082, Ap
28	89.5	10.3	257	1	PCT-US02-03987-13845	Sequence 13845, A
29	89.5	10.3	257	22	US-09-815-242-13845	Sequence 13845, A
30	89.5	10.3	257	24	US-10-072-851-13845	Sequence 13845, A
31	88.5	10.2	180	1	PCT-US99-22918-7	Sequence 7451, Ap
32	88.5	10.2	180	15	US-09-164-714-7	Sequence 7, Appl
33	88.5	10.2	573	23	US-09-952-267-3	Sequence 7, Appl
34	88.5	10.2	573	23	US-09-952-267A-3	Sequence 3, Appl
35	88.5	10.2	573	23	US-09-952-267A-3	Sequence 3, Appl
36	88	10.1	359	8	US-08-065-442-2	Sequence 2, Appl
37	88	10.1	359	8	US-08-457-997-2	Sequence 2, Appl
38	88	10.1	359	8	US-08-457-997A-2	Sequence 2, Appl
39	88	10.1	359	18	US-08-467-722-2	Sequence 2, Appl
40	88	10.1	359	18	US-09-451-184-2	Sequence 2, Appl
41	88	10.1	397	23	US-09-902-540-16267	Sequence 16267, A
42	88	10.1	610	23	US-09-952-267-11	Sequence 11, Appl
43	88	10.1	610	23	US-09-952-267A-11	Sequence 11, Appl
44	88	10.1	624	23	US-09-952-267-7	Sequence 7, Appl
45	88	10.1	624	23	US-09-952-267A-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-08-406-362-2
Sequence 2, Application US/08406362
GENERAL INFORMATION:
APPLICANT: Brodeur, Bernard R
APPLICANT: Martin, Denis
TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESS: Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/406,362
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr, James F
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: Pharma-43

```
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-406-362-2

Query Match          100.0%; Score 868; DB 8; Length 174;
Best Local Similarity 100.0%; Pred. No. 3.9e-91;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGAKGFSRISAGYRINDLR 60
DB 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGAKGFSRISAGYRINDLR 60
QY 61 FAVDYTRYKNYKAPSTDEFLYSIGASAIYDPTQSPVKPYLGARLSLRASVLDGSDSF 120
DB 61 FAVDYTRYKNYKAPSTDEFLYSIGASAIYDPTQSPVKPYLGARLSLRASVLDGSDSF 120
QY 121 SQTSGIGLVGVSAVPPNVDLDAGYRNYIGKYNVKNVSGELSVGRVKE 174
DB 121 SQTSGIGLVGVSAVPPNVDLDAGYRNYIGKYNVKNVSGELSVGRVKE 174

RESULT 2
US-09-870-759-36
Sequence 36, Application US/09870759
GENERAL INFORMATION:
APPLICANT: TERMAN, David S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REFERENCE: 870759
CURRENT FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: US 60/208,128
NUMBER OF SEQ ID NOS: 166
SOFTWARE: PatentIn version 3.1
SEQ ID NO 36
LENGTH: 174
TYPE: PRT
ORGANISM: Neisseria meningitidis
US-09-870-759-36

Query Match          100.0%; Score 868; DB 22; Length 174;
Best Local Similarity 100.0%; Pred. No. 3.9e-91;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGAKGFSRISAGYRINDLR 60
DB 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGAKGFSRISAGYRINDLR 60
QY 61 FAVDYTRYKNYKAPSTDEFLYSIGASAIYDPTQSPVKPYLGARLSLRASVLDGSDSF 120
DB 61 FAVDYTRYKNYKAPSTDEFLYSIGASAIYDPTQSPVKPYLGARLSLRASVLDGSDSF 120
QY 121 SQTSGIGLVGVSAVPPNVDLDAGYRNYIGKYNVKNVSGELSVGRVKE 174
DB 121 SQTSGIGLVGVSAVPPNVDLDAGYRNYIGKYNVKNVSGELSVGRVKE 174

RESULT 3
US-08-479-520-20
Sequence 20, Application US/08479520
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
```

```
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,520
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/105/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-479-520-20

Query Match          15.6%; Score 135; DB 8; Length 170;
Best Local Similarity 26.3%; Pred. No. 1.1e-06;
Matches 41; Conservative 20; Mismatches 47; Indels 48; Gaps 4;

QY 6 ATITLALPAALAEAGSGFYVQADAAHAKASSLSGAKGFSRISAGYRINDLR 45
DB 15 SLLFSSAAQASDRSPYVQADLAIAERTHDYPOATGANNSTVSDFRNRRAAS 74
QY 46 FSPRISAGYRINDLRFAVDYTRYKNYKAPSTDEK 79
DB 75 IHPKVSVDYDFEGGRADYASFRKNNNNKYVNTKELEKHNKKDLKTENQENCTFHA 134
QY 80 LYSIGASAIYDPTQSPVKPYLGARLSLRASVLD 113
DB 135 ASSLGLSAIYDFLKGKFKPYIGARAVAYGHVRSID 170

RESULT 4
US-08-486-050-20
Sequence 20, Application US/08486050
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
```


OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,050
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/103/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-486-050A-20

Query Match 15.6%; Score 135; DB 8; Length 170;
Best Local Similarity 26.3%; Pred. No. 1,1e-06;
Matches 41; Conservative 20; Mismatches 47; Indels 48; Gaps 4;

QY 6 ATTLALPAAALAGASGFYVQADAAH-----AKASSLSG-----AKG 45
DB 15 SSLFSSAAQAASBDRSPYVQADLAYAERITHDYPQATGANNSTVSDYFRNIRAH 74
QY 46 FSPRISAGYRINDREFADVTRYKNY-----KAPSTDFK 79
DB 75 IHPRVSVGYDPCGWRILADYASYRKMNKNKYSVNTRKLENNHNNKDKLTENGCTFHA 134
QY 80 LYSIGASAIYDPTQSPVKPYLGARLSLN--RASVD 113
DB 135 ASLSGLSAIYDFKLGKFKRPYIGARVAGVHRHSID 170

RESULT 5
US-08-486-050A-20
Sequence 20, Application US/08486050A
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,050A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/103/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-486-050A-20

Query Match 15.6%; Score 135; DB 8; Length 170;
Best Local Similarity 26.3%; Pred. No. 1,1e-06;
Matches 41; Conservative 20; Mismatches 47; Indels 48; Gaps 4;

QY 6 ATTLALPAAALAGASGFYVQADAAH-----AKASSLSG-----AKG 45
DB 15 SSLFSSAAQAASBDRSPYVQADLAYAERITHDYPQATGANNSTVSDYFRNIRAH 74
QY 46 FSPRISAGYRINDREFADVTRYKNY-----KAPSTDFK 79
DB 75 IHPRVSVGYDPCGWRILADYASYRKMNKNKYSVNTRKLENNHNNKDKLTENGCTFHA 134
QY 80 LYSIGASAIYDPTQSPVKPYLGARLSLN--RASVD 113
DB 135 ASLSGLSAIYDFKLGKFKRPYIGARVAGVHRHSID 170

RESULT 6
US-08-988-44-20
Sequence 20, Application US/08988444
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/988,444
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/486,050
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/103/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids

TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-988-444-20

Query Match 15.6%; Score 135; DB 13; Length 170;
Best Local Similarity 26.3%; Pred. No. 1.1e-06;
Matches 41; Conservative 20; Mismatches 47; Indels 48; Gaps 4;

QY 6 ATLIALPALPAALAEAGSGFYVQADAAH-----AKASSLSG-----AKG 45
DB 15 SSLFSSAAQAASEDRSPYVQADLAIAERITHDYPOATGANNSTVSDYFRNIRAH 74
QY 46 FSPRISAGYRINDLRFVAVDYTRYKNY-----KAPSTDFK 79
DB 75 IHPRVSVGYDFGGMRIADYASYRKNNNNKYSVNTKELENKNNKKDKLTENGCTFHA 134
QY 80 LYSIGASATYDDTQSPVRYGARGLSLN--RASVD 113
DB 135 ASSLGSAIYDFKLGKFKRPYIGARVAYGVHRSID 170

RESULT 7
US-09-217-849-20
Sequence 20, Application US/09217849

GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/217,849
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/486,050
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/103/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-09-217-849-20

Query Match 15.6%; Score 135; DB 16; Length 170;
Best Local Similarity 26.3%; Pred. No. 1.1e-06;
Matches 41; Conservative 20; Mismatches 47; Indels 48; Gaps 4;

QY 6 ATLIALPALPAALAEAGSGFYVQADAAH-----AKASSLSG-----AKG 45
DB 15 SSLFSSAAQAASEDRSPYVQADLAIAERITHDYPOATGANNSTVSDYFRNIRAH 74
QY 46 FSPRISAGYRINDLRFVAVDYTRYKNY-----KAPSTDFK 79
DB 75 IHPRVSVGYDFGGMRIADYASYRKNNNNKYSVNTKELENKNNKKDKLTENGCTFHA 134
QY 80 LYSIGASATYDDTQSPVRYGARGLSLN--RASVD 113
DB 135 ASSLGSAIYDFKLGKFKRPYIGARVAYGVHRSID 170

RESULT 8
US-09-489-850-20
Sequence 20, Application US/09489850

GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/489,850
FILING DATE: 24-Jan-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/988,444
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/103/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-489-850-20

Query Match 15.6%; Score 135; DB 18; Length 170;
Best Local Similarity 26.3%; Pred. No. 1.1e-06;
Matches 41; Conservative 20; Mismatches 47; Indels 48; Gaps 4;

QY 6 ATLIALPALPAALAEAGSGFYVQADAAH-----AKASSLSG-----AKG 45
DB 15 SSLFSSAAQAASEDRSPYVQADLAIAERITHDYPOATGANNSTVSDYFRNIRAH 74
QY 46 FSPRISAGYRINDLRFVAVDYTRYKNY-----KAPSTDFK 79
DB 75 IHPRVSVGYDFGGMRIADYASYRKNNNNKYSVNTKELENKNNKKDKLTENGCTFHA 134

[illegible]

```

RESULT 13
US-09-543-681A-7922
: Sequence 7922, Application US/09543681A
: GENERAL INFORMATION:
: APPLICANT: GARY BRETTON
: TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
: TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
: FILE REFERENCE: 2/09.1002-001
: CURRENT APPLICATION NUMBER: US/09/543,681A
: CURRENT FILING DATE: 2000-04-05
: PRIOR APPLICATION NUMBER: US 60/128,706
: PRIOR FILING DATE: 1999-04-09
: NUMBER OF SEQ ID NOS: 8344
: SEQ ID NO 7922
: LENGTH: 384
: TYPE: PRT
: ORGANISM: Proteus mirabilis
US-09-543-681A-7922

```

[illegible]

```

RESULT 14
US-10-082-014-124
; Sequence 124, Application US/10082014
; GENERAL INFORMATION:
; APPLICANT: Birkett, Ashley J.
; TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES STABILIZED WITH AN N-TERMINAL C
; FILE REFERENCE: ICC-130.0.4564/85124
; CURRENT APPLICATION NUMBER: US/10/082.014
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 09/930,915
; PRIOR FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 290
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 124
; LENGTH: 21
; TYPE: PRT

```

```

; ORGANISM Neisseria meningitidis
US-10-082-014-124

Query Match      11.6%; Score 101; DB 24; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.00038;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      153 GKAVTVANNVRSGLSYGVRYK 173
      |||
Db      1 GKAVTVANNVRSGLSYGVRYK 21

```

```

RESULT 15
US-60-358-618-48
; Sequence 48, Application US/60358618
; GENERAL INFORMATION:
; APPLICANT: Birkett, Ashley J.
; TITLE OF INVENTION: STABILIZED HBC CHIMER PARTICLES HAVING MENINGOCOCCAL IMMUNOGEN
; FILE REFERENCE: IC107 (4564/82044)
; CURRENT APPLICATION NUMBER: US/60/358,618
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48
; LENGTH: 21
; TYPE: PRF
; ORGANISM: Neisseria meningitidis
US-60-358-618-48

```

Query Match	11.6%	Score 101	DB 26	Length 21
Best Local Similarity	100.0%	Pred. No. 0	00038	
Matches 21	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	153	GKVTYVANKVNSGELSYGVRYK	173	
DB	1	GKVTYVANKVNSGELSYGVRYK	21	

Search completed: October 28, 2002, 16:11:21
Job time : 106.601 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 28, 2002, 16:01:19 ; Search time 35.6987 Seconds
(without alignments)
1465.185 Million cell updates/sec

Title: US-09-684-883-2
Perfect score: 868
Sequence: 1 MKKALATIALALPAALAE.....VNTYKNVRSGLSVGRVKE 174

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1112697 seqs, 300604653 residues

Total number of hits satisfying chosen parameters: 1112697

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New:*
1: /cgn2_6/ptodata/2/paa/PCF_NEW_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/PCF_NEW_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
6: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
7: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
8: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
9: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
10: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
11: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
12: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*
13: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	868	100.0	174	9	US-09-684-883-2
2	854	98.4	174	9	US-09-684-883-6
3	838.5	96.6	175	9	US-09-684-883-30
4	825	95.0	174	9	US-09-684-883-8
5	824.5	95.0	175	9	US-09-684-883-4
6	133	15.3	25	9	US-10-203-942-9
7	94	10.8	353	11	US-10-219-999-45753
8	89	10.3	187	11	US-10-219-999-59699
9	89	10.3	229	11	US-09-791-537-117254
10	88.5	10.2	576	9	US-09-791-537-117254
11	88.5	10.2	765	9	US-09-791-537-117254
12	87	10.0	16	9	US-09-684-883-15
13	87	10.0	500	9	US-09-990-004A-149
14	87	10.0	500	11	US-10-219-220-149
15	86	9.9	213	9	US-09-791-537-112202
16	85.5	9.9	339	9	US-09-513-966A-67258
17	85.5	9.9	534	9	US-09-513-966A-7956
18	84	9.7	165	9	US-09-540-209B-7537
19	83.5	9.6	576	9	US-09-458-180-2
20	83	9.6	364	9	US-09-545-199F-151

21	82	9.4	433	9	US-09-791-537-118678	Sequence 118678,
22	81	9.3	15	9	US-09-684-883-23	Sequence 23, Appl
23	80.5	9.3	330	9	US-09-120-051C-47	Sequence 47, Appl
24	80.5	9.3	330	9	US-09-120-051D-47	Sequence 47, Appl
25	80.5	9.3	573	9	US-09-540-209B-2271	Sequence 24508, A
26	80.5	9.3	695	9	US-09-791-537-118424	Sequence 8424, Ap
27	80.5	9.3	792	11	US-10-179-131-8424	Sequence 67259, A
28	80	9.2	511	9	US-09-513-966A-67259	Sequence 7957, Ap
29	80	9.2	511	9	US-09-513-966A-7957	Sequence 39219, A
30	80	9.2	369	9	US-09-545-199F-153	Sequence 153, App
31	79.5	9.2	421	9	US-09-791-537-118429	Sequence 114829, A
32	79.5	9.2	431	9	US-09-791-537-128171	Sequence 28171, A
33	79.5	9.2	516	9	US-09-791-537-29175	Sequence 29175, A
34	79.5	9.2	15	9	US-09-684-883-18	Sequence 18, Appl
35	79	9.1	264	9	US-09-956-508A-14	Sequence 4, Appl
36	79	9.1	293	11	US-10-059-964-54	Sequence 54, Appl
37	79	9.1	427	9	US-09-540-209B-6145	Sequence 6145, Ap
38	79	9.1	1114	11	US-10-069-799-1	Sequence 3443, Ap
39	78.5	9.0	189	11	US-10-108-260A-3443	Sequence 3443, Ap
40	78.5	9.0	189	11	US-10-108-260A-3443	Sequence 3443, Ap
41	78.5	9.0	332	11	US-10-193-002-53	Sequence 53, Appl
42	78.5	9.0	652	11	US-10-193-002-350	Sequence 350, App
43	78.5	9.0	802	11	US-10-193-002-209	Sequence 209, App
44	78.5	9.0	802	11	US-10-193-002-346	Sequence 346, App
45	78.5	9.0	802	11	US-10-193-002-346	

ALIGNMENTS

RESULT 1
US-09-684-883-2
Sequence 2, Application US/09684883
GENERAL INFORMATION:
APPLICANT: Brodeur, Bernard R
Martin, Denis
Hamel, Josée
Rioux, Clement
TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
OF NEISSERIA MENINGITIDIS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/684,883
FILING DATE: 06-Oct-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
APPLICATION NUMBER: US 60/001,983
FILING DATE: 04-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 047998/0128
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-684-883-2

Query Match 100.0%; Score 868; DB 9; Length 174;
Best Local Similarity 100.0%; Pred. No. 7.4e-83;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKALATLIALPAAALAEAGSGFYQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
DB 1 MKKALATLIALPAAALAEAGSGFYQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
QY 61 FAVDYTRKKNKAPSTDFKLTSGASATYDFDTPQSPVKPYLGARLSLNRAVDLGSDSF 120
DB 61 FAVDYTRKKNKAPSTDFKLTSGASATYDFDTPQSPVKPYLGARLSLNRAVDLGSDSF 120
QY 121 SQTSGIGLVLAGSYAVTPNVLDAGYRNYIGKVTYKNVRSGLSVGYRVKF 174
DB 121 SQTSGIGLVLAGSYAVTPNVLDAGYRNYIGKVTYKNVRSGLSVGYRVKF 174

RESULT 2

US-09-684-883-6
Sequence 6, Application US/09684883
GENERAL INFORMATION:

APPLICANT: Brodeur, Bernard R

Hamel, Denis
Hamel, Josee
Rioux, Clement

TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
OF NEISSERIA MENINGITIDIS

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/684,883

FILING DATE: 06-Oct-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/913,362

FILING DATE: 13-NOV-1997

APPLICATION NUMBER: US 08/406,362

FILING DATE: 17-MAR-1995

APPLICATION NUMBER: US 60/001,983

FILING DATE: 04-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: Bent, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 047998/0128

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399

TELEFAX: 904136

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 174 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-09-684-883-6

Query Match 98.4%; Score 854; DB 9; Length 174;
Best Local Similarity 98.3%; Pred. No. 2.2e-81;
Matches 171; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKKALATLIALPAAALAEAGSGFYQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
DB 1 MKKALATLIALPAAALAEAGSGFYQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
QY 61 FAVDYTRKKNKAPSTDFKLTSGASATYDFDTPQSPVKPYLGARLSLNRAVDLGSDSF 120
DB 61 FAVDYTRKKNKAPSTDFKLTSGASATYDFDTPQSPVKPYLGARLSLNRAVDLGSDSF 120
QY 121 SQTSGIGLVLAGSYAVTPNVLDAGYRNYIGKVTYKNVRSGLSVGYRVKF 174
DB 121 SQTSGIGLVLAGSYAVTPNVLDAGYRNYIGKVTYKNVRSGLSVGYRVKF 174

RESULT 3

US-09-684-883-30
Sequence 30, Application US/09684883
GENERAL INFORMATION:

APPLICANT: Brodeur, Bernard R

Hamel, Denis
Hamel, Josee
Rioux, Clement

TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
OF NEISSERIA MENINGITIDIS

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/684,883

FILING DATE: 06-Oct-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/913,362

FILING DATE: 13-NOV-1997

APPLICATION NUMBER: US 08/406,362

FILING DATE: 17-MAR-1995

APPLICATION NUMBER: US 60/001,983

FILING DATE: 04-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: Bent, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 047998/0128

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399

TELEFAX: 904136

INFORMATION FOR SEQ ID NO: 30:

SEQUENCE CHARACTERISTICS:

LENGTH: 175 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 30:

US-09-684-883-30

Query Match 96.6%; Score 838.5; DB 9; Length 175;
Best Local Similarity 97.1%; Pred. No. 9.2e-80;
Matches 170; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

```

Db      61 FAVDYTRYKNYKAPSIDFKLYSIGASVYIDFDQTQSPVKPYFGARLSLNRAASHLGSGSDS 120
Oy      121 SOTSIGVLGVTSYAVTPNVDDACGYRNYTGNKYNNKNSGELSGCYRVKF 174
       |::| |||| | ||||||| :|||:|||||:||||| ||||| 
Db      121 SKTAGAGLGVLAGSYANTPNVDLDAGYRYNKYTKNVRSGELSGAYRVKF 174

RESULT 5
US-09-684-883-4
; Sequence 4, Application US/09664883
GENERAL INFORMATION:
APPLICANT: Brodeur, Bernard R
           Martin, Denis
           Hamel, Josee
           Rioux, Clement
TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSER: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/684,883
FILING DATE: 06-Oct-2000
Prior APPLICATION DATA:
APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-Nov-1997
APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
APPLICATION NUMBER: US 60/001,983
FILING DATE: 04-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 04/998/0128
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acids
TYPE: amino acid
MOLECULE TYPE: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-684-883-4

Query Match          95.0%; Score 824.5; DB 9; Length 175;
Best Local Similarity 95.4%; Fred. No. 2.7e-78;
Matches 167; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

Oy      1 MKRALATLLALPAALALEGASGFYYOADAHHAKASSIGSAKGSPRTSAGYRIINDLR 60
       | |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| |
Db      1 MKRLAALLIALPALPAALALEGASGFYYOADAHAHAKASSIGSAKGSPRTISAQYRIINDLR 60

Oy      61 FAVDYTRYKNYK APSTDFKLXYSIGASAIYDPTQSPVKPYTGARLSLNRAASYDLGGSDS 119
       | |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| |
Db      61 FAVDYTRYKNYKVPESTDCKLYSIGASAIYDFQSPVKPYTLGARLSLNRAASYDFNGSDS 120

Oy      120 FSQTSIGLVGVTSYAVTPNVDDLACGYRNYTGNKYNNKNSGELSGCYRVKF 174
       | |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| |
Db      121 FSQTSIGLVGVTSYAVTPNVDDLACGYRNYTGNKYNNKNSGELSGAYRVKF 175

```

```

RESULT 6
US-09-684-883-26
: Sequence 26, Application US/09684883
: GENERAL INFORMATION:
: APPLICANT: Brodeur, Bernard R
:      Martin, Denis
:      Hamel, Josée
:      Roux, Clement
: TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
: NUMBER OF SEQUENCES: 30
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Foley & Lardher
: STREET: 3000 K Street, N.W., Suite 500
: CITY: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20007-5109
: COMPUTER READABLE FORM:
: MEDIUM TYPE: floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/684,883
: FILING DATE: 06-Oct-2000
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/913,362
: FILING DATE: 13-NOV-1997
: APPLICATION NUMBER: US 08/406,362
: FILING DATE: 17-MAR-1995
: APPLICATION NUMBER: US 60/001,583
: FILING DATE: 04-AUG-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Bent, Stephen A.
: REGISTRATION NUMBER: 29,768
: REFERENCE/DOCKET NUMBER: 04/998/0128
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202)672-5300
: TELEFAX: (202)672-5399
: TELEX: 904136
: INFORMATION FOR SEQ ID NO: 26:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 25 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: ORIGINAL SOURCE:
: ORGANISM: Neisseria meningitidis
: STRAIN: 608B
: SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-684-883-26

Query Match      15.3%: Score 133; DB 9; Length 25;
Best Local Similarity 100.0%: Pred. No. 6.1e-07;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY      61 FAVDYTRYKNYKAPSTDFKLYSIGA 85
Db      1 FAVDYTRYKNYKAPSTDFKLYSIGA 25

RESULT 7
US-10-203-942-9
: Sequence 9, Application US/10203942
: GENERAL INFORMATION:
: APPLICANT: BERTHET, FRANCOIS-XAVIER
: APPLICANT: DENOEL, PHILIPPE
: APPLICANT: POOLMAN, JAN
: APPLICANT: THONNARD, JOELLE
: TITLE OF INVENTION: HAEMOPHILUS INFLUENZA OUTER MEMBRANE
: TITLE OF INVENTION: PROTEIN AND USE THEREOF IN VACCINATION

```

```

FILE REFERENCE: B45210
CURRENT APPLICATION NUMBER: US/10/203_942
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: PCT/EP01/01556
PRIOR FILING DATE: 2001-02-13
PRIOR APPLICATION NUMBER: GB 0003502.2
PRIOR FILING DATE: 2000-02-15
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9
LENGTH: 353
TYPE: PRF
ORGANISM: Haemophilus influenzae
US-10-203-942-9

Query Match          10.8% Score 94; DB 11; Length 353;
Best Local Similarity 23.8%; Pred. No. 0.24; Mismatches 93; Indels 40; Gaps 9;
Matches 51; Conservative 30;

QY      1 MKKALATLIALPALPAALAEGA--SGFYVADAAHAHAKASSSLGS-----AKGFS 47
       ||| | : | :::: | : | | | | : | | : | | : | | : | : | : | 
Db     1 MKKTALIALVVAGLAASVAQAAPQNTFTFYAGYKAQGASFHDRLRALREKYGVHRNSFT 60
QY      48 PRISAGYI---NDLRFAV----DYTYKKTKAPSTPFKLXSTA--SAIDPDTOSPV 97
       : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db     61 YGFVGFGYLINNNILGLAVELGYDPFGRAKGREGKITYVKHTNHSTHLSLGSEVLLEG 120
QY      98 KPYIGARLSLNRASVDLGSDSFQSOTSIG-----LGVL-TGVSVAYTPNVLDLAGY-- 147
       | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db    121 DYTGAGAVALVRSDYDKTLNENNSTLKLTGEHHRRASAQLFAVGAEYAIVPELVAFLEYTOW 180
QY     148 -----RNYIGKVNTVKNVRS--GELSVCGRVKE 174
           : | | | | | : | : | : | : | : |
Db    181 LTRVGKYPPODEKPPTALMYNPWICGINAGISYRF 214


RESULT 8
US-10-219-999-45753
Sequence 45753, Application US/10219999
GENERAL INFORMATION:
APPPLICANT: Cao, Yongwei
APPPLICANT: Edgerton, Michael D
APPPLICANT: Hinkle, Gregory J.
APPPLICANT: Kovacic, David K.
APPPLICANT: Liu, Jingdong
APPPLICANT: Stein, Joshua
TITLE OF INVENTION: cDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-10(52726)C
CURRENT APPLICATION NUMBER: US/10/219_999
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: US 60/324,109
PRIOR FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: US 60/312,544
PRIOR FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 63520
SEQ ID NO 45753
LENGTH: 187
TYPE: PRF
ORGANISM: Zea mays
US-10-219-999-45753

Query Match          10.3% Score 89; DB 11; Length 187;
Best Local Similarity 29.2%; Pred. No. 0.35; Mismatches 42; Indels 40; Gaps 5;
Matches 40; Conservative 15;

QY      4 ALATITLALPLAALAEAGSGFYVOADAHAHAKASSSLGSKFSPRISAGYRIINDLRFAV 63
       | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db     82 AAASLYSAIAISSASTGAALASVSAGAAAAGSASLSGASVASGNASATA----- 130
QY      64 DYTRYKNRKAPTDFKLYSIGSAIFYDPTOSPKVPYLCARLSLNRAVDLGDSDFSOT 123
       : | | | | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db    131 -----SASTSTSIDSVSASA-----DTGS-----LATTSVSAAGAAYS----- 164
```


QY 124 SIGGLVLTGVSAYV-TP 139
DB 165 --SFGVSTASMASTP 179

RESULT 9

US-10-219-999-59699
; Sequence 59699, Application US/10219999
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Edgerton, Michael D
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jindong
; APPLICANT: Stein, Joshua
; TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-10(52726)C
; CURRENT APPLICATION NUMBER: US/10/219,999
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 60/324,109
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: US 60/312,544
; PRIOR FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 63520
; SEQ ID NO 59699
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Zea mays
US-10-219-999-59699

Query Match 10.3%; Score 89; DB 11; Length 229;
Best Local Similarity 29.2%; Pred. No. 0.46;
Matches 40; Conservative 15; Mismatches 42; Indels 40; Gaps 5;

QY 4 ALATLALPAALAEAGSGFYVQDAHAHAKASSLSGAKGFSRISAGYRINDLRFAV 63
DB 82 AASLVSAISGSASTGAAASVSAGAAAGSASLSGASASATP----- 130
QY 64 DTRYKNYAPSTDFKLYSGAAYDFDTQSPVPRYLGARLSLRASVDLGSDSFSQT 123
DB 131 -----SASTSTLSDVSASA-----DTGS-----LAATTSVSAAGAAVS----- 164
QY 124 SIGGLVLTGVSAYV-TP 139
DB 165 --SFGVSTASMASTP 179

RESULT 10

US-09-791-537-117254
; Sequence 117254, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Biocomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 117254
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
US-09-791-537-117254

Query Match 10.2%; Score 88.5; DB 9; Length 576;
Best Local Similarity 24.6%; Pred. No. 1.7;
Matches 42; Conservative 29; Mismatches 59; Indels 41; Gaps 9;
QY 19 AEGASGFYVQADA-----AHAKASSLSGS-AKGFSPRISA-GYRINDLRFAVDYTR 67
DB 165 --SFGVSTASMASTP 179

DB 432 ASADTKFAATADATYKNGNATYKNAKSITDGTGKVDGDFGRVTAIDTKVNA----- 483

QY 68 YKNYKAPSTDFKLYSGAAYDFDTQSPV-----KPLIGARLSLRASVDLGSDSFSQT 123

DB 484 --DTRYKNYAPSTDFKLYSGAAYDFDTQSPVPRYLGARLSLRASVDLGSDSFSQT 123

QY 124 SIGGLVLTGVSAYVTPVNDLDAGYRNYIKGNTKVNVRSGELSGYRVE 174
DB 539 AIGAG-----YRVPNPLAFKAG-----AINTSGN-KKGSYINIGVYEF 576

RESULT 11

US-09-791-537-22674
; Sequence 22674, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Biocomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22674
; LENGTH: 765
; TYPE: PRT
; ORGANISM: Synechocystis sp
US-09-791-537-22674

Query Match 10.2%; Score 88.5; DB 9; Length 765;
Best Local Similarity 26.1%; Pred. No. 2.5;
Matches 29; Conservative 20; Mismatches 49; Indels 13; Gaps 4;

QY 46 FSPRISAGYRINDLRFAVDYTRYKNYAPSTDFKLYSGAAYDFDTQSPVPRYLGARL 105
DB 630 FEPIY--GARLINLSPALDQT--TNYRNSLSVL--AGQFOINETASRTWINDLVGCKL 683
QY 106 SLNRASV-----DLGSDSFSQTSIGGLVLTGVSAYVTPVNDLDAGYR 149
DB 684 GVQLTDLTALMLRGDVSQFSLGSDWMMNALIGLDYVRENAIQGYRF 734

RESULT 12

US-09-684-883-15
; Sequence 15, Application US/09684883
; GENERAL INFORMATION:
; APPLICANT: Brodeur, Bernard R
; APPLICANT: Hamel, Joseph
; APPLICANT: Rioux, Clement
; TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
; TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/684,883
; FILING DATE: 06-Oct-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/913,362
; FILING DATE: 13-Nov-1997

APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
APPLICATION NUMBER: US 60/001,983
FILING DATE: 04-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 04/998/0128
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Neisseria meningitidis
STRAIN: 608B
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-684-883-15

Query Match 10.0%; Score 87; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 FAVDYTRYKNYKAPST 76
DB 1 FAVDYTRYKNYKAPST 16

RESULT 13
US-09-990-004A-149
Sequence 149, Application US/09990004A
GENERAL INFORMATION:
APPLICANT: Flihn, Barry
TITLE OF INVENTION: Methods for Modulating Cellular Development and Programmed Cell De
FILE REFERENCE: 11000.103861
CURRENT APPLICATION NUMBER: US/09/990,004A
CURRENT FILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: US 09/327,373
PRIOR FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 204
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 149
LENGTH: 500
TYPE: PRT
ORGANISM: Eucalyptus grandis
US-09-990-004A-149

Query Match 10.0%; Score 87; DB 9; Length 500;
Best Local Similarity 23.7%; Pred. No. 2.1;
Matches 41; Conservative 19; Mismatches 81; Indels 32; Gaps 4;

QY 4 ALATLIALPALAALAEASGFYQADAAHAKASSLSGAKGFSPTISAGYRI-----56
DB 32 AAVALALALALTITIASALDMSIVSYDRAGDRSSSSSSWRSDDEVMAYYESWLAKHGK 91
QY 57 -----NDLRFAY--DYTRYKNYKAPSTDFKLYSIGASAIYEDTQSPVKPYLGARLSL 107
DB 92 AYNALGEKEKRFQYFKNLRFIDHNGGD--RTYVGLNGFADLTNEYRSMTLGARMOR 150
QY 108 NRASVDLGSDSFSQTSIGLVGVSAYTPNVDLDAGRYNYNIGKYNVYKN 160
DB 151 SGRRLGRARSD-----RYAVALAGEELPASVDMRREGAVVDVKD 188

RESULT 14
US-10-219-220-149
Sequence 149, Application US/10219220

GENERAL INFORMATION:
APPLICANT: Flihn, Barry
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: death and their use in the modification of plant development
FILE REFERENCE: 11000.102261
CURRENT APPLICATION NUMBER: US/10/219,220
CURRENT FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: U.S. No. 09/325,932
PRIOR FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 299
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 149
LENGTH: 500
TYPE: PRT
ORGANISM: Eucalyptus grandis
US-10-219-220-149

Query Match 10.0%; Score 87; DB 11; Length 500;
Best Local Similarity 23.7%; Pred. No. 2.1;
Matches 41; Conservative 19; Mismatches 81; Indels 32; Gaps 4;

QY 4 ALATLIALPALAALAEASGFYQADAAHAKASSLSGAKGFSPTISAGYRI-----56
DB 32 AAVALALALALTITIASALDMSIVSYDRAGDRSSSSSSWRSDDEVMAYYESWLAKHGK 91
QY 57 -----NDLRFAY--DYTRYKNYKAPSTDFKLYSIGASAIYEDTQSPVKPYLGARLSL 107
DB 92 AYNALGEKEKRFQYFKNLRFIDHNGGD--RTYVGLNGFADLTNEYRSMTLGARMOR 150
QY 108 NRASVDLGSDSFSQTSIGLVGVSAYTPNVDLDAGRYNYNIGKYNVYKN 160
DB 151 SGRRLGRARSD-----RYAVALAGEELPASVDMRREGAVVDVKD 188

RESULT 15
US-09-791-537-112202
Sequence 112202, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Biomomix, Inc.
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 112202
LENGTH: 213
TYPE: PRT
ORGANISM: Brucella canis
US-09-791-537-112202

Query Match 9.9%; Score 86; DB 9; Length 213;
Best Local Similarity 25.3%; Pred. No. 0.85;
Matches 47; Conservative 32; Mismatches 71; Indels 34; Gaps 9;

QY 14 PAALAEASGFYQADAAHAKASSLSGAKGFSPTISAGYRI-----GYRINDLRFAYDYTRYK 69
DB 41 PYSWAGGTGTGLTYLGYGNKKAK--TSTVGSINPDDMKAKAFAGWNPQKQIYVYEGDAGY 99
QY 70 NYKAPSTD-----FKLYSIGASAIYEDTQSPVKPYL-----GARLSINRASVDLGGS 117
DB 100 SWAKSKSGDLEVKQGFEE--GLSLARVGYDL--NPWMPYLTGAGISQIKLN-----NGL 149
QY 118 DSFSQTSIGLVGVSAYTPNVDLDAGYRI-----NYIGKYNVYKN--VRSGLSISGV 170
DB 150 DGSKFRVGTAGGLEAKLDNLTIGRVEYRYTOYSNKNYDLACTYTNKLDTDIDIRGI 209
QY 171 RYKF 174

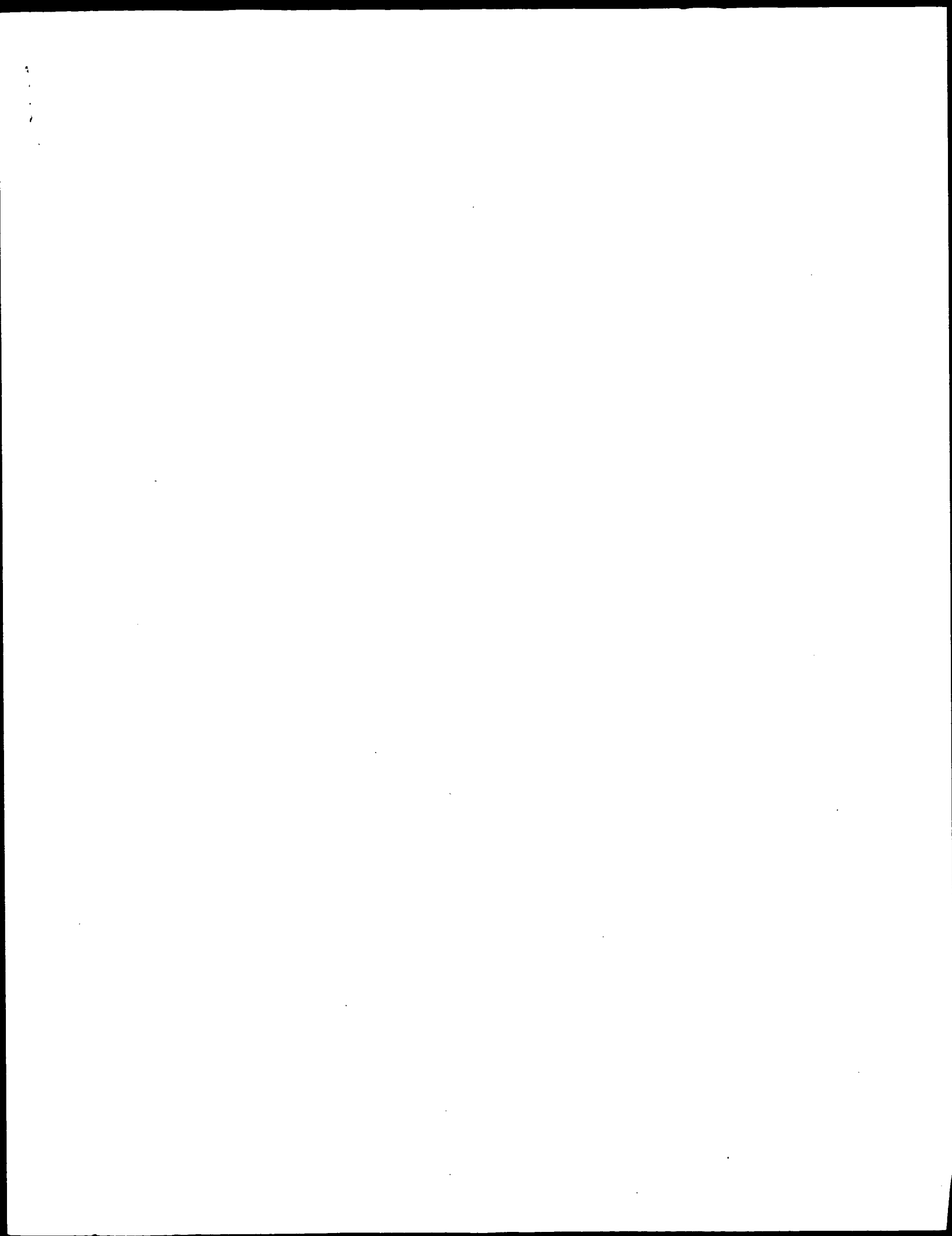
Tue Oct 29 09:23:07 2002

us-09-684-883-2.rapn

Page 7

Db 210 GYKF 213

Search completed: October 28, 2002, 16:13:49
Job time : 36.6987 secs



GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 28, 2002, 16:00:44 ; Search time 104.197 Seconds

(without alignments)
591.158 Million cell updates/sec

Title: US-09-684-883-4

Sequence: 1 MKKALALIALALPAALAE.....VNTKVNRSGLSGAVRK 175

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Pending_Patents_AA_Main:*
1: /cgn2_6/ptodata/1/paa/PCMS.COMB.pep:*
2: /cgn2_6/ptodata/1/paa/US06.COMB.pep:*
3: /cgn2_6/ptodata/1/paa/US07.COMB.pep:*
4: /cgn2_6/ptodata/1/paa/US08.COMB.pep:*
5: /cgn2_6/ptodata/1/paa/US081.COMB.pep:*
6: /cgn2_6/ptodata/1/paa/US082.COMB.pep:*
7: /cgn2_6/ptodata/1/paa/US083.COMB.pep:*
8: /cgn2_6/ptodata/1/paa/US084.COMB.pep:*
9: /cgn2_6/ptodata/1/paa/US085.COMB.pep:*
10: /cgn2_6/ptodata/1/paa/US086.COMB.pep:*
11: /cgn2_6/ptodata/1/paa/US087.COMB.pep:*
12: /cgn2_6/ptodata/1/paa/US088.COMB.pep:*
13: /cgn2_6/ptodata/1/paa/US089.COMB.pep:*
14: /cgn2_6/ptodata/1/paa/US090.COMB.pep:*
15: /cgn2_6/ptodata/1/paa/US091.COMB.pep:*
16: /cgn2_6/ptodata/1/paa/US092.COMB.pep:*
17: /cgn2_6/ptodata/1/paa/US093.COMB.pep:*
18: /cgn2_6/ptodata/1/paa/US094.COMB.pep:*
19: /cgn2_6/ptodata/1/paa/US095.COMB.pep:*
20: /cgn2_6/ptodata/1/paa/US096.COMB.pep:*
21: /cgn2_6/ptodata/1/paa/US097.COMB.pep:*
22: /cgn2_6/ptodata/1/paa/US098.COMB.pep:*
23: /cgn2_6/ptodata/1/paa/US099.COMB.pep:*
24: /cgn2_6/ptodata/1/paa/US100.COMB.pep:*
25: /cgn2_6/ptodata/1/paa/US101.COMB.pep:*
26: /cgn2_6/ptodata/1/paa/US60.COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	824.5	94.3	174	8	US-08-406-362-2
2	824.5	94.3	174	22	US-09-870-759-36
3	138.5	15.8	170	8	US-08-479-520-20
4	138.5	15.8	170	8	US-08-486-050-20
5	138.5	15.8	170	8	US-08-486-050A-20
6	138.5	15.8	170	13	US-08-988-444-20
7	138.5	15.8	170	16	US-09-217-849-20

8	138.5	15.8	170	18	US-09-489-850-20	Sequence 20, Appl
9	128	14.6	281	21	US-09-739-449-11638	Sequence 11638, A
10	128	14.6	281	22	US-09-803-110-11638	Sequence 11638, A
11	116	13.3	187	18	US-09-489-039A-13699	Sequence 13699, A
12	114.5	13.1	98	19	US-09-540-236-2245	Sequence 2245, Ap
13	107.5	12.3	190	19	US-09-543-681A-7684	Sequence 7684, Ap
14	104	11.9	487	17	US-09-328-352-5331	Sequence 5331, Ap
15	101.5	11.6	217	16	US-09-252-691C-9162	Sequence 9162, Ap
16	101.5	11.6	217	16	US-09-252-691C-9162	Sequence 9162, Ap
17	101	11.6	21	24	US-10-082-014-124	Sequence 124, Ap
18	101	11.6	21	26	US-09-358-618-47	Sequence 47, Appl
19	99.5	11.4	257	1	PCT-US02-03987-13845	Sequence 13845, A
20	99.5	11.4	257	22	US-09-815-242-13845	Sequence 13845, A
21	99.5	11.4	257	24	US-10-072-851-13845	Sequence 13845, A
22	98.5	11.3	643	17	US-09-328-352-5146	Sequence 5146, Ap
23	97	11.1	21	24	US-10-082-014-124	Sequence 124, Ap
24	97	11.1	21	26	US-09-358-618-48	Sequence 48, Appl
25	97	11.1	384	19	US-09-543-681A-7922	Sequence 7922, Ap
26	95.5	10.9	212	1	PCT-US02-03987-10149	Sequence 10149, A
27	95.5	10.9	212	22	US-09-815-242-10149	Sequence 10149, A
28	95.5	10.9	212	24	US-10-072-851-10149	Sequence 10149, A
29	95.5	10.9	568	7	US-08-331-393-5	Sequence 5, Appl
30	95	10.9	955	24	US-10-015-127-11706	Sequence 11706, A
31	93.5	10.7	350	14	US-09-080-025-3	Sequence 3, Appl
32	93.5	10.7	351	16	US-09-252-991A-30094	Sequence 30094, A
33	93.5	10.7	359	4	US-08-065-442-2	Sequence 2, Appl
34	93.5	10.7	359	8	US-08-457-997A-2	Sequence 2, Appl
35	93.5	10.7	359	8	US-08-457-997A-2	Sequence 2, Appl
36	93.5	10.7	359	8	US-08-457-997A-2	Sequence 2, Appl
37	93.5	10.7	359	18	US-09-451-184-2	Sequence 2, Appl
38	93.5	10.7	369	18	US-09-418-980-10	Sequence 10, Appl
39	93.5	10.7	369	19	US-09-506-078-46	Sequence 46, Appl
40	93.5	10.7	369	19	US-09-545-159C-153	Sequence 153, App
41	93.5	10.7	369	19	US-09-545-159D-153	Sequence 153, App
42	93.5	10.7	369	22	US-09-809-665A-153	Sequence 46, Appl
43	93.5	10.7	369	26	US-09-418-980-46	Sequence 46, Appl
44	90	10.3	215	18	US-09-418-980-46	Sequence 4, Appl
45	90	10.3	215	19	US-09-506-078-44	Sequence 44, Appl

ALIGNMENTS

RESULT 1
US-08-406-362-2
Sequence 2, Application US/08406362
GENERAL INFORMATION:
APPLICANT: Brodeur, Bernard R
APPLICANT: Martin, Denis
TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/406,362
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr, James F
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: Pharma-43

TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-406-362-2

Query Match
Best Local Similarity 94.3%; Score 824.5; DB 8; Length 174;
Matches 167; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 1 MKKALALIALPAAALAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
DB 1 MKKALATLIALPAAALAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
QY 61 FAVDYTRYKNKYKVPSTDFELYSIGASAIYDFDTQSPVPRYLGARLSLRASVDNGSDS 120
DB 61 FAVDYTRYKNKYK-APSTDRLKYSIGASAIYDFDTQSPVPRYLGARLSLRASVDLGGSDS 119
QY 121 FSQTSIGLVLAGVSYAVTPNVDLDAGYRYNYIGKYNIVKVRSGELSGAVRYKF 175
DB 120 FSQTSIGLVLAGVSYAVTPNVDLDAGYRYNYIGKYNIVKVRSGELSGAVRYKF 174

RESULT 2
US-09-870-759-36
Sequence 36, Application US/09870759
GENERAL INFORMATION:
APPLICANT: TERMAN, David S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REFERENCE: 870759
CURRENT APPLICATION NUMBER: US/09/870,759
CURRENT FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: US 60/208,128
PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 166
SOFTWARE: PatentIn version 3.1
SEQ ID NO 36
LENGTH: 174
TYPE: PRT
ORGANISM: Neisseria meningitidis
US-09-870-759-36

Query Match
Best Local Similarity 94.3%; Score 824.5; DB 22; Length 174;
Matches 167; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 1 MKKALALIALPAAALAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
DB 1 MKKALATLIALPAAALAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
QY 61 FAVDYTRYKNKYKVPSTDFELYSIGASAIYDFDTQSPVPRYLGARLSLRASVDNGSDS 120
DB 61 FAVDYTRYKNKYK-APSTDRLKYSIGASAIYDFDTQSPVPRYLGARLSLRASVDLGGSDS 119
QY 121 FSQTSIGLVLAGVSYAVTPNVDLDAGYRYNYIGKYNIVKVRSGELSGAVRYKF 175
DB 120 FSQTSIGLVLAGVSYAVTPNVDLDAGYRYNYIGKYNIVKVRSGELSGAVRYKF 174

RESULT 3
US-08-479-520-20
Sequence 20, Application US/08479520
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF

NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,520
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/105/INB1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-479-520-20

Query Match
Best Local Similarity 15.8%; Score 138.5; DB 8; Length 170;
Matches 42; Conservative 19; Mismatches 48; Indels 47; Gaps 4;

QY 6 AALIALPAAALAGSGFYVQADAAH-----AKASSLSG-----AKG 45
DB 15 SLSFSSAAQASSEDPRSPTVQDLAYAAERITHYPOATGANNTSTVDYRNRRAHS 74
QY 46 FSPRISAGYRINDLRFVADYTRYKNY-----KQVPSTDFK 80
DB 75 IHPRVSVGDFGWRADYASYRRKMNWNNKYSVNTKELENKHNKKDKLTENGTFEHA 134
QY 81 LYSTGASAIYDFDTQSPVPRYLGARLSLN--RASVD 114
DB 135 ASSLSGSAIYDFKLGKRPYIGARVAVGHVRSID 170

RESULT 4
US-08-486-050-20
Sequence 20, Application US/08486050
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,050
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/103/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-486-050-20

Query Match 15.8%; Score 138.5; DB 8; Length 170;
Best Local Similarity 26.9%; Pred. No. 1e-06;
Matches 42; Conservative 19; Mismatches 48; Indels 47; Gaps 4;

QY 6 AALIALPAAALAEAGSGFYVQADAAH-----AKASSLSG-----AKG 45
DB 15 SSLFSSAAQAASEDRSPYVQADLAFAERITHDYPOATGANNTSTVSDYFRNIRAH 74
QY 46 FSPRISAGYRINDLRFADVTRYKNY-----KQVSTDFK 80
DB 75 IHRPVSVGYDFGGRILADYASTRKNNNNKYSVNTELEKHNKKDKLTENGCTFHA 134
QY 81 LYSIGASAIYDFDQSPVKPYLGARLSLN--RASVD 114
DB 135 ASSIGLSAIYDFKLGKFKPYIGARVAVGHVRSID 170

RESULT 5
US-08-486-050A-20
Sequence 20, Application US/08486050A
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,050A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/103/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-486-050A-20

Query Match 15.8%; Score 138.5; DB 8; Length 170;
Best Local Similarity 26.9%; Pred. No. 1e-06;
Matches 42; Conservative 19; Mismatches 48; Indels 47; Gaps 4;

QY 6 AALIALPAAALAEAGSGFYVQADAAH-----AKASSLSG-----AKG 45
DB 15 SSLFSSAAQAASEDRSPYVQADLAFAERITHDYPOATGANNTSTVSDYFRNIRAH 74
QY 46 FSPRISAGYRINDLRFADVTRYKNY-----KQVSTDFK 80
DB 75 IHRPVSVGYDFGGRILADYASTRKNNNNKYSVNTELEKHNKKDKLTENGCTFHA 134
QY 81 LYSIGASAIYDFDQSPVKPYLGARLSLN--RASVD 114
DB 135 ASSIGLSAIYDFKLGKFKPYIGARVAVGHVRSID 170

RESULT 6
US-08-988-444-20
Sequence 20, Application US/08988444
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/988,444
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/486,050
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/103/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids

; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: unknown
 US-08-988-444-20

Query Match	15.8%;	Score 138.5;	DB 13;	Length 170;
Best Local Similarity	26.9%;	Pred. No. 1e-06;		
Matches	42;	Conservative	19;	Mismatches 48;
			Indels	47;
			Gaps	4;

[illegible]

RESULT 7

US-09-217-849-20
; Sequence 20, Application US/09217849

GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THERIETIC
TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:

Query Match	15.8%;	Score 138.5;	DB 16;	Length 170;
Best Local Similarity	26.9%;	Pred. No. 1e-06;		
Matches 42;	Conservative 19;	Mismatches 48;	Indels 47;	Gaps 4;

```
QY      6 AALIALALPAALAEASGEFYVQADAAH-----AKSSSLGS-----AKG 45
Db      15 SLLFSFSAQAASEDRSRSPYQADLAVALAERLTHDYPOATGANNTSTVSDFERNIRAHS 74
QY      46 FSPISAGRYINDLRRAVDYTRYKNY-----KQVSTDFK 80
Db      75 IHRPVSYGVIDFGWRILADYASYRKMNNNKYSVTKLEKNHNKKDKLTENQNGTFPHA 134
QY      81 LYSIGASAIYDFDQSPPVYPYLGARLSLN--RASVD 114
Db      135 ASSTGLSATIYDFRLKGFRFPYIGARVAAGVHRHSID 170
```

RESULT 8
ITS-09-489-850-20

; Sequence 20, Application US/09489850

GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
SHARMA, Lawrence Rajendra
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
NUMBER OF SEQUENCES: 75

Query Match	15.8%;	Score 138.5;	DB 18;	Length 170;
Best Local Similarity	26.9%;	Pred. No. 1e-06;		
Matches 42;	Conservative 19;	Mismatches 48;	Indels 47;	Gaps 4

```
QY      6 AATIALAPPAALAGASGEVVOADAH-----AKSSISGS-----AKG 45  
       ::::|P::::||::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
Db     15 SLLSESAQAAMSEDREBPYYOADLVAERITHDYPOATGANNTSYSDYFRITRAHS 74  
  
QY     46 FSPRISACGRINDLEAFANDYRYKNT-----KOVSIDFK 80  
       ||:||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
Db     75 IHRPVSGVDGEGWILADVASTYRNANNTKYSVNTELENKHNNKKDKLTENOENGFFHA 13
```


Matches 50; Conservative 24; Mismatches 61; Indels 36; Gaps 9;

Search completed: October 28, 2002, 16:11:22
Job time : 105.197 secs

Search completed: October 28, 2002, 16:11:22
Job time : 105.197 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 28, 2002, 16:01:19 ; Search time 35.9039 Seconds

(without alignments)
1465.185 Million cell updates/sec

Title: US-09-684-883-4

Perfect score: 874
Sequence: 1 MKKALALALALPAALAE.....VTVKNSGSELSAGVRYKF 175

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1112697 segs, 300604653 residues

Total number of hits satisfying chosen parameters: 1112697

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/2/paa/PCF_NEW_COMB.pep.*
2: /cgn2_6/ptodata/2/paa/PCF_NEW_COMB.pep1.*
3: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep.*
4: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep.*
5: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep.*
6: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep1.*
7: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep.*
8: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep.*
9: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep1.*
10: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep.*
11: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep1.*
12: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep.*
13: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep1.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	874	100.0	175	US-09-684-883-4	Sequence 4, Appl
2	843	96.5	175	US-09-684-883-30	Sequence 30, Appl
3	838.5	95.9	174	US-09-684-883-6	Sequence 6, Appl
4	824.5	94.3	174	US-09-684-883-2	Sequence 2, Appl
5	813.5	93.1	174	US-09-684-883-8	Sequence 8, Appl
6	118.5	13.6	25	US-09-684-883-26	Sequence 26, Appl
7	93.5	10.7	353	US-10-203-942-9	Sequence 9, Appl
8	93.5	10.7	350	US-09-545-199F-153	Sequence 153, App
9	89.5	10.2	500	US-09-990-004A-149	Sequence 149, App
10	89.5	10.2	500	US-10-219-220-149	Sequence 149, App
11	87.5	10.0	229	US-10-219-999-99699	Sequence 35699, A
12	86.5	9.9	213	US-09-791-537-112202	Sequence 112202,
13	86.5	9.9	431	US-09-540-209B-7041	Sequence 7041, Ap
14	86.5	9.9	501	US-09-540-209B-7077	Sequence 7077, Ap
15	86	9.8	332	US-10-193-002-53	Sequence 53, Appl
16	86	9.8	364	US-09-545-199F-151	Sequence 151, App
17	86	9.8	652	US-10-193-002-250	Sequence 350, App
18	86	9.8	765	US-09-791-537-22674	Sequence 22674, A
19	86	9.8	802	US-10-193-002-209	Sequence 209, App
20	86	9.8	802	US-10-193-002-346	Sequence 346, App

21	85.5	9.8	490	US-09-791-537-119822	Sequence 119822,
22	85	9.7	334	US-10-206-576-106	Sequence 106, App
23	85	9.7	471	US-09-791-537-52271	Sequence 52271, A
24	83	9.5	396	US-10-179-131-9383	Sequence 9383, Ap
25	83	9.5	634	US-09-791-537-98668	Sequence 58668, A
26	83	9.5	634	US-09-791-537-99400	Sequence 99400, A
27	82.5	9.4	634	US-09-791-537-99401	Sequence 99401, A
28	82.5	9.4	187	US-10-219-999-45753	Sequence 45753, A
29	82.5	9.4	228	US-09-791-537-67314	Sequence 67314, A
30	82	9.4	243	US-10-053-853A-1674	Sequence 1674, Ap
31	81	9.3	15	US-09-684-883-23	Sequence 23, Appl
32	81	9.3	641	US-10-108-605-61	Sequence 61, Appl
33	80.5	9.2	421	PCT-US02-12532-123	Sequence 123, App
34	80	9.2	581	US-09-513-996A-64105	Sequence 64105, A
35	80	9.2	645	US-09-513-996A-64105	Sequence 64105, A
36	79.5	9.1	390	US-09-791-537-89799	Sequence 89799, A
37	79.5	9.1	433	US-09-791-537-118678	Sequence 118678,
38	79.5	9.1	527	US-09-791-537-108323	Sequence 108323,
39	79.5	9.1	2214	US-60-360-039-22147	Sequence 22147, A
40	79	9.0	15	US-09-684-883-18	Sequence 18, Appl
41	79	9.0	294	US-09-513-996A-13642	Sequence 13642, A
42	79	9.0	294	US-09-513-996A-58290	Sequence 58290, A
43	79	9.0	339	US-09-513-996A-67258	Sequence 67258, A
44	79	9.0	385	US-09-513-996A-13641	Sequence 13641, A
45	79	9.0	385	US-09-513-996A-58289	Sequence 58289, A

ALIGNMENTS

RESULT 1
US-09-684-883-4
Sequence 4, Application US/09684883
GENERAL INFORMATION:
APPLICANT: Brodeur, Bernard R
Martlin, Denis
Hamel, Josee
Roux, Clement
TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
OF NEISSERIA MENINGITIDIS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/684,883
FILING DATE: 06-Oct-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
APPLICATION NUMBER: US 60/001,983
FILING DATE: 04-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 047998/0128
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:

LENGTH: 175 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-684-883-4

Query Match 100.0%; Score 874; DB 9; Length 175;
Best Local Similarity 100.0%; Pred. No. 9, 1e-84;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKALALIALALPAALALAEAGSGFYQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
DB 1 MKKALALIALALPAALALAEAGSGFYQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
QY 61 FAVDYTRYKNYKQVSTDFKLYSGASAIYDPTQSPVRYKPYLGARLSLNRAVDGSDS 120
DB 61 FAVDYTRYKNYKQVSTDFKLYSGASAIYDPTQSPVRYKPYLGARLSLNRAVDGSDS 120
QY 121 FSQSTGLGVLAGVSYAVTPNVLDAGRYRNYIGKVTYKVRSGELSGAGRYVRF 175
DB 121 FSQSTGLGVLAGVSYAVTPNVLDAGRYRNYIGKVTYKVRSGELSGAGRYVRF 175

RESULT 2
US-09-684-883-30

Sequence 30, Application US/09684883
GENERAL INFORMATION:

APPLICANT: Brodeur, Bernard R

Hamel, Josee
Rioux, Clement

TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/684,883

FILING DATE: 06-Oct-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/913,362

FILING DATE: 13-NOV-1997

APPLICATION NUMBER: US 08/406,362

FILING DATE: 17-MAR-1995

APPLICATION NUMBER: US 60/001,983

FILING DATE: 04-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: Bent, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 047998/0128

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 30:

SEQUENCE CHARACTERISTICS:

LENGTH: 175 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 30:

US-09-684-883-30

Query Match 96.5%; Score 843; DB 9; Length 175;
Best Local Similarity 96.6%; Pred. No. 1,7e-80;
Matches 169; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MKKALALIALALPAALALAEAGSGFYQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
DB 1 MKKALALIALALPAALALAEAGSGFYQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
QY 61 FAVDYTRYKNYKQVSTDFKLYSGASAIYDPTQSPVRYKPYLGARLSLNRAVDGSDS 120
DB 61 FAVDYTRYKNYKQVSTDFKLYSGASAIYDPTQSPVRYKPYLGARLSLNRAVDGSDS 120
QY 121 FSQSTGLGVLAGVSYAVTPNVLDAGRYRNYIGKVTYKVRSGELSGAGRYVRF 175
DB 121 FSQSTGLGVLAGVSYAVTPNVLDAGRYRNYIGKVTYKVRSGELSGAGRYVRF 175

RESULT 3
US-09-684-883-6

Sequence 6, Application US/09684883
GENERAL INFORMATION:

APPLICANT: Brodeur, Bernard R

Hamel, Josee
Rioux, Clement

TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/684,883

FILING DATE: 06-Oct-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/913,362

FILING DATE: 13-NOV-1997

APPLICATION NUMBER: US 08/406,362

FILING DATE: 17-MAR-1995

APPLICATION NUMBER: US 60/001,983

FILING DATE: 04-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: Bent, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 047998/0128

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 174 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-09-684-883-6

Query Match 95.9%; Score 838.5; DB 9; Length 174;

Best Local Similarity 97.1%; Pred. No. 4.9e-80;

Matches 170; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

RESULT 6
US-09-684-883-26
; Sequence 26, Application US/09684883
; GENERAL INFORMATION:
; APPLICANT: Brodeur, Bernard R
; Hamel, Denis
; Hamel, Josée
; Rioux, Clement
; TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
; OF NEISSERIA MENINGITIDIS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/684,883
; FILING DATE: 06-Oct-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/913,362
; FILING DATE: 13-NOV-1997
; APPLICATION NUMBER: US 08/406,362
; FILING DATE: 17-MAR-1995
; APPLICATION NUMBER: US 60/001,983
; FILING DATE: 04-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 047998/0128
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Neisseria meningitidis
; STRAIN: 608B
; SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-684-883-26
Query Match 13.6%; Score 118.5; DB 9; Length 25;
Best Local Similarity 92.3%; Pred. No. 1.9e-05;
Matches 24; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
OY 61 FAVDYTRYKNKQVSTDFKLYSIGA 86
DB 1 FAVDYTRYKNK-APSTDFKLYSIGA 25
RESULT 7
US-10-203-942-9
; Sequence 9, Application US/10203942
; GENERAL INFORMATION:
; APPLICANT: BERTHE, FRANCOIS-XAVIER
; APPLICANT: DEMOEL, PHILIPPE
; APPLICANT: POOLMAN, JAN
; APPLICANT: THONNARD, JOELLE
; TITLE OF INVENTION: HAEMOPHILUS INFLUENZA OUTER MEMBRANE
; PROTEIN AND USE THEREOF IN VACCINATION

FILE REFERENCE: B45210
; CURRENT APPLICATION NUMBER: US/10/203,942
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: PCT/EP01/01556
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: GB 0003502.2
; PRIOR FILING DATE: 2000-02-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-10-203-942-9
Query Match 10.7%; Score 93.5; DB 11; Length 353;
Best Local Similarity 24.9%; Pred. No. 0.27;
Matches 54; Conservative 29; Mismatches 89; Indels 45; Gaps 10;
OY 1 MKKALALIALALPAALAEGA---SGFYQADAAHAKASSLSGS-----AKGFS 47
DB 1 MKKALALVAVGAAASVAQAAPQENTFYAGVKAGQASHDGLALAREYKVGYHRNSFT 60
OY 48 PRISAGYRI---NDIRPAV-----DYTRYKNKQVSTDFKLYSIGA--SATYDFTQSP 97
DB 61 YGVFGYQIILNQNNLGLAVELGYDDFCRAKG-REKGTIVVHTNHTLSIKGSYEVLHG 119
OY 98 VKPYGLARLSINRASVDNGSDSFQSTGTG-----VLASYATPVRVDAG 147
DB 120 LDVYKAGVALVR--DYKLNENSTLTKLGEHHRARASGLFVAGETAVLPPLAVRL 177
OY 148 Y-----RYNYIGKVTNVKVR--GELSAGVRKF 175
DB 178 YQMLFRVGKVRPQDKPNTALVYNPMWISINMGISYRF 214
RESULT 8
US-09-545-199F-153
; Sequence 153, Application US/09545199F
; GENERAL INFORMATION:
; APPLICANT: Lowery E., David
; APPLICANT: Fuller E., Troy
; APPLICANT: Kennedy J., Michael
; TITLE OF INVENTION: Anti-Bacterial Vaccine Compositions
; FILE REFERENCE: 28341/6227.NCP
; CURRENT APPLICATION NUMBER: US/09/545,199F
; CURRENT FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/153,453
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/128,689
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 153
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Actinobacillus pleuropneumoniae
US-09-545-199F-153
Query Match 10.7%; Score 93.5; DB 9; Length 369;
Best Local Similarity 23.2%; Pred. No. 0.28;
Matches 54; Conservative 34; Mismatches 78; Indels 67; Gaps 12;
OY 1 MKKALALIALALPAALAEGA---SGFYQADAAHAKASSLSGSK-GFSPRI---SAG 53
DB 1 MKKSLVALAVLS--AAAVQAAPQONTFYAGAKVGOSSFFHGVGNLKGCHDRYNDKTRK 58
OY 54 YINIDLRFAVDYTRYKNKQVSTDFKLYSIGASAIYDF-----DT 94
DB 59 YGIN--RNSVTYGVFGYQIILNQNNF---GLAAELGYDYVGRVGNVDFRTVHSAHGL 113
OY 95 QSPVVK-----YIGARLSINRASVDNGSDSFQSTGTGLGLV-----AGSYA 137

; SOFTWARE: PatentIn version 3.0

```

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000
1001
1002
1003
1004
1005
1006
1007
1008
1009
1010
1011
1012
1013
1014
1015
1016
1017
1018
1019
1020
1021
1022
1023
1024
1025
1026
1027
1028
1029
1030
1031
1032
1033
1034
1035
1036
1037
1038
1039
1040

```

SEQ ID NO 112202
 LENGTH: 213
 TYPE: PRT
 ORGANISM: Brucella canis
 US-09-791-537-112202

Query Match
 Best Local Similarity 26.5%; Score 86.5; DB 9; Length 213;
 Matches 49; Conservative 30; Mismatches 71; Indels 35; Gaps 10;

QY 14 PAAALAGAGFYVQADAHAKASSLSGAKGSPRISA-----GYRINDLRFAVD---Y 65
 DB 41 PYSWAGAGFYVQADAHAKASSLSGAKGSPRISA-----GYRINDLRFAVD---Y 65
 QY 66 TRKNTYQVSTDEKLT---YSASAIYDEDTQSPVKPYL-----GARSLNRSYDFNG 117
 DB 100 SNAKSD--GLEVKQGFESGLRVRGYDL--NPWAPYTLGAIASQIKLN-----NG 148
 QY 118 SDSPSTSTGLVAGSYAVTPNVDLAGRY-----NYIGKVTYKN-VRSGLSAG 170
 DB 149 LDGSEKFRVGMTAGAGLEAKLTDLNIGRVEYRTQYSNNKYDLAGTTRKLDLTDIRVG 208
 QY 171 VRXAF 175
 DB 209 IGYKF 213

RESULT 13
 US-09-540-209B-7041
 Sequence 7041, Application US/09540209B

GENERAL INFORMATION:
 APPLICANT: Gary L. Breton
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTERIOIDES FR
 FILE REFERENCE: 2709,1001-001
 CURRENT APPLICATION NUMBER: US/09/540, 209B
 NUMBER OF SEQ ID NOS: 2000-04-04
 SEQ ID NO 7041
 LENGTH: 431
 TYPE: PRT
 ORGANISM: B.fragilis
 US-09-540-209B-7041

Query Match
 Best Local Similarity 25.8%; Score 86.5; DB 9; Length 431;
 Matches 34; Conservative 24; Mismatches 41; Indels 33; Gaps 6;

QY 48 PRISAGTRINDLRPAVDYTRYKNK-----QVPSD-----FKLYSIGASAIYD 91
 DB 197 PNGSAFYRTQDLSYMC--KLKNKFGVGVEMPSVDGTNOYLINTQRPDFTASQYN 254
 QY 92 FDTQSPKPYLGARLSLNRSYDFNGS--DSFQSTSTGLVAGSYAVTPNVDLAGRY 150
 DB 255 WNAASHLK-----LAIVSMYSSSVYDKAKSKAGYGLQASTSENVTP-----KW 300
 QY 151 NYIGKVTYKNV 162
 DB 301 QYVGQVNYGKGI 312

RESULT 14
 US-09-540-209B-7077
 Sequence 7077, Application US/09540209B
 GENERAL INFORMATION:
 APPLICANT: Gary L. Breton
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTERIOIDES FR
 FILE REFERENCE: 2709,1001-001
 CURRENT APPLICATION NUMBER: US/09/540, 209B
 NUMBER OF SEQ ID NOS: 2000-04-04
 SEQ ID NO 7077

LENGTH: 501
 TYPE: PRT
 ORGANISM: B.fragilis
 US-09-540-209B-7077

Query Match
 Best Local Similarity 23.6%; Score 86.5; DB 9; Length 501;
 Matches 45; Conservative 32; Mismatches 65; Indels 49; Gaps 10;

QY 16 AALAGAGFYVQADAHAKASSLSGAKGSPRISGYRINDR-----F 61
 DB 53 AGVAEMGFSLSLNGSAGFYQRTTST--FAP--FAGFGSNAYKYGASADFTFSVF 108
 QY 62 ANDYTRYKNKYQVSTDEKLTYSIGASAIYD-----FDTQSPKPYLGARLSLNRSYD-- 114
 DB 109 AV-----YKKDKRAFSGNRAVYGGGKATFNGLSFSFESLYSVF--GMLVAAGNEMVDKG 162
 QY 115 -----FNGSDSFQTS-----TGLVAGSYAVTPNVDLAGRYNYI-----GKVN 157
 DB 163 VLPINIFNGTNYKYSVDSYMRKOMIFGLQATYRTIDYLSAFAGVRYNVSNGEGHIR 222
 QY 158 TVK-NVRSGL 167
 DB 223 NIANIGGEM 233

RESULT 15
 US-10-193-002-53
 Sequence 53, Application US/10193002

GENERAL INFORMATION:
 APPLICANT: Reed, Steven G.
 SKEIKY, Yasir A.W.
 DILLON, Davin C.
 Campos-Neto, Antonia
 Houghton, Raymond
 Vedvick, Thomas S.
 Twardzik, Daniel R.
 Lodes, Michael J.
 Hendrickson, Ronald C.
 TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
 TUBERCULOSIS
 NUMBER OF SEQUENCES: 350
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SEED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98104-7092
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/193,002
 FILING DATE: 10-Jul-2002
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/072,596
 FILING DATE: 05-MAY-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: Makl, David J.
 REGISTRATION NUMBER: 31,392
 REFERENCE/DOCKET NUMBER: 210121.417C9
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 53:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 332 amino acids
 TYPE: amino acid
 STRANDEDNESS: single

TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 53:
US-10-193-002-53

Query Match 9.8%; Score 86; DB 11; Length 332;
Best Local Similarity 27.9%; Pred. No. 1.5;
Matches 43; Conservative 15; Mismatches 60; Indels 36; Gaps 7;

```

QY 10 ALALPAAALAEAGSGFYVOADAAHAKASSLSGA-----KGFSPRISAGYRINDLRFA 62
   : ||||| : ||||| : |||
Db 128 SFALPAG-----WVESDAHFDDYGSALSKTTGDPFFGQPPYVA-----NDTRIV 173
   : ||||| : ||||| : |||
QY 63 VDYTRKKNYKQVPSDFKLYSIGASAIYDEFTQSPVKKPYLGARLSLNRAVDENGSD--- 119
   : ||||| : ||||| : |||
Db 174 LGRLDOKLYASAFAATDSK-----AAARLGSMDGFEFMPYPGTGRINQETVSLDANGVSGSA 228
   : ||||| : ||||| : |||
QY 120 -----SFQSTSTGLG-VLAGVSYAVTPNVDLDAG 147
   : ||||| : ||||| : |||
Db 229 SYEYKFSDFPSKPNQIWTGVIIGSPANAP-DAG 261
   : ||||| : ||||| : |||

```

Search completed: October 28, 2002, 16:13:51
Job time : 37.9039 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 28, 2002, 16:00:44 ; Search time 103.601 Seconds

(without alignments)
591.158 Million cell updates/sec

Title: US-09-684-883-6

Sequence: 1 MKKALATLIALALPAALAE.....VNYKVNNSGLSAGRVK 174

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Pending_Patents_AA_Main:*
1: /cgn2_6/ptodata/1/paa/US086.COMB.pep:*
2: /cgn2_6/ptodata/1/paa/US086.COMB.pep:*
3: /cgn2_6/ptodata/1/paa/US086.COMB.pep:*
4: /cgn2_6/ptodata/1/paa/US086.COMB.pep:*
5: /cgn2_6/ptodata/1/paa/US086.COMB.pep:*
6: /cgn2_6/ptodata/1/paa/US086.COMB.pep:*
7: /cgn2_6/ptodata/1/paa/US086.COMB.pep:*
8: /cgn2_6/ptodata/1/paa/US086.COMB.pep:*
9: /cgn2_6/ptodata/1/paa/US086.COMB.pep:*
10: /cgn2_6/ptodata/1/paa/US086.COMB.pep:*
11: /cgn2_6/ptodata/1/paa/US086.COMB.pep:*
12: /cgn2_6/ptodata/1/paa/US086.COMB.pep:*
13: /cgn2_6/ptodata/1/paa/US086.COMB.pep:*
14: /cgn2_6/ptodata/1/paa/US086.COMB.pep:*
15: /cgn2_6/ptodata/1/paa/US086.COMB.pep:*
16: /cgn2_6/ptodata/1/paa/US086.COMB.pep:*
17: /cgn2_6/ptodata/1/paa/US086.COMB.pep:*
18: /cgn2_6/ptodata/1/paa/US086.COMB.pep:*
19: /cgn2_6/ptodata/1/paa/US086.COMB.pep:*
20: /cgn2_6/ptodata/1/paa/US086.COMB.pep:*
21: /cgn2_6/ptodata/1/paa/US086.COMB.pep:*
22: /cgn2_6/ptodata/1/paa/US086.COMB.pep:*
23: /cgn2_6/ptodata/1/paa/US086.COMB.pep:*
24: /cgn2_6/ptodata/1/paa/US086.COMB.pep:*
25: /cgn2_6/ptodata/1/paa/US086.COMB.pep:*
26: /cgn2_6/ptodata/1/paa/US086.COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	854	98.4	174	8	US-08-406-362-2
2	854	98.4	174	22	US-09-870-759-36
3	135	15.6	170	8	US-08-479-520-20
4	135	15.6	170	8	US-08-486-050-20
5	135	15.6	170	8	US-08-486-050A-20
6	135	15.6	170	13	US-08-988-444-20
7	135	15.6	170	16	US-09-217-849-20

8	135	15.6	170	18	US-09-489-850-20	Sequence 20, Appl
9	130.5	15.0	281	21	US-09-739-449-11638	Sequence 11638, A
10	130.5	15.0	281	22	US-09-803-110-11638	Sequence 11638, A
11	115.5	13.3	187	18	US-09-489-039A-13699	Sequence 13699, A
12	114.5	13.3	187	18	US-09-489-039A-13699	Sequence 13699, A
13	106.5	12.3	384	19	US-09-540-236-2245	Sequence 2245, Ap
14	102	11.8	217	16	US-09-552-691-9162	Sequence 9922, Ap
15	102	11.8	217	16	US-09-552-691-9162	Sequence 9162, Ap
16	101	11.6	21	24	US-10-082-014-123	Sequence 9162, Ap
17	101	11.6	21	26	US-10-082-014-123	Sequence 123, App
18	97	11.2	21	24	US-10-082-014-124	Sequence 47, Appl
19	97	11.2	21	26	US-10-082-014-124	Sequence 124, App
20	96	11.1	212	22	PCT-US02-03987-10149	Sequence 10149, A
21	96	11.1	212	22	US-09-815-242-10149	Sequence 10149, A
22	96	11.1	212	24	US-10-072-851-10149	Sequence 5331, A
23	95.5	11.0	487	17	US-09-328-352-5331	Sequence 7684, Ap
24	94	10.8	190	19	US-09-543-681A-7684	Sequence 19759, A
25	93.5	10.8	261	16	US-09-252-991A-19759	Sequence 2, Appl
26	93	10.7	359	4	US-08-055-442-2	Sequence 2, Appl
27	93	10.7	359	8	US-08-457-997-2	Sequence 2, Appl
28	93	10.7	359	8	US-08-457-997-2	Sequence 2, Appl
29	93	10.7	359	8	US-08-457-997-2	Sequence 2, Appl
30	93	10.7	359	18	US-09-451-184-2	Sequence 2, Appl
31	92	10.6	257	1	PCT-US02-03987-13845	Sequence 13845, A
32	92	10.6	257	22	US-09-815-242-13845	Sequence 13845, A
33	92	10.6	257	24	US-10-072-851-13845	Sequence 5, Appl
34	92	10.6	568	7	US-08-331-393-5	Sequence 7451, Ap
35	90.5	10.4	385	18	US-09-489-039A-7451	Sequence 16367, A
36	90	10.4	397	23	US-09-902-540-16367	Sequence 5146, Ap
37	90	10.4	643	17	US-09-328-352-5146	Sequence 13821, A
38	89	10.3	225	24	US-10-015-127-13821	Sequence 153, App
39	89	10.3	369	19	US-09-545-199C-153	Sequence 153, App
40	89	10.3	369	19	US-09-545-199C-153	Sequence 9372, Ap
41	89	10.3	369	22	US-09-809-665A-153	Sequence 9372, Ap
42	88.5	10.2	178	21	US-09-739-449-9372	Sequence 8555, Ap
43	88.5	10.2	178	22	US-09-803-110-9372	Sequence 8555, Ap
44	87.5	10.1	213	21	US-09-739-449-8555	Sequence 8555, Ap
45	87.5	10.1	213	22	US-09-803-110-8555	Sequence 8555, Ap

ALIGNMENTS

RESULT 1
US-08-406-362-2
Sequence 2, Application US/08406362
GENERAL INFORMATION:
APPLICANT: Brodeur, Bernard R
APPLICANT: Martin, Denis
TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/406,362
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr, James F
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: Pharma-43

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-596-9000
 TELEFAX: 212-596-9090
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 174 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-406-362-2

Query Match 98.4%; Score 854; DB 8; Length 174;
 Best Local Similarity 98.3%; Pred. No. 3.9e-88;
 Matches 171; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 DB 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 QY 61 FAVDYTRYKRYKAPSTDFKLYSGASAIYDFPTQSPVKRYLGARLSLNASVDLGSDSF 120
 DB 61 FAVDYTRYKRYKAPSTDFKLYSGASAIYDFPTQSPVKRYLGARLSLNASVDLGSDSF 120
 QY 121 SQTSLGLVLAGVYAVTPNVDLDAGRYRYNGKVTYKVRSGELSGYRVKF 174
 DB 121 SQTSLGLVLAGVYAVTPNVDLDAGRYRYNGKVTYKVRSGELSGYRVKF 174

RESULT 2

US-09-870-759-36
 Sequence 36, Application US/09870759

GENERAL INFORMATION:
 APPLICANT: TERMAN, David S
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
 FILE REFERENCE: 870759
 CURRENT APPLICATION NUMBER: US/09/870,759
 PRIOR FILING DATE: 2002-01-14
 PRIOR APPLICATION NUMBER: US 60/208,128
 PRIOR FILING DATE: 2000-05-30
 NUMBER OF SEQ ID NOS: 166
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 36
 LENGTH: 174
 TYPE: PRT
 ORGANISM: Neisseria meningitidis
 US-09-870-759-36

Query Match 98.4%; Score 854; DB 22; Length 174;
 Best Local Similarity 98.3%; Pred. No. 3.9e-88;
 Matches 171; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 DB 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
 QY 61 FAVDYTRYKRYKAPSTDFKLYSGASAIYDFPTQSPVKRYLGARLSLNASVDLGSDSF 120
 DB 61 FAVDYTRYKRYKAPSTDFKLYSGASAIYDFPTQSPVKRYLGARLSLNASVDLGSDSF 120
 QY 121 SQTSLGLVLAGVYAVTPNVDLDAGRYRYNGKVTYKVRSGELSGYRVKF 174
 DB 121 SQTSLGLVLAGVYAVTPNVDLDAGRYRYNGKVTYKVRSGELSGYRVKF 174

RESULT 3

US-08-479-520-20
 Sequence 20, Application US/08479520

GENERAL INFORMATION:
 APPLICANT: VAN ALSTYNE, Diane
 APPLICANT: SHARMA, Lawrence Rajendra
 TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
 TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
 TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THEREOF, AND USES THEREOF

NUMBER OF SEQUENCES: 40
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner
 STREET: 3000 K Street, N.W., Suite 500
 CITY: Washington

STATE: D.C.
 COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/479,520

FILING DATE: 07-JUN-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/127,499

FILING DATE: 28-SEP-1993

ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 51916/105/INBI

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 170 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

US-08-479-520-20

Query Match 15.6%; Score 135; DB 8; Length 170;
 Best Local Similarity 26.3%; Pred. No. 1.6e-06;
 Matches 41; Conservative 20; Mismatches 47; Indels 48; Gaps 4;

QY 6 ATLLALPAALAEAGSGFYVQADAAH-----AKASSLSG-----AKG 45
 DB 15 SLLFSSAAQASSEDRSPYVQADLAAERITHDYPOATGANNSTVSDYFRNRAHS 74
 QY 46 FSPRISAGYRINDLRFAVDYTRYKRY-----KAPSTDFK 79
 DB 75 IHPRVSVGDFGWRIRIADYASRYKMNKYSVTKELKNNKKDKLTQNGTFHA 134
 QY 80 LYSTGASAIYDFDQSPVKRYLGARLSLN--RASVD 113
 DB 135 ASSLGLSAIYDFKLGKFKPYIGARVAVAGVHRSID 170

RESULT 4

US-08-486-050-20
 Sequence 20, Application US/08486050

GENERAL INFORMATION:
 APPLICANT: VAN ALSTYNE, Diane
 APPLICANT: SHARMA, Lawrence Rajendra
 TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
 TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
 TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THEREOF, AND USES THEREOF
 NUMBER OF SEQUENCES: 75
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Foley & Lardner
 STREET: 3000 K Street, N.W., Suite 500
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20007-5109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,050
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/103/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-486-050-20

Query Match 15.6%; Score 135; DB 8; Length 170;
Best Local Similarity 26.3%; Pred. NO. 1.6e-06;
Matches 41; Conservative 20; Mismatches 47; Indels 48; Gaps 4;

QY 6 ATLIALPMAALAGASGYVQADAAH-----AKSSSLGS-----AKG 45
DB 15 SLIFSSAAQAASEDRSPYVQADLAVAAERITHDYPOATGANNSTVSDYFNIRAH 74
QY 46 FSPRISAGYRINDLRFVADYTRYKNY-----KAPSTDFK 79
DB 75 IHPRVSVGYDEGWMRIADYASVRKNNKYSVNTKELENKNNKDKLTENGNGTFHA 134
QY 80 LYSIGASAIYDPDQSPVYPYLGARSLN--RASVD 113
DB 135 ASSLGSAIYDFKLGKFKFYIGARVAGVHRSID 170

RESULT 5
US-08-486-050A-20
Sequence 20, Application US/08486050A
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THEREO, AND USES THEREOF
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,050A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/103/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-486-050A-20

Query Match 15.6%; Score 135; DB 8; Length 170;
Best Local Similarity 26.3%; Pred. NO. 1.6e-06;
Matches 41; Conservative 20; Mismatches 47; Indels 48; Gaps 4;

QY 6 ATLIALPMAALAGASGYVQADAAH-----AKSSSLGS-----AKG 45
DB 15 SLIFSSAAQAASEDRSPYVQADLAVAAERITHDYPOATGANNSTVSDYFNIRAH 74
QY 46 FSPRISAGYRINDLRFVADYTRYKNY-----KAPSTDFK 79
DB 75 IHPRVSVGYDEGWMRIADYASVRKNNKYSVNTKELENKNNKDKLTENGNGTFHA 134
QY 80 LYSIGASAIYDPDQSPVYPYLGARSLN--RASVD 113
DB 135 ASSLGSAIYDFKLGKFKFYIGARVAGVHRSID 170

RESULT 6
US-08-988-444-20
Sequence 20, Application US/08988444
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THEREO, AND USES THEREOF
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/988,444
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/486,050
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/103/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids

TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-988-444-20

Query Match 15.6%; Score 135; DB 13; Length 170;
Best Local Similarity 26.3%; Pred. No. 1.6e-06;
Matches 41; Conservative 20; Mismatches 47; Indels 48; Gaps 4;

QY 6 ATLLALPAAALAGASGFYQADAAH-----AKASSSLGS-----AKG 45
DB 15 SSLFSSAAQAASEDRSPYYQADLAFAERITHDYPQATGANNSTVSDYFNNIRAS 74
QY 46 FSPRISAGYRINDLRFADVTRYKNY-----KAPSTDFK 79
DB 75 IHPRVSVGYDGGWRIADYASRYKNNKYSVNTKELENKHNKKDKLTENGNGTFHA 134
QY 80 LYSIGASAIYDFDQSPVYKPYLGARLSLN--RASVD 113
DB 135 ASSLGSAIYDFKLGKFKPKYIGARVAYGHVHSHID 170

RESULT 7

US-09-217-849-20
Sequence 20, Application US/09217849
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/217,849
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/486,050
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/103/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-09-217-849-20

Query Match 15.6%; Score 135; DB 16; Length 170;
Best Local Similarity 26.3%; Pred. No. 1.6e-06;
Matches 41; Conservative 20; Mismatches 47; Indels 48; Gaps 4;

QY 6 ATLLALPAAALAGASGFYQADAAH-----AKASSSLGS-----AKG 45
DB 15 SSLFSSAAQAASEDRSPYYQADLAFAERITHDYPQATGANNSTVSDYFNNIRAS 74
QY 46 FSPRISAGYRINDLRFADVTRYKNY-----KAPSTDFK 79
DB 75 IHPRVSVGYDGGWRIADYASRYKNNKYSVNTKELENKHNKKDKLTENGNGTFHA 134
QY 80 LYSIGASAIYDFDQSPVYKPYLGARLSLN--RASVD 113
DB 135 ASSLGSAIYDFKLGKFKPKYIGARVAYGHVHSHID 170

RESULT 8

US-09-489-850-20
Sequence 20, Application US/09489850
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/489,850
FILING DATE: 24-Jan-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/988,444
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/103/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-489-850-20

Query Match 15.6%; Score 135; DB 18; Length 170;
Best Local Similarity 26.3%; Pred. No. 1.6e-06;
Matches 41; Conservative 20; Mismatches 47; Indels 48; Gaps 4;

QY 6 ATLLALPAAALAGASGFYQADAAH-----AKASSSLGS-----AKG 45
DB 15 SSLFSSAAQAASEDRSPYYQADLAFAERITHDYPQATGANNSTVSDYFNNIRAS 74
QY 46 FSPRISAGYRINDLRFADVTRYKNY-----KAPSTDFK 79
DB 75 IHPRVSVGYDGGWRIADYASRYKNNKYSVNTKELENKHNKKDKLTENGNGTFHA 134

Query Match	15.08;	Score 130.5;	DB 22;	Length 281;
-------------	--------	--------------	--------	-------------

FILE REFERENCE: Z/09.2003-001
CURRENT APPLICATION NUMBER: US/09/540.236

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 28, 2002, 16:01:19 ; Search time 35.6987 Seconds

(without alignments)
1465.185 Million cell updates/sec

Title: US-09-684-883-6

Sequence: 1 MKKALATIALALPAAALAE.....VNTVKNVRSGLSGVRYKF 174

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1112697 seqs, 300604653 residues

Total number of hits satisfying chosen parameters: 1112697

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Pending_Patents_AA_New:*

1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
6: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
7: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
8: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
9: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
10: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
11: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
12: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*
13: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	868	100.0	174	9	US-09-684-883-6
2	854	98.4	174	9	US-09-684-883-2
3	847.5	97.6	175	9	US-09-684-883-30
4	838.5	96.6	175	9	US-09-684-883-4
5	834	96.1	174	9	US-09-684-883-8
6	133	15.3	25	9	US-09-684-883-26
7	99	11.4	353	11	US-10-203-942-9
8	89.5	10.3	339	9	US-09-513-996A-67258
9	89.5	10.3	534	9	US-09-513-996A-7956
10	89.5	10.3	765	9	US-10-701-537-22674
11	89	10.3	229	11	US-10-219-999-59699
12	89	10.3	369	9	US-09-545-199F-153
13	88	10.1	165	9	US-09-540-209B-7537
14	87	10.0	16	9	US-09-684-883-15
15	87	10.0	500	9	US-09-990-004A-149
16	87	10.0	500	11	US-10-219-999-45753
17	85	9.8	187	11	US-10-219-999-45753
18	85	9.8	388	9	US-09-791-537-60560
19	85	9.8	388	13	US-60-360-039-22903
20	84	9.7	316	9	US-09-513-996A-67259

21	84	9.7	364	9	US-09-545-199F-151	Sequence 151, App
22	84	9.7	511	9	US-09-513-996A-7957	Sequence 7957, Ap
23	84	9.7	511	9	US-09-513-996A-39219	Sequence 39219, A
24	83	9.6	213	9	US-09-791-537-112202	Sequence 112202,
25	81	9.3	15	9	US-09-684-883-23	Sequence 23, Appl
26	81	9.3	431	9	US-09-540-209B-7041	Sequence 7041, Ap
27	81	9.3	509	9	US-09-791-537-80797	Sequence 80797, A
28	81	9.3	573	9	US-09-540-209B-55271	Sequence 115703,
29	79.5	9.2	576	9	US-09-513-996A-64105	Sequence 5271, Ap
30	79.5	9.2	581	9	US-09-513-996A-64106	Sequence 117254,
31	79.5	9.2	645	9	US-09-513-996A-64105	Sequence 64106, A
32	79.5	9.2	15	9	US-09-684-883-18	Sequence 18, Appl
33	79	9.1	207	9	US-09-570-214B-7	Sequence 7, Appl
34	79	9.1	264	9	US-09-956-508A-4	Sequence 80, Appl
35	79	9.1	273	9	US-09-882-227-80	Sequence 123, App
36	79	9.1	421	2	PCT-US02-12532-123	Sequence 6145, Ap
37	79	9.1	427	9	US-09-540-209B-6145	Sequence 119822,
38	79	9.1	431	9	US-09-791-537-119822	Sequence 3443, Ap
39	78.5	9.0	153	9	US-09-905-176-22	Sequence 3443, Ap
40	78.5	9.0	189	11	US-10-108-260A-3443	Sequence 8424, Ap
41	78.5	9.0	189	11	US-10-179-131-8424	Sequence 2, Appl
42	78.5	9.0	792	11	US-10-179-131-8424	Sequence 14, Appl
43	78.5	9.0	576775	9	US-09-458-180-2	
44	78.5	9.0	15	9	US-09-684-883-14	
45	78					

ALIGNMENTS

RESULT 1
US-09-684-883-6
Sequence 6, Application US/0968483
GENERAL INFORMATION:
APPLICANT: Brodeur, Bernard R
Martin, Denis
Hamel, Josee
Rioux, Clement
TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
OF NEISSERIA MENINGITIDIS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/684, 883
FILING DATE: 06-Oct-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/913, 362
FILING DATE: 13-Nov-1997
APPLICATION NUMBER: US 08/406, 362
FILING DATE: 17-Mar-1995
APPLICATION NUMBER: US 60/001, 983
FILING DATE: 04-Aug-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 047998/0128
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:

LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-684-883-6

Query Match 100.0%; Score 868; DB 9; Length 174;
Best Local Similarity 100.0%; Pred. No. 1.6e-81;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
DB 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
QY 61 FAVDYTRKNNKAPSTDFPKLSTIGASAIYDPDQSPYKPYLGARLSLNRAVDLGSDSF 120
DB 61 FAVDYTRKNNKAPSTDFPKLSTIGASAIYDPDQSPYKPYLGARLSLNRAVDLGSDSF 120
QY 121 SQTSTGLVLAGSVAVTPNVDDAGRYRNYIGKNTVKNVRSGLSAGYRVKF 174
DB 121 SQTSTGLVLAGSVAVTPNVDDAGRYRNYIGKNTVKNVRSGLSAGYRVKF 174

RESULT 2

US-09-684-883-2

Sequence 2, Application US/09684883

GENERAL INFORMATION:

APPLICANT: Brodeur, Bernard R

Hamel, Josee

Rioux, Clement

TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
OF NEISSERIA MENINGITIDIS

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/684,883

FILING DATE: 06-Oct-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/913,362

FILING DATE: 13-NOV-1997

APPLICATION NUMBER: US 08/406,362

FILING DATE: 17-MAR-1995

APPLICATION NUMBER: US 60/001,983

FILING DATE: 04-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: Bent, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 047998/0128

TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 174 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-684-883-2

Query Match 98.4%; Score 854; DB 9; Length 174;
Best Local Similarity 98.3%; Pred. No. 4.4e-80;
Matches 171; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
DB 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
QY 61 FAVDYTRKNNKAPSTDFPKLSTIGASAIYDPDQSPYKPYLGARLSLNRAVDLGSDSF 120
DB 61 FAVDYTRKNNKAPSTDFPKLSTIGASAIYDPDQSPYKPYLGARLSLNRAVDLGSDSF 120
QY 121 SQTSTGLVLAGSVAVTPNVDDAGRYRNYIGKNTVKNVRSGLSAGYRVKF 174
DB 121 SQTSTGLVLAGSVAVTPNVDDAGRYRNYIGKNTVKNVRSGLSAGYRVKF 174

RESULT 3

US-09-684-883-30

Sequence 30, Application US/09684883

GENERAL INFORMATION:

APPLICANT: Brodeur, Bernard R

Hamel, Josee

Rioux, Clement

TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
OF NEISSERIA MENINGITIDIS

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/684,883

FILING DATE: 06-Oct-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/913,362

FILING DATE: 13-NOV-1997

APPLICATION NUMBER: US 08/406,362

FILING DATE: 17-MAR-1995

APPLICATION NUMBER: US 60/001,983

FILING DATE: 04-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: Bent, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 047998/0128

TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 30:

SEQUENCE CHARACTERISTICS:

LENGTH: 175 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 30:

US-09-684-883-30

Query Match 97.6%; Score 847.5; DB 9; Length 175;
Best Local Similarity 98.3%; Pred. No. 2.1e-79;
Matches 172; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

61 FAVDYTRYKNYK-APSTDEKLYSIGASAIYDEFTQSPVKPYLGLRLSLNRASVDLGGSDS 119

Db 121 SRTSAGLGVLGVSIAVTPNVDLDAGYRYNNYGVKNTVKNVRSGELSAGVRK 174

```

RESULT 6
US-09-684-883-26
; Sequence 26, Application US/09684883
; GENERAL INFORMATION:
; APPLICANT: Brodeur, Bernard R
; Hamel, Josée
; Martin, Denis
; Rioux, Clement
; TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
; OF NEISSERIA MENINGITIDIS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/684,883
; FILING DATE: 06-Oct-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/913,362
; FILING DATE: 13-NOV-1997
; APPLICATION NUMBER: US 08/406,362
; FILING DATE: 17-MAR-1995
; APPLICATION NUMBER: US 60/001,983
; FILING DATE: 04-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 047998/0128
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Neisseria meningitidis
; STRAIN: 608B
; SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-684-883-26

Query Match 15.3%; Score 133; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.3e-07;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 FAVDYTRYKNYKAPSTDFKLYSIGA 85
DB 1 FAVDYTRYKNYKAPSTDFKLYSIGA 25

```

```

; FILE REFERENCE: B45210
; CURRENT APPLICATION NUMBER: US/10/203,942
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: PCT/EP01/01556
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: GB 0003502.2
; PRIOR FILING DATE: 2000-02-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-10-203-942-9

Query Match 11.4%; Score 99; DB 11; Length 353;
Best Local Similarity 24.8%; Pred. No. 0.095;
Matches 53; Conservative 29; Mismatches 92; Indels 40; Gaps 9;

QY 1 MKKALATLIALALPAAALAEGA---SGFYQAADAHAHAKASSLSGS-----AKGFS 47
DB 1 MKKTAIALVAVGLAASVQAAPQENTFYAGVRKAGQASFDGLRALAREYKGYHRNSFT 60
QY 48 PRISAGYFI---NDLRAY-----DYTRYKNYKAPSTDFKLYSIGA--SAIYDFDQSPV 97
DB 61 YGVGGYQIILNQNNIGLAVELGYDPPGAKGREGKTVVXHTNGLSLKSGSYEVLEGL 120
QY 98 KPYLGARSLNRASVDLGGSDFSQTSFG-----LGVLG-VSYAVTPNVVDLAGY-- 147
DB 121 DYGAGAGALVRSIDYKLYNENSTLKKLGEHHRARASGLFVAVGLAVLELAVRLEYQW 180
QY 148 ----RYNYIGKVTYKVNRS--GELSGAVRYKF 174
DB 181 LTRVGKYPQDKPMTALYNPWNIGSINAGISYRF 214

RESULT 8
US-09-513-996A-67258
; Sequence 67258, Application US/09513996A
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
; FILE OF INVENTION: ENCODED THEREBY
; FILE REFERENCE: 2750-709P
; CURRENT APPLICATION NUMBER: US/09/513,996A
; CURRENT FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 81028
; SEQ ID NO 67258
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 1..339
; OTHER INFORMATION: any n or Xaa = unknown
; OTHER INFORMATION: Location 1..339 / Ceres Seq. ID 2177695
US-09-513-996A-67258

Query Match 10.3%; Score 89.5; DB 9; Length 339;
Best Local Similarity 27.7%; Pred. No. 0.87;
Matches 39; Conservative 20; Mismatches 53; Indels 29; Gaps 8;

QY 39 SLGSAKF-----SPRISAGYRINDLRFADV--TRYKNYKAPSTDFKLYSIGASAIY 89
DB 18 SFSAKMFIESPKVESPVWK--YTENEIHSYVDYETFEVHEKYNQYQWIVPKYKY 75
QY 90 DEDTQSPYKPYLGARSLNRASVDLGGSDFSQTSFGVLA---GVSYAVTPNVVDLAG 146
DB 76 DKTDIRY-PKLGVM-----VGLGGNNGSTLTA---GVLNKGISWATKDKVQ---- 121
QY 147 RYNYIGKVTYKVNRSGLS 167
; | | | : : | | :

```

Db 122 -QANFGSLTQASSIRVGSFN 141

RESULT 9
US-09-513-996A-7956

; Sequence 7956, Application US/09513996A

; GENERAL INFORMATION:

; APPLICANT: N. ALEXANDROV et al.

; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

; FILE REFERENCE: 2750-709P

; CURRENT APPLICATION NUMBER: US/09/513,996A

; NUMBER OF SEQ ID NOS: 81028

; SEQ ID NO 7956

; LENGTH: 534

; ORGANISM: Arabidopsis thaliana

; TYPE: PRT

; NAME/KEY: UNSURE

; LOCATION: 1..534

; OTHER INFORMATION: any n or Xaa = unknown

; FEATURE:

; OTHER INFORMATION: Location 1..534 / Ceres Seq. ID 1026819

US-09-513-996A-7956

Query Match 10.3%; Score 89.5; DB 9; Length 534;
Best Local Similarity 27.7%; Pred. No. 1.6;

Matches 39; Conservative 20; Mismatches 53; Indels 29; Gaps 8;

QY 39 SLSAGKGF-----SPRISAGYRINDLFAVDY--TRYKNKAPSTDEKLYSGASAIY 89

Db 18 SSSSAMFLESKEVESPKNK--YTENEHLSVYDTEETTEVYHKKTYNGYOWIVKPKTYKY 75

QY 90 DFDGOSPVKPYLGARLSLRASVDLGSDFSQSTGIGVLA---GVSAVTPNVDLAAG 146

Db 76 DEKTDIRV--PKIGVML-----VGLGNNGSTLTA---GVANKKSGISMATDKYQ----- 121

QY 147 YRYNYGKNTYKKNVRSGLS 167

Db 122 -QANFGSLTQASSIRVGSFN 141

RESULT 10

US-09-791-537-22674

; Sequence 22674, Application US/09791537

; GENERAL INFORMATION:

; APPLICANT: Biomimix, Inc.

; APPLICANT: Debe, Derek

; APPLICANT: Danzer, Joseph

; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB

; FILE REFERENCE: 261/210

; CURRENT APPLICATION NUMBER: US/09/791,537

; CURRENT FILING DATE: 2001-02-22

; NUMBER OF SEQ ID NOS: 153055

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 22674

; LENGTH: 765

; TYPE: PRT

; ORGANISM: Synecocystis sp

US-09-791-537-22674

Query Match 10.3%; Score 89.5; DB 9; Length 765;
Best Local Similarity 26.1%; Pred. No. 2.5;

Matches 29; Conservative 20; Mismatches 49; Indels 13; Gaps 4;

QY 46 FSPRISAGYRINDLFAVDYTRYKNKAPSTDEKLYSGASAIYDFDGSVPKPYLGARL 105

Db 630 FEPYI--GARLINSFALDQ--TWRYNSSVLSL--AGQFOINETSRTWNPVVGKGL 683

QY 106 SLNRASV-----DLGSDSFSQSTGTLGVLGVSAVTPNVDLAAGRY 149

Db 684 GVOULTLALMLRGDVGSGFDLSCGADNMNMAILLDYVRENAVLQGYKE 734

RESULT 11

US-10-219-999-59699

; Sequence 59699, Application US/10219999

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Edgerton, Michael D

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Kovacic, David K.

; APPLICANT: Lin, Jindong

; APPLICANT: Stein, Joshua

; TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT

; FILE REFERENCE: 38-10(52726)C

; CURRENT APPLICATION NUMBER: US/10/219,999

; PRIOR FILING DATE: 2002-08-15

; PRIOR APPLICATION NUMBER: US 60/324,109

; PRIOR FILING DATE: 2001-09-21

; PRIOR FILING DATE: 2001-08-15

; NUMBER OF SEQ ID NOS: 63520

; SEQ ID NO 59699

; LENGTH: 229

; TYPE: PRT

; ORGANISM: Zea mays

US-10-219-999-59699

Query Match 10.3%; Score 89; DB 11; Length 229;
Best Local Similarity 28.8%; Pred. No. 0.58;

Matches 45; Conservative 15; Mismatches 52; Indels 44; Gaps 5;

QY 4 ALATIALALPAALACASGFFVQADAAHAKSSSSIGSAKGSPPRISAGYRINDLFAV 63

Db 82 AASLVSAIGSASGAAASVSAAAGAAASGSASIGSASVSASAKTA----- 130

QY 64 DYTRYKNKAPSTDEKLYSGASAIYDFDGSVPKPYLGARLSLRASV---DLGSDSF 120

Db 131 -----SASTSTSLDSVASA---DTGS-----LAFTVSAAAGAVSSFGVSTAA 172

QY 121 S-----QTSGLGYLAGVSAVTPNVDL 144

Db 173 SWAASTPAAAAAASSTGAAGVGTWTSTAGAVQLD 208

RESULT 12

US-09-545-199F-153

; Sequence 153, Application US/09545199F

; GENERAL INFORMATION:

; APPLICANT: Lowery E., David

; APPLICANT: Fuller E., Troy

; APPLICANT: Kennedy J., Michael

; TITLE OF INVENTION: Anti-Bacterial Vaccine Compositions

; FILE REFERENCE: 28341/6227.NCP

; CURRENT APPLICATION NUMBER: US/09/545,199F

; CURRENT FILING DATE: 2000-04-06

; PRIOR APPLICATION NUMBER: 60/153,453

; PRIOR FILING DATE: 1999-09-10

; PRIOR APPLICATION NUMBER: 60/128,689

; PRIOR FILING DATE: 1999-04-09

; NUMBER OF SEQ ID NOS: 165

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 153

; LENGTH: 369

; TYPE: PRT

; ORGANISM: Actinobacillus pleuropneumoniae

US-09-545-199F-153

Query Match 10.3%; Score 89; DB 9; Length 369;
Best Local Similarity 21.5%; Pred. No. 1.1;

Matches 49; Conservative 36; Mismatches 85; Indels 58; Gaps 11;

QY 1 MKKRAITLIALALPAALAEGA---SGFYVQADAAHAKSSSSIGSAK-GFSPP----- 49

```

Db      1  |||:| | :| |:| :| :| :| | :| :| :| |
1 MKKSLVALAAYLS--AAVVAQAAPQÖNMFYGAAGVGGSSFFHHGNÖLKGSGDDDYNDKTRK 58

QY      50  -----ISAGYRI--NDLRFAVD--YTRYKNKYKAPSTDFKLYTSGISAAIY----- 89
59 YGIRNSVTVYGVFEGGYOILNONNEGFLAELGYDYIGRVNRGVNDDEFIRKYVSHAGHLALAK 118

Db      90  -DFFQSGPVKPYLCARISLRNASVDLGSGDSFSQTSNGLCVL-----AGVSYAVTPNV 141
119 PSYVLEPDLDVYIGKVGIAVVRKNDYKKYGAENTNESTTKFHKLASITLLGAGVEYAIILP-- 176

QY      142 DLDAGYRYNTYIGKVNFKN--VRSG-----ELISAGVRYKF 174
177 ELAARVEYQYLNKAGNLNKLALVNSGTDVDVQYAPRDHSTYALSLTRF 224

```

```

RESULT 13
US-09-540-209B-7537
; Sequence 7537, Application US/09540209B
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTERIOIDES FR
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1001-001
; CURRENT APPLICATION NUMBER: US/09/540,209B
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 10444
; SEQ ID NO 7537
; LENGTH: 165
; TYPE: PRF
; ORGANISM: B.fragilis
US-09-540-209B-7537

```

Query Match	10.1%	Score 88;	DB 9;	Length 165;
Best Local Similarity	22.8%;	Pred. No. 0.46;		
Matches 41; Conservative	30;	Mismatches	30;	Gaps 7;

[illegible]

RESULT 14
 US-09-684-883-15
 ; Sequence 15, Application US/09684883
 ; GENERAL INFORMATION:
 ; APPLICANT: Brodeur, Bernard R
 ; Hamel, Josee
 ; Martin, Denis
 ; Rioux, Clement
 ;
 TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
 OF NEISSERIA MENINGITIDIS
 ;
 ; NUMBER OF SEQUENCES: 30
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Foley & Lardner
 ; STREET: 3000 K Street, N.W., Suite 500
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20007-5109
 ;
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30

```

1 CURRENT APPLICATION DATA:
2 APPLICATION NUMBER: US/09/684,883
3 FILING DATE: 06-Oct-2000
4
5 PRIOR APPLICATION DATA:
6 APPLICATION NUMBER: US/08/913,362
7 FILING DATE: 13-NOV-1997
8 APPLICATION NUMBER: US 08/406,362
9 FILING DATE: 17-MAR-1995
10 APPLICATION NUMBER: US 60/001,983
11 FILING DATE: 04-AUG-1995
12
13 ATTORNEY/AGENT INFORMATION:
14 NAME: Bent, Stephen A.
15 REGISTRATION NUMBER: 29,768
16 REFERENCE/DOCKET NUMBER: 497998/0128
17
18 TELECOMMUNICATION INFORMATION:
19 TELEPHONE: (202) 672-5500
20 TELEFAX: (202) 672-5399
21
22 TELEX: 904136
23
24 INFORMATION FOR SEQ ID NO: 15:
25 SEQUENCE CHARACTERISTICS:
26 LENGTH: 16 amino acids
27 TYPE: amino acid
28 TOPOLOGY: linear
29 MOLECULE TYPE: protein
30 ORIGINAL SOURCE:
31 ORGANISM: Neisseria meningitidis
32 STRAIN: 608B
33
34 SEQUENCE DESCRIPTION: SEQ ID NO: 15:
35
36 US-09-684-883-15

```

Query Match	10.0%;	Score 87;	DB 9;	Length 16;
Best Local Similarity	100.0%;	Pred. No. 0.029;		
Matches 16;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	61	FAVDYTRYKNYKAPST	76
Db	1	FAVDYTRYKNYKAPST	16

```

RESULT 5
US-09-990-004A-149
; Sequence 149, Application US/09990004A
; GENERAL INFORMATION:
; APPLICANT: Film, Barry
; APPLICANT: Lasham, Annette
; TITLE OF INVENTION: Methods for Modulating
; FILE REFERENCE: 11000.1038c1
; CURRENT APPLICATION NUMBER: US/09/990, 004A
; CURRENT FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: US 09/327,373
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 149
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-09-990-004A-149

```

Query Match	10.0%	Score 87	DB 9	Length 500
Best Local Similarity	23.7%	Pred. No. 2.6		
Matches	41	Conservative 19	Mismatches 81	Indels 32
			Gaps	4

QY	4	AATLIALALPAAALAEAGSGFYQADAAHAKASSSLGAKFSPRISAGYRI-----	56
		: : : : : : : : : : : : : : : : : : : : : : : : :	
Db	32	AAVAVALIALATLTITIASALDMSIVSYDRAHGDRSSSSSSSWRSDDEVAAVYESWLAKHGK	91
QY	57	-----NDLRPAV--DYTRYKNYKAPSTDFELYSIGASAIYDPTQSGVYKRYLGARSL	107
		: : : : : : : : : : : : : : : : : : : : : : : : :	
Db	92	AYNALGEKKEKRFQVFKDNLRFIDHNAGCD--RTYYTGLNQFADLTNEEYSRMYTGARM--	148
QY	108	NRAVDLGGSDSFQSOTSTGLGVLACYSYAVTENVVDLACRYRNYIGKVTATYAN	160
		: : : : : : : : : : : : : : : : : : : : : : : : :	

Tue Oct 29 09:23:19 2002

us-09-684-883-6.rapn

Page 7

Db 149 -----DRSGRRIGRARSDRYAVANGELLPASVDMRKEGAVYDVKD 188

Search completed: October 28, 2002, 16:13:52
Job time : 36.6987 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 28, 2002, 16:00:44 ; Search time 103.601 Seconds

(without alignments)
591.158 Million cell updates/sec

Title: US-09-684-883-8

Sequence: 1 MKKALALIALALPAALAE.....VNTKVNRSGLSAGVRVK 174

Scoring table: BLOSOM62
Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Pending Patents_AA_Main:*

1: /cgn2_6/ptodata/1/paa/US086_COMB.pep:*

2: /cgn2_6/ptodata/1/paa/US086_COMB.pep:*

3: /cgn2_6/ptodata/1/paa/US086_COMB.pep:*

4: /cgn2_6/ptodata/1/paa/US086_COMB.pep:*

5: /cgn2_6/ptodata/1/paa/US086_COMB.pep:*

6: /cgn2_6/ptodata/1/paa/US086_COMB.pep:*

7: /cgn2_6/ptodata/1/paa/US086_COMB.pep:*

8: /cgn2_6/ptodata/1/paa/US086_COMB.pep:*

9: /cgn2_6/ptodata/1/paa/US086_COMB.pep:*

10: /cgn2_6/ptodata/1/paa/US086_COMB.pep:*

11: /cgn2_6/ptodata/1/paa/US086_COMB.pep:*

12: /cgn2_6/ptodata/1/paa/US086_COMB.pep:*

13: /cgn2_6/ptodata/1/paa/US086_COMB.pep:*

14: /cgn2_6/ptodata/1/paa/US086_COMB.pep:*

15: /cgn2_6/ptodata/1/paa/US086_COMB.pep:*

16: /cgn2_6/ptodata/1/paa/US086_COMB.pep:*

17: /cgn2_6/ptodata/1/paa/US086_COMB.pep:*

18: /cgn2_6/ptodata/1/paa/US086_COMB.pep:*

19: /cgn2_6/ptodata/1/paa/US086_COMB.pep:*

20: /cgn2_6/ptodata/1/paa/US086_COMB.pep:*

21: /cgn2_6/ptodata/1/paa/US086_COMB.pep:*

22: /cgn2_6/ptodata/1/paa/US086_COMB.pep:*

23: /cgn2_6/ptodata/1/paa/US086_COMB.pep:*

24: /cgn2_6/ptodata/1/paa/US086_COMB.pep:*

25: /cgn2_6/ptodata/1/paa/US086_COMB.pep:*

26: /cgn2_6/ptodata/1/paa/US086_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	825	94.8	174	8	US-08-406-362-2
2	825	94.8	174	22	US-09-870-759-36
3	125	14.4	170	8	US-08-479-520-20
4	125	14.4	170	8	US-08-486-050-20
5	125	14.4	170	8	US-08-486-050A-20
6	125	14.4	170	13	US-08-988-444-20
7	125	14.4	170	16	US-09-217-849-20

8	125	14.4	170	18	US-09-489-850-20	Sequence 20, Appl
9	124.5	14.3	281	21	US-09-739-449-11638	Sequence 11638, A
10	124.5	13.0	187	18	US-09-803-110-11638	Sequence 11638, A
11	113.5	13.0	187	18	US-09-489-039A-13699	Sequence 13699, A
12	112.5	12.9	98	19	US-09-540-236-2245	Sequence 2245, Ap
13	107	12.3	217	16	US-09-252-691-9162	Sequence 9162, Ap
14	107	12.3	217	16	US-09-252-691C-9162	Sequence 9162, Ap
15	104	12.0	359	8	US-08-065-442-2	Sequence 2, Appl
16	104	12.0	359	8	US-08-457-997-2	Sequence 2, Appl
17	104	12.0	359	8	US-08-457-997A-2	Sequence 2, Appl
18	104	12.0	359	8	US-08-457-122-2	Sequence 2, Appl
19	104	12.0	359	18	US-09-451-184-2	Sequence 2, Appl
20	101	11.6	21	24	US-10-082-014-123	Sequence 123, Appl
21	101	11.6	21	26	US-09-358-618-47	Sequence 47, Appl
22	97.5	11.2	384	19	US-09-543-681A-7922	Sequence 7922, Ap
23	97	11.1	21	24	US-10-082-014-124	Sequence 124, Ap
24	97	11.1	21	26	US-09-358-618-48	Sequence 48, Appl
25	96	11.0	369	19	US-09-418-980-10	Sequence 10, Appl
26	96	11.0	369	19	US-09-506-078-46	Sequence 46, Appl
27	96	11.0	369	26	US-09-120-454-46	Sequence 46, Appl
28	95.5	11.0	212	1	PCT-US02-03987-10149	Sequence 10149, A
29	95.5	11.0	212	22	US-09-815-242-10149	Sequence 10149, A
30	95.5	11.0	212	24	US-10-072-851-10149	Sequence 10149, A
31	95.5	11.0	487	17	US-09-328-352-5331	Sequence 5331, Ap
32	95	10.9	257	1	PCT-US02-03987-13845	Sequence 13845, A
33	95	10.9	257	22	US-09-815-242-13845	Sequence 13845, A
34	95	10.9	257	24	US-10-072-851-13845	Sequence 153, App
35	95	10.9	369	19	US-09-545-199C-153	Sequence 153, App
36	95	10.9	369	19	US-09-545-199D-153	Sequence 153, App
37	95	10.9	369	22	US-09-809-665A-153	Sequence 153, App
38	95	10.9	397	23	US-09-902-540-16267	Sequence 16267, A
39	94.5	10.9	799	16	US-09-201-228A-203	Sequence 203, App
40	93	10.7	190	19	US-09-543-681A-7684	Sequence 7684, Ap
41	92	10.6	364	18	US-09-418-980-8	Sequence 8, Appl
42	92	10.6	364	19	US-09-506-078-45	Sequence 45, Appl
43	92	10.6	364	19	US-09-545-199C-151	Sequence 151, App
44	92	10.6	364	19	US-09-545-199D-151	Sequence 151, App
45	92	10.6	364	22	US-09-809-665A-151	Sequence 151, App

ALIGNMENTS

RESULT 1
US-08-406-362-2
Sequence 2, Application US/08406362
GENERAL INFORMATION:
APPLICANT: Brodeur, Bernard R
APPLICANT: Martin, Denis
TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
Zip: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/406,362
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr, James F
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: Pharma-43

```
TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9000
; TELEFAX: 212-596-9090
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 174 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-406-362-2

Query Match          94.8%; Score 825; DB 8; Length 174;
Best Local Similarity 94.3%; Pred. No. 9.7e-85;
Matches 164; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 MKKALALIALPALAALAGAGSGFYVOADAHAHAKASSLSGSAKGSPPRISAGRYINDLR 60
DB 1 MKKALALIALPALAALAGAGSGFYVOADAHAHAKASSLSGSAKGSPPRISAGRYINDLR 60
QY 61 FAVDYTRYKNTKAPSTDFKLYSIGASVYDFTQSPVKPYFGARLSLNRAHLLGSDSF 120
DB 61 FAVDYTRYKNTKAPSTDFKLYSIGASVYDFTQSPVKPYFGARLSLNRAHLLGSDSF 120
QY 121 SKTSAGIGVLAGVSYAVTPNVDLAGRYRYVGVNTVKVNRSGELSGARYKVF 174
DB 121 SKTSAGIGVLAGVSYAVTPNVDLAGRYRYVGVNTVKVNRSGELSGARYKVF 174

RESULT 2
; Sequence 36, Application US/09870759
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
; US-09-870-759-36

Query Match          94.8%; Score 825; DB 22; Length 174;
Best Local Similarity 94.3%; Pred. No. 9.7e-85;
Matches 164; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 MKKALALIALPALAALAGAGSGFYVOADAHAHAKASSLSGSAKGSPPRISAGRYINDLR 60
DB 1 MKKALALIALPALAALAGAGSGFYVOADAHAHAKASSLSGSAKGSPPRISAGRYINDLR 60
QY 61 FAVDYTRYKNTKAPSTDFKLYSIGASVYDFTQSPVKPYFGARLSLNRAHLLGSDSF 120
DB 61 FAVDYTRYKNTKAPSTDFKLYSIGASVYDFTQSPVKPYFGARLSLNRAHLLGSDSF 120
QY 121 SKTSAGIGVLAGVSYAVTPNVDLAGRYRYVGVNTVKVNRSGELSGARYKVF 174
DB 121 SKTSAGIGVLAGVSYAVTPNVDLAGRYRYVGVNTVKVNRSGELSGARYKVF 174

RESULT 3
; Sequence 20, Application US/08479520
; GENERAL INFORMATION:
; APPLICANT: VAN ALSTYNE, Diane
; APPLICANT: SHARMA, Lawrence Rajendra
; TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
; TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
; TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THEREOF, AND USES THEREOF
```

```
NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,520
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 42A
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/127,499
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 51916/105/INBI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; US-08-479-520-20

Query Match          14.4%; Score 125; DB 8; Length 170;
Best Local Similarity 25.2%; Pred. No. 2.4e-05;
Matches 37; Conservative 18; Mismatches 46; Indels 46; Gaps 3;

QY 6 AALIALPALAALAGAGSGFYVOADAHAHAKASSLSGSAKGSPPRISAGRYINDLR 60
DB 15 SLLTSSNAQAASDEDRREPPYVOADLAIAERITHTDYQATGANNSTVSDFRNIAHS 74
QY 46 FSPRISAGRYINDLRFAVDYTRYKNTKAPSTDFKLYSIGASVYDFTQSPVKPYFGARLS 106
DB 75 IHPRVSVGYDEFGWRIADYASRYRKNMNNKYSVNTKELENKHNKKDKLTENQNGTFHA 134
QY 80 LYSIGASVYDFTQSPVKPYFGARLS 106
DB 135 ASSLSGASVYDFTQSPVKPYFGARVA 161

RESULT 4
; Sequence 20, Application US/08486050
; GENERAL INFORMATION:
; APPLICANT: VAN ALSTYNE, Diane
; APPLICANT: SHARMA, Lawrence Rajendra
; TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
; TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
; TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THEREOF, AND USES THEREOF
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
```

```

?      REGISTRATION NUMBER: 29, 768
?      REFERENCE/DOCKET NUMBER: 51916/103/INBI
?      TELECOMMUNICATION INFORMATION:
?      TELEPHONE: (202)672-5300
?      TELEFAX: (202)672-5399
?      TELEX: 904136
?      INFORMATION FOR SEQ ID NO: 20:
?      SEQUENCE CHARACTERISTICS:
?      LENGTH: 170 amino acids
?      TYPE: amino acid
?      STRANDEDNESS:
?      TOPOLOGY: unknown
?      US-08-486-050A-20

Query Match          14.4%; Score 125; DB 8; Length 170;
Best Local Similarity 25.2%; Pred. No. 2,4e-05;
Matches 37; Conservative 18; Mismatches 46; Indels 46; Gaps 3

```

Query Match	14.48;	Score 125;	DB 8;	Length 170;
Best Local Similarity	25.28;	Pred. No. 2.4e-05;		
Matches 37;	Conservative 18;	Mismatches 46;	Indels 46;	Gaps 3;

```
QY      6 AALIALALPAALAGASGSPVQAADAH-----AKASSLIGS-----AKG 45
Dd      15 SSLLFFSSAAQAASERPSRPYYQAADLAHYAERLTHDPQTATGANNSTYSODEFRIRRAHS 74
QY      46 FSPRIASGRINDLEFAYDYIRRYKNY-----KASTDEK 79
Dd      75 IHRPVSVCVDPCGGWILIAADYASIKRWNNNKTSYATKELENHNNKKDLKTENQENGTFPH 134
QY      80 LYSIGASYIIDPDIOSPVKPFYGARLS 106
Dd      135 ASSLGSLSYIDFKLGKTRFPYIGARA 161
```

QY 80 LYSIGASVITDEDTQSPVKPFYFGARLS 106
|:| | ||| : || | ||:
Db 135 ASSIGLSAIVDFKLKGKFKPYIGARVA 161

QY 80 LYSIGASVITDEDTQSPVKPFYFGARLS 106
|:| | ||| : || | ||:
Db 135 ASSIGLSAIVDFKLKGKFKPYIGARVA 161

QY 80 LYSIGASVITDEDTQSPVKPFYFGARLS 106
|:| | ||| : || | ||:
Db 135 ASSIGLSAIVDFKLKGKFKPYIGARVA 161

QY 80 LYSIGASVITDEDTQSPVKPFYFGARLS 106
|:| | ||| : || | ||:
Db 135 ASSIGLSAIVDFKLKGKFKPYIGARVA 161

QY 80 LYSIGASVITDEDTQSPVKPFYFGARLS 106
|:| | ||| : || | ||:
Db 135 ASSIGLSAIVDFKLKGKFKPYIGARVA 161

QY 80 LYSIGASVITDEDTQSPVKPFYFGARLS 106
|:| | ||| : || | ||:
Db 135 ASSIGLSAIVDFKLKGKFKPYIGARVA 161

QY 80 LYSIGASVITDEDTQSPVKPFYFGARLS 106
|:| | ||| : || | ||:
Db 135 ASSIGLSAIVDFKLKGKFKPYIGARVA 161

QY 80 LYSIGASVITDEDTQSPVKPFYFGARLS 106
|:| | ||| : || | ||:
Db 135 ASSIGLSAIVDFKLKGKFKPYIGARVA 161

RESULT 6
 US-08-988-444-20
 : Sequence 20. Application US/08988444
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: VAN ALSTYNE, Diane
 : APPLICANT: SHARMA, Lawrence Rajendra
 : TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
 : TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
 : TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THEREO, AND USES THEREOF
 : NUMBER OF SEQUENCES: 75
 :
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Foley & Lardner
 : STREET: 3000 K Street, N.W., Suite 500
 : City: Washington
 : STATE: D.C.
 : COUNTRY: USA
 : ZIP: 20007-5109
 :
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent In Release #1.0, Version #1.30
 :
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/988,444
 : FILING DATE:
 : CLASSIFICATION:
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 08/486,050
 : FILING DATE: 07-JUN-1995
 : APPLICATION NUMBER: US 08/127,499
 : FILING DATE: 28-SEP-1993
 : ATTORNEY/AGENT INFORMATION:
 : NAME: BENT, Stephen A.
 : REGISTRATION NUMBER: 29,768
 : REFERENCE/DOCKET NUMBER: 51916/103/IMBI
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (202)672-5300
 : TELEFAX: (202)672-5399
 : TELEX: 904136
 :
 : INFORMATION FOR SEQ ID NO: 20:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 170 amino acids

TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-988-444-20

Query Match 14.4%; Score 125; DB 13; Length 170;
Best Local Similarity 25.2%; Pred. No. 2.4e-05;
Matches 37; Conservative 18; Mismatches 46; Indels 46; Gaps 3;

QY 6 AALIALPAAALAEAGSGFYVOADAH-----AKASSLSGS-----AKG 45
DB 15 SLLFSSAAQAASEDRSPYYOADLAYAERITHDYPOATGANNSTVSDYFRNIRAH 74
QY 46 FSPRISAGYRINDLRFADVTRYKNY-----KAPSTDFK 79
DB 75 IHPRVSVGYDFGWMRIAADYASRKNNKYSVNTKELENKNNKKDLKTENQENGTFHA 134
QY 80 LYSIGASVYDFDQSPKPYFGARLS 106
DB 135 ASSIGLSAIDFKKFKPKYIGARVA 161

RESULT 7
US-09-217-849-20

Sequence 20, Application US/09217849
GENERAL INFORMATION:

APPLICANT: VAN ALSTYNE, Diane
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/217,849
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/486,050
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/103/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136

INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-09-217-849-20

Query Match 14.4%; Score 125; DB 16; Length 170;
Best Local Similarity 25.2%; Pred. No. 2.4e-05;
Matches 37; Conservative 18; Mismatches 46; Indels 46; Gaps 3;

QY 6 AALIALPAAALAEAGSGFYVOADAH-----AKASSLSGS-----AKG 45
DB 15 SLLFSSAAQAASEDRSPYYOADLAYAERITHDYPOATGANNSTVSDYFRNIRAH 74
QY 46 FSPRISAGYRINDLRFADVTRYKNY-----KAPSTDFK 79
DB 75 IHPRVSVGYDFGWMRIAADYASRKNNKYSVNTKELENKNNKKDLKTENQENGTFHA 134
QY 80 LYSIGASVYDFDQSPKPYFGARLS 106
DB 135 ASSIGLSAIDFKKFKPKYIGARVA 161

RESULT 8
US-09-489-850-20

Sequence 20, Application US/09489850
GENERAL INFORMATION:

APPLICANT: VAN ALSTYNE, Diane
SHARMA, Lawrence Rajendra
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/489,850
FILING DATE: 24-Jan-2000
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/988,444
FILING DATE: <unknown>
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/103/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136

INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
TYPE: amino acid
STRANDEDNESS: <unknown>
TOPOLOGY: unknown
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-489-850-20

Query Match 14.4%; Score 125; DB 18; Length 170;
Best Local Similarity 25.2%; Pred. No. 2.4e-05;
Matches 37; Conservative 18; Mismatches 46; Indels 46; Gaps 3;

QY 6 AALIALPAAALAEAGSGFYVOADAH-----AKASSLSGS-----AKG 45
DB 15 SLLFSSAAQAASEDRSPYYOADLAYAERITHDYPOATGANNSTVSDYFRNIRAH 74
QY 46 FSPRISAGYRINDLRFADVTRYKNY-----KAPSTDFK 79
DB 75 IHPRVSVGYDFGWMRIAADYASRKNNKYSVNTKELENKNNKKDLKTENQENGTFHA 134

QY 80 LKSGASVITDFDQSPYKPYFGARLS 106
DB 135 ASSLSGLAIYDFLKGKFKPYIGARVA 161

RESULT 9

US-09-739-449-11638
; Sequence 11638, Application US/09739449
; GENERAL INFORMATION:
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15490)C
; CURRENT APPLICATION NUMBER: US/09/739,449
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/514,000
; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 13351
; SEQ ID NO 11638
; LENGTH: 281
; TYPE: PRS
; ORGANISM: Agrobacterium tumefaciens
US-09-739-449-11638

Query Match 14.3%; Score 124.5; DB 21; Length 281;
Best Local Similarity 21.6%; Pred. No. 5.6e-05;
Matches 58; Conservative 29; Mismatches 78; Indels 103; Gaps 11;

QY 1 MKKALALIAL-----PAALAE-----ASGYVAD----- 30
DB 1 MKKALAGFLAVLLTGTSAIADLYQAEPAVYDAPEVTVQASGYLKGDCVGSFNKL 60
QY 31 AAHAKSSSLGSAKGFSPRI-----SAGYRINDL-----RFVDTYRYKNYKAPSTDF 78
DB 61 GAHYGGPGGLQDFDITATIKDSVYIGGVGYQFNNTFRSDVTIDYMGKSDFRGSTSGF 120
QY 79 -----KLVSIGASVITDFDQSPYKPYFGARLSLNRAHAGS-----D 118
DB 121 CGSVPRCVSADLSLAVTLMANAYVDLGTGISTPYVG-----GGIGGSYKWD 171
QY 119 SFSKTSIA-----GLG-----VLGVSYAVTPVNDLADAGRYNYVGYKNT 157
DB 172 KLRNTSCSVNGLGCDPTTEHGKGMKRPAYALMAGASIDVTCNLKADIGYRHRHINKGDM 231
QY 158 V-----KNVSGELSGAVRYKF 174
DB 232 FAYENGSGPRGDKGLYSHVAVGGRYVF 259

RESULT 10

US-09-803-110-11638
; Sequence 11638, Application US/09803110
; GENERAL INFORMATION:
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15490)D
; CURRENT APPLICATION NUMBER: US/09/803,110
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 09/739,449
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/514,000
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: US 60/168,139
; PRIOR FILING DATE: 1999-12-01
; NUMBER OF SEQ ID NOS: 13351
; SEQ ID NO 11638
; LENGTH: 281
; TYPE: PRS
; ORGANISM: Agrobacterium tumefaciens
US-09-803-110-11638

Query Match 14.3%; Score 124.5; DB 22; Length 281;

Best Local Similarity 21.6%; Pred. No. 5.6e-05;
Matches 58; Conservative 29; Mismatches 78; Indels 103; Gaps 11;

QY 1 MKKALALIAL-----PAALAE-----ASGYVAD----- 30
DB 1 MKKALAGFLAVLLTGTSAIADLYQAEPAVYDAPEVTVQASGYLKGDCVGSFNKL 60
QY 31 AAHAKSSSLGSAKGFSPRI-----SAGYRINDL-----RFVDTYRYKNYKAPSTDF 78
DB 61 GAHYGGPGGLQDFDITATIKDSVYIGGVGYQFNNTFRSDVTIDYMGKSDFRGSTSGF 120
QY 79 -----KLVSIGASVITDFDQSPYKPYFGARLSLNRAHAGS-----D 118
DB 121 CGSVPRCVSADLSLAVTLMANAYVDLGTGISTPYVG-----GGIGGSYKWD 171
QY 119 SFSKTSIA-----GLG-----VLGVSYAVTPVNDLADAGRYNYVGYKNT 157
DB 172 KLRNTSCSVNGLGCDPTTEHGKGMKRPAYALMAGASIDVTCNLKADIGYRHRHINKGDM 231
QY 158 V-----KNVSGELSGAVRYKF 174
DB 232 FAYENGSGPRGDKGLYSHVAVGGRYVF 259

RESULT 11
US-09-489-039A-13699
; Sequence 13699, Application US/09489039A
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 13699
; LENGTH: 187
; TYPE: PRS
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13699

Query Match 13.0%; Score 113.5; DB 18; Length 187;
Best Local Similarity 25.7%; Pred. No. 0.00055;
Matches 52; Conservative 25; Mismatches 78; Indels 47; Gaps 7;

QY 1 MKKALALIA--LALPAALAEAGSGFYVQDAHAHAKSSSLGSAK----- 44
DB 5 MKSIAAKWVAATIALGASSACAANLHGEAGAEFTNLISFGAGBPMTFSSQMAHSDN 64
QY 45 -GFSPRISAGYRINDLRAVDYTRYKNYKAPSTDFKLYSGASVY---DEFQSPYK 99
DB 65 DGDVSLGDMGNFNLGPR-----LMTLGGKAVYINPKDGGEGVIAA 106
QY 100 YFGARLSINRAHAGSDPSFKTSAGLV-----LAGSYAVTPVNDLADAGRY- NYV 152
DB 107 GGGAELPLGQYFT-LFEGGYSPDSMSGVEDYEAANAGRLNRPDLNLEAGRYIDMA 165
QY 153 GKVTVMKVRSGELSGAVRYKF 174
DB 166 GKDGNDTTLADGAYAGVNERF 187

RESULT 12

US-09-540-236-2245
; Sequence 2245, Application US/09540236
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CA
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236

```

; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2245
; LENGTH: 98
; TYPE: PRT
; ORGANISM: M. catarrhalis
US-09-540-236-2245

```

```

Query Match      12.9%; Score 112.5; DB 19; Length 98;
Best Local Similarity 39.7%; Pred. No. 0.00027;
Matches 23; Conservative 12; Mismatches 18; Indels 5; Gaps 2;

```

```

QY 122 KTSGAGLVLAGVAVTPVDLDAGYRYNVG---KVNTVKVRSGLSAGV---GVRYKF 174
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 41 ETVAGGVLAGAAGYALNPOLSVAGVEYNLGRKYLKLDTSKIKAKQYAKKGLRHN 98

```

```

RESULT 13
US-09-252-691-9162
; Sequence 9162, Application US/09252691B
; GENERAL INFORMATION:
; APPLICANT: Keith G. Weinstein et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROBACTER
; FILE REFERENCE: 107196.135
; CURRENT APPLICATION NUMBER: US/09/252,691B
; CURRENT FILING DATE: 1999-02-18
; NUMBER OF SEQ ID NOS: 11324
; SEQ ID NO 9162
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Enterobacter cloacae
US-09-252-691-9162

```

```

Query Match      12.3%; Score 107; DB 16; Length 217;
Best Local Similarity 22.9%; Pred. No. 0.0037;
Matches 49; Conservative 38; Mismatches 79; Indels 48; Gaps 9;

```

```

QY 1 MKK-ALNALALPAAALFEGAGFYVQADAAHAKASSISGAKGSPRISAGYRI-ND 58
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 8 MKKLAVALLLSSISGAYAHAGFEPRIRAGSATVPRTEGSDNVLGM-----GCFVNSNN 62
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 59 LRFADYV-----RYKNYKAPSTDV-KIYSIGASVY---YDFDTQSPV 97
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 63 TOLGTFYMATDNGVELLAATPFRRHVGIGPTGDIATVHLPPTLMAQWYFGDSSSKV 122
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 98 KPYFGARLS-----LNRASAHLGSDSFSKTSAGLGVLAGVSAVTPN----- 140
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 123 RPTIGAGVNYTTTFDEFKNDTGKEAGLSDSLKDSMGAGQGLDYLINRDLINASVWY 182
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 141 VDLADGARYNYVGR---VNTVKVRSGLSAGV 171
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 183 MDIDTVRFKAGGQGSINTRLDPWVWFMSAGYR 216

```

```

RESULT 14
US-09-252-691C-9162
; Sequence 9162, Application US/09252691C
; GENERAL INFORMATION:
; APPLICANT: Keith G. Weinstein et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROBACTER
; FILE REFERENCE: 107196.135
; CURRENT APPLICATION NUMBER: US/09/252,691C
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/094,145
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: US 60/074,787
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 11326
; SEQ ID NO 9162
; LENGTH: 217
; TYPE: PRT

```

```

; ORGANISM: Enterobacter cloacae
US-09-252-691C-9162

```

```

Query Match      12.3%; Score 107; DB 16; Length 217;
Best Local Similarity 22.9%; Pred. No. 0.0037;
Matches 49; Conservative 38; Mismatches 79; Indels 48; Gaps 9;

```

```

QY 1 MKK-ALNALALPAAALFEGAGFYVQADAAHAKASSISGAKGSPRISAGYRI-ND 58
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 8 MKKLAVALLLSSISGAYAHAGFEPRIRAGSATVPRTEGSDNVLGM-----GCFVNSNN 62
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 59 LRFADYV-----RYKNYKAPSTDV-KIYSIGASVY---YDFDTQSPV 97
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 63 TOLGTFYMATDNGVELLAATPFRRHVGIGPTGDIATVHLPPTLMAQWYFGDSSSKV 122
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 98 KPYFGARLS-----LNRASAHLGSDSFSKTSAGLGVLAGVSAVTPN----- 140
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 123 RPTIGAGVNYTTTFDEFKNDTGKEAGLSDSLKDSMGAGQGLDYLINRDLINASVWY 182
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 141 VDLADGARYNYVGR---VNTVKVRSGLSAGV 171
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 183 MDIDTVRFKAGGQGSINTRLDPWVWFMSAGYR 216

```

```

RESULT 15
US-08-065-442-2
; Sequence 2, Application US/08065442
; GENERAL INFORMATION:
; APPLICANT: Kolattukudy, P. E.
; TITLE OF INVENTION: Otitis Media Vaccine
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESS: Calfee, Halter and Griswold
; STREET: Suite 1800 800 Superior Avenue
; CITY: Cleveland
; STATE: Ohio
; COUNTRY: U.S.A.
; ZIP: 44114-2688
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/065,442
; FILING DATE: 19930518
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Goltick, Mary E.
; REGISTRATION NUMBER: 34,829
; REFERENCE/DOCKET NUMBER: 22727/00102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (216) 622-8458
; TELEFAX: (216) 241-0816
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-065-442-2

```

```

Query Match      12.0%; Score 104; DB 4; Length 359;
Best Local Similarity 24.7%; Pred. No. 0.017;
Matches 56; Conservative 29; Mismatches 82; Indels 60; Gaps 11;

```

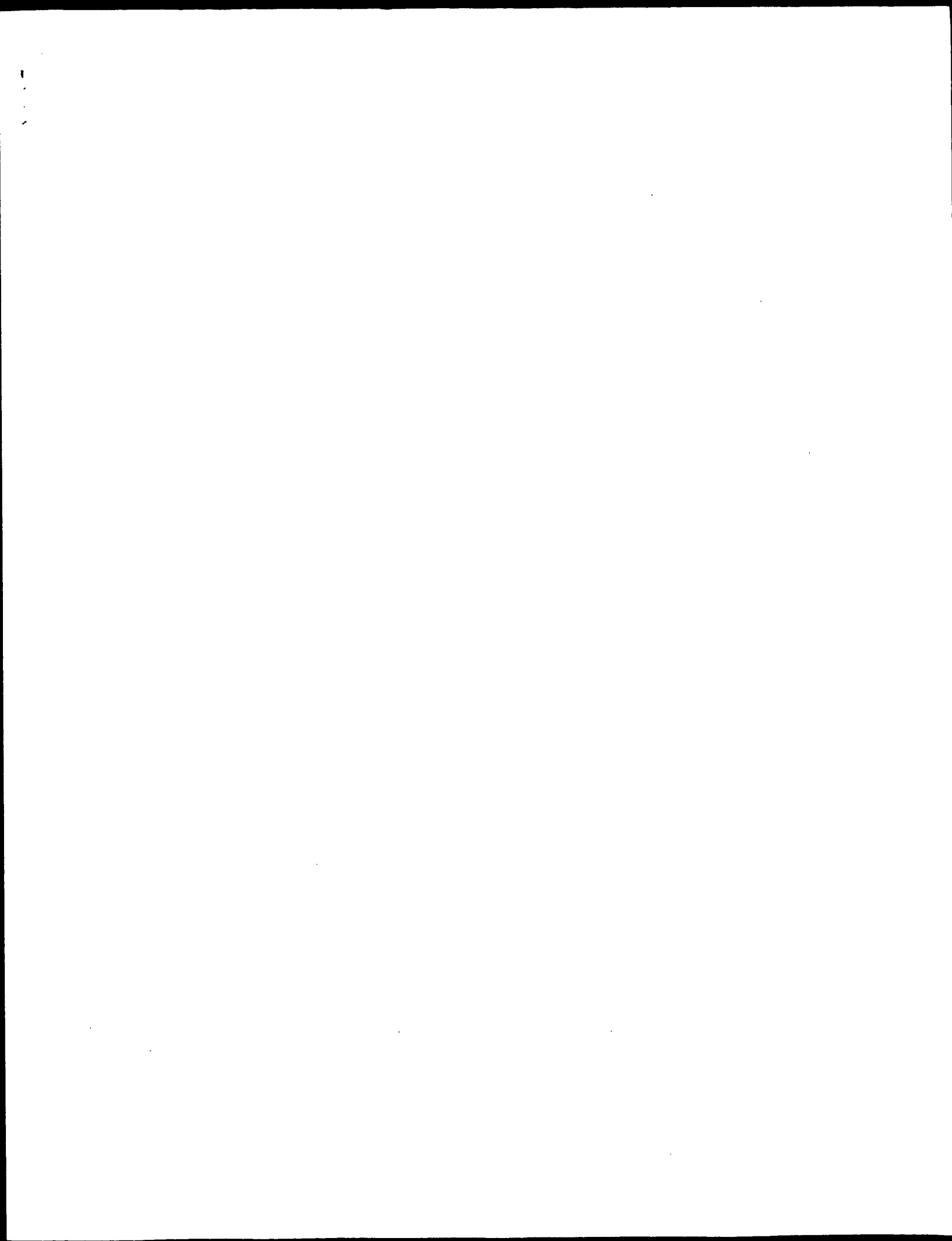
```

QY 1 MKKALALIALPAAALFEGAGFYVQADAA---HAKASSISGASGSPRISAG 53
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1 MKKTAIAIVVAGIAAASVAQAAPQENTFYAGYKAGQGSFHHGGINNCAIKKGLSS- NYG 59
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 54 YRINDRFVADYTRRYKNKAPSTDVFKLTSIGASVYDFDTQSPV-----KPF-----YFGAR 104
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 60 YRKNFTTYGV-----FGYQIILNQD--NFGIAAEIGYDDFGRAKLRKAGKPRAKHTNHGAY 113

```

QY 105 LSLNRASAHLGSDSEKTSAGL-----GVLA-GVSYA 136
| | : | | : |
Db 114 LSLKGSYEVLGDLDVYGKAGVALVRSDYKFYEDANGTRDHKGRHTARASGLFAVGAETA 173
| | : | | : |
QY 137 VTPNVDLDAGY-----RYNYGKYNFTVKNRS--GELSAGYRVKF 174
| | : | | : |
Db 174 VLPBLAVRLEYQMLTRYGKYRPQDKPNTALNPNWIGICINAGISYRF 220
| | : | | : |

Search completed: October 28, 2002, 16:11:24
Job time : 104.601 secs



GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 28, 2002, 16:01:19 ; Search time 35.6987 Seconds

(without alignments)
1465.185 Million cell updates/sec

Title: US-09-684-883-8

Perfect score: 870
Sequence: 1 MKKALALIALALPAALAE.....VNTKKNVSGELSGVRVKE 174

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1112697 seqs, 300604653 residues

Total number of hits satisfying chosen parameters: 1112697

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents-AA-New:*

1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
6: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
7: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
8: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
9: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
10: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
11: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
12: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*
13: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	870	100.0	174	US-09-684-883-8	Sequence 8, Appli
2	834	95.9	174	US-09-684-883-6	Sequence 6, Appli
3	825	94.8	174	US-09-684-883-2	Sequence 2, Appli
4	823.5	94.7	175	US-09-684-883-30	Sequence 30, Appli
5	813.5	93.5	175	US-09-684-883-4	Sequence 4, Appli
6	133	15.3	25	US-09-684-883-26	Sequence 26, Appli
7	106	12.2	353	US-10-203-942-9	Sequence 153, App
8	95	10.9	369	US-09-545-199F-153	Sequence 151, App
9	92	10.6	364	US-09-545-199F-151	Sequence 149, App
10	90	10.3	500	US-09-990-004A-149	Sequence 147, App
11	90	10.3	500	US-10-219-220-149	Sequence 145, App
12	87.5	10.1	576	US-09-791-537-117254	Sequence 117254,
13	87	10.0	16	US-09-684-883-15	Sequence 15, Appli
14	87	10.0	213	US-09-791-537-112202	Sequence 112202,
15	85	9.8	250	US-09-540-209B-9349	Sequence 9349, Ap
16	84.5	9.7	199	US-10-053-853A-8	Sequence 8, Appli
17	84.5	9.7	199	US-10-053-853A-80	Sequence 80, Appli
18	84.5	9.7	199	US-10-053-853A-760	Sequence 760, App
19	83.5	9.6	339	US-09-513-996A-67258	Sequence 67258, A
20	83.5	9.6	534	US-09-513-996A-7956	Sequence 7956, Ap

21	83	9.5	431	9	US-09-540-209B-7041	Sequence 7041, Ap
22	82.5	9.5	423	9	US-09-791-537-129337	Sequence 129337,
23	82.5	9.5	1082	13	US-60-360-039-17890	Sequence 17890, A
24	81.5	9.4	199	11	US-10-053-853A-970	Sequence 970, App
25	81	9.3	165	9	US-09-540-209B-7537	Sequence 7537, App
26	81	9.3	187	11	US-10-219-999-45753	Sequence 45753, A
27	81	9.3	229	11	US-10-219-999-59699	Sequence 59699, A
28	80	9.2	15	9	US-09-684-883-23	Sequence 23, Appli
29	80	9.2	163	9	US-09-791-537-98389	Sequence 98389, A
30	80	9.2	259	9	US-09-513-996A-57141	Sequence 57141, A
31	80	9.2	274	9	US-09-513-996A-57139	Sequence 57139, A
32	80	9.2	383	9	US-09-513-996A-45591	Sequence 45591, A
33	80	9.2	490	9	US-09-513-996A-45590	Sequence 45590, A
34	80	9.2	539	9	US-09-513-996A-45589	Sequence 45589, A
35	79	9.1	264	9	US-09-956-508A-4	Sequence 4, Appli
36	79	9.1	273	9	US-09-882-227-80	Sequence 80, Appli
37	79	9.1	400	9	US-09-513-996A-19382	Sequence 19382, A
38	79	9.1	507	9	US-09-513-996A-19381	Sequence 19381, A
39	79	9.1	551	13	US-60-360-039-15697	Sequence 15697, A
40	79	9.1	551	13	US-60-360-039-16088	Sequence 16088, A
41	79	9.1	556	9	US-09-513-996A-19380	Sequence 19380, A
42	79	9.1	624	13	US-60-360-039-15330	Sequence 15330, A
43	79	9.1	896	11	US-10-210-296-5	Sequence 5, Appli
44	78.5	9.0	199	11	US-10-053-853A-388	Sequence 388, Appli
45	78	9.0	15	9	US-09-684-883-14	Sequence 14, Appli

ALIGNMENTS

RESULT 1
US-09-684-883-8
Sequence 8, Application US/09684883
GENERAL INFORMATION:
APPLICANT: Brodeur, Bernard R
Hamel, Josee
Rioux, Clement
TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
OF NEISSERIA MENINGITIDIS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/684,883
FILING DATE: 06-Oct-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
APPLICATION NUMBER: US 60/001,983
FILING DATE: 04-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,766
REFERENCE/DOCKET NUMBER: 047998/0128
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:

LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 8
US-09-684-883-8

Query Match 100.0%; Score 870; DB 9; Length 174;
Best Local Similarity 100.0%; Pred. No. 1,6e-81;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKALALIALALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
DB 1 MKKALALIALALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
QY 61 FAVDTYRKKNKAPSTDEKLYSIGASYIDPDQSPVKPYFGARLSLNRASVHLGSSDSF 120
DB 61 FAVDTYRKKNKAPSTDEKLYSIGASYIDPDQSPVKPYFGARLSLNRASVHLGSSDSF 120
QY 121 SKTSAGLVLGVSAYVTPNVDLDAGYRNYVGKVTYKVRSGELSGAGYRVKF 174
DB 121 SKTSAGLVLGVSAYVTPNVDLDAGYRNYVGKVTYKVRSGELSGAGYRVKF 174

RESULT 2

US-09-684-883-6
Sequence 6, Application US/09684883

GENERAL INFORMATION:

APPLICANT: Brodeur, Bernard R

Martin, Denis

Hamel, Josee

Rioux, Clement

TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
OF NEISSERIA MENINGITIDIS

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA: US/09/684,883

APPLICATION NUMBER: US/09/684,883

FILING DATE: 06-Oct-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/913,362

FILING DATE: 13-NOV-1997

APPLICATION NUMBER: US 08/406,362

FILING DATE: 17-MAR-1995

APPLICATION NUMBER: US 60/001,983

FILING DATE: 04-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: Bent, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 047998/0128

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399

TELEX: 904136

SEQUENCE CHARACTERISTICS:

LENGTH: 174 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-684-883-6

Query Match 95.9%; Score 834; DB 9; Length 174;
Best Local Similarity 95.4%; Pred. No. 8.1e-78;
Matches 166; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 MKKALALIALALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
DB 1 MKKALALIALALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
QY 61 FAVDTYRKKNKAPSTDEKLYSIGASYIDPDQSPVKPYFGARLSLNRASVHLGSSDSF 120
DB 61 FAVDTYRKKNKAPSTDEKLYSIGASYIDPDQSPVKPYFGARLSLNRASVHLGSSDSF 120
QY 121 SKTSAGLVLGVSAYVTPNVDLDAGYRNYVGKVTYKVRSGELSGAGYRVKF 174
DB 121 SKTSAGLVLGVSAYVTPNVDLDAGYRNYVGKVTYKVRSGELSGAGYRVKF 174

RESULT 3

US-09-684-883-2
Sequence 2, Application US/09684883

GENERAL INFORMATION:

APPLICANT: Brodeur, Bernard R

Martin, Denis

Hamel, Josee

Rioux, Clement

TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
OF NEISSERIA MENINGITIDIS

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA: US/09/684,883

APPLICATION NUMBER: US/09/684,883

FILING DATE: 06-Oct-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/913,362

FILING DATE: 13-NOV-1997

APPLICATION NUMBER: US 08/406,362

FILING DATE: 17-MAR-1995

APPLICATION NUMBER: US 60/001,983

FILING DATE: 04-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: Bent, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 047998/0128

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399

TELEX: 904136

SEQUENCE CHARACTERISTICS:

LENGTH: 174 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-684-883-2

Query Match 94.8%; Score 825; DB 9; Length 174;
Best Local Similarity 94.3%; Pred. No. 6.9e-77;
Matches 164; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 MKKALALIALALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

DB 1 MKKALALIALPALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
QY 61 FAVDYTRYKNKAPSTDFKLYSIGASVYDFDTQSPVKPYFGARLSLNRASAHLGSDSF 120
DB 61 FAVDYTRYKNKAPSTDFKLYSIGASVYDFDTQSPVKPYFGARLSLNRASAHLGSDSF 120
QY 121 SKTSAGLGVLAGSVYAVTPNVDLDAGRYRNYGKVTYKRVNVSSELGELSGAGYRVKF 174
DB 121 SKTSAGLGVLAGSVYAVTPNVDLDAGRYRNYGKVTYKRVNVSSELGELSGAGYRVKF 174

RESULT 4
US-09-684-883-30
Sequence 30, Application US/09684883
GENERAL INFORMATION:
APPLICANT: Brodeur, Bernard R
Martlin, Denis
Hamel, Josee
Rioux, Clement
TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/684,883
FILING DATE: 06-Oct-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
APPLICATION NUMBER: US 60/001,983
FILING DATE: 04-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 047998/0128
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acids
TYPE: amino acid
STRANDEDNESS: <unknown>
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-684-883-30

Query Match 94.7%; Score 823.5; DB 9; Length 175;
Best Local Similarity 94.9%; Pred. No. 9.9e-77;
Matches 166; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

QY 1 MKKALALIALPALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
DB 1 MKKALALIALPALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
QY 61 FAVDYTRYKNKAPSTDFKLYSIGASVYDFDTQSPVKPYFGARLSLNRASAHLGSDSF 119

DB 61 FAVDYTRYKNKAPSTDFKLYSIGASVYDFDTQSPVKPYFGARLSLNRASAHLGSDSF 120
QY 120 FSKTSAGLGVLAGSVYAVTPNVDLDAGRYRNYGKVTYKRVNVSSELGELSGAGYRVKF 174
DB 121 FSKTSAGLGVLAGSVYAVTPNVDLDAGRYRNYGKVTYKRVNVSSELGELSGAGYRVKF 175

RESULT 5
US-09-684-883-4
Sequence 4, Application US/09684883
GENERAL INFORMATION:
APPLICANT: Brodeur, Bernard R
Martlin, Denis
Hamel, Josee
Rioux, Clement
TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/684,883
FILING DATE: 06-Oct-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
APPLICATION NUMBER: US 60/001,983
FILING DATE: 04-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 047998/0128
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acids
TYPE: amino acid
STRANDEDNESS: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-684-883-4

Query Match 93.5%; Score 813.5; DB 9; Length 175;
Best Local Similarity 93.7%; Pred. No. 1.1e-75;
Matches 164; Conservative 2; Mismatches 8; Indels 1; Gaps 1;

QY 1 MKKALALIALPALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
DB 1 MKKALALIALPALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
QY 61 FAVDYTRYKNKAPSTDFKLYSIGASVYDFDTQSPVKPYFGARLSLNRASAHLGSDSF 119
DB 61 FAVDYTRYKNKAPSTDFKLYSIGASVYDFDTQSPVKPYFGARLSLNRASAHLGSDSF 119
QY 120 FSKTSAGLGVLAGSVYAVTPNVDLDAGRYRNYGKVTYKRVNVSSELGELSGAGYRVKF 174
DB 120 FSKTSAGLGVLAGSVYAVTPNVDLDAGRYRNYGKVTYKRVNVSSELGELSGAGYRVKF 175

[illegible]

Db 119 PSEVEPLDGVYGVKCIAYVRNDYKKY-GAE-NTNESTT-----KFKKRASTILGAGV 170
 QY 134 STAATPNDLDAGRYRNVYKVNKN--VRSG-----ELSAQVRYKF 174
 Db 171 EXAIIIP--ELAAVREYQYLKAGNINIKALVRSQTQDVDFQVAPDIHSTVAGLSYRF 224

RESULT 9
 US-09-545-199F-151
 ; Sequence 151, Application US/09545199F
 ; GENERAL INFORMATION:
 ; APPLICANT: Lowery E., David
 ; APPLICANT: Fuller E., Troy
 ; APPLICANT: Kennedy J., Michael
 ; TITLE OF INVENTION: Anti-Bacterial Vaccine Compositions
 ; FILE REFERENCE: 28341/6227.NCP
 ; CURRENT APPLICATION NUMBER: US/09/545, 199F
 ; CURRENT FILING DATE: 2000-04-06
 ; PRIOR APPLICATION NUMBER: 60/153,453
 ; PRIOR FILING DATE: 1999-09-10
 ; PRIOR APPLICATION NUMBER: 60/128,689
 ; PRIOR FILING DATE: 1999-04-09
 ; NUMBER OF SEQ ID NOS: 165
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 151
 ; LENGTH: 364
 ; TYPE: PRT
 ; ORGANISM: Actinobacillus pleuropneumoniae
 US-09-545-199F-151

Query Match 10.6%; Score 92; DB 9; Length 364;
 Best Local Similarity 25.6%; Pred. No. 0.53;
 Matches 58; Conservative 24; Mismatches 85; Indels 60; Gaps 11;

QY 1 MKKALALALALPAALAEAGA---SGFYQADAAHAK---ASSLSGSAKGFSPRISAGY 54
 Db 1 MKKSLVALVLVS--AAVAQAAPQONTFYAGAKAGMASHDIEOLDSKNTDRGTKKGI 58
 QY 55 RINDREFAV-----DY-----TRYKNYKAPSTDYFKLISIGAS-- 86
 Db 59 NNSVYVYGVFGYQIINODKLGLAEELGYDFGRVRSSEKPGKADKTFRIAHAGATIA 118
 QY 87 -----VIIDPTQSPVRYKFFGARLSINRASHLGGSDSEFT---SAGLGVLAVSYAV 137
 Db 119 LRPSEVEPLDLDVYGVK---GIAL-VNNTYKTFMAADEKVTTRFQSSLLIGAGVEYAI 173
 QY 138 TPNVDLDAGRY-NTYGVNTVKNVRSG-----ELSAQVRYKF 174
 Db 174 LPELAARVEYQWLNNAKASYSTLRMGKTDYRSDISSVSAGLSYRF 220

RESULT 10
 US-09-990-004A-149
 ; Sequence 149, Application US/09990004A
 ; GENERAL INFORMATION:
 ; APPLICANT: Plinn, Barry
 ; APPLICANT: Lasham, Annette
 ; TITLE OF INVENTION: Methods for Modulating Cellular Development and Programmed Cell De
 ; FILE REFERENCE: 11000.1038c1
 ; CURRENT APPLICATION NUMBER: US/09/990,004A
 ; CURRENT FILING DATE: 2002-04-08
 ; PRIOR APPLICATION NUMBER: US 09/327,373
 ; PRIOR FILING DATE: 1999-06-04
 ; NUMBER OF SEQ ID NOS: 204
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO: 149
 ; LENGTH: 500
 ; TYPE: PRT
 ; ORGANISM: Eucalyptus grandis
 US-09-990-004A-149

Query Match 10.3%; Score 90; DB 9; Length 500;
 Best Local Similarity 24.9%; Pred. No. 1.3;

Matches 43; Conservative 20; Mismatches 78; Indels 32; Gaps 5;

QY 4 ALAALALALPAALAEAGSGFYQADAAHAKSSLSGSAKGFSPRISAGYRI----- 56
 Db 32 AAVALALALALTTIASALDMSTVYRAHGDNRSSSSSSMRSDDEVMAYEESWLAKHK 91
 QY 57 -----NDLRFAY--DYTRYKNYKAPSTDYFKLISIGASVYDFDQSPVKPYFGARLSL 107
 Db 92 AYNALGEKERKFFQYKFNLDLRFIDHNGCD-RFTYVGLNCFADLTNEYRSMTLGAR--M 148
 QY 108 NRAAHLGGSDSEFTKTSAGLGVLAGVSYAVTPNVDLDAGRYRNVYKVNKN 160
 Db 149 DRSGRRILGRARS-----DRYAAVAGGELPASVDMRREGAVVDVKD 188

RESULT 11
 US-10-219-220-149
 ; Sequence 149, Application US/10219220
 ; GENERAL INFORMATION:
 ; APPLICANT: Plinn, Barry
 ; APPLICANT: Lasham, Annette
 ; TITLE OF INVENTION: Compositions affecting programmed cell
 ; TITLE OF INVENTION: death and their use in the modification of plant development
 ; FILE REFERENCE: 11000.1022c1
 ; CURRENT APPLICATION NUMBER: US/10/219,220
 ; CURRENT FILING DATE: 2002-08-14
 ; PRIOR APPLICATION NUMBER: U.S. No. 09/325,932
 ; PRIOR FILING DATE: 1999-06-04
 ; NUMBER OF SEQ ID NOS: 290
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO: 149
 ; LENGTH: 500
 ; TYPE: PRT
 ; ORGANISM: Eucalyptus grandis
 US-10-219-220-149

Query Match 10.3%; Score 90; DB 11; Length 500;
 Best Local Similarity 24.9%; Pred. No. 1.3;
 Matches 43; Conservative 20; Mismatches 78; Indels 32; Gaps 5;

QY 4 ALAALALALPAALAEAGSGFYQADAAHAKSSLSGSAKGFSPRISAGYRI----- 56
 Db 32 AAVALALALALTTIASALDMSTVYRAHGDNRSSSSSSMRSDDEVMAYEESWLAKHK 91
 QY 57 -----NDLRFAY--DYTRYKNYKAPSTDYFKLISIGASVYDFDQSPVKPYFGARLSL 107
 Db 92 AYNALGEKERKFFQYKFNLDLRFIDHNGCD-RFTYVGLNCFADLTNEYRSMTLGAR--M 148
 QY 108 NRAAHLGGSDSEFTKTSAGLGVLAGVSYAVTPNVDLDAGRYRNVYKVNKN 160
 Db 149 DRSGRRILGRARS-----DRYAAVAGGELPASVDMRREGAVVDVKD 188

RESULT 12
 US-09-791-537-117254
 ; Sequence 117254, Application US/09791537
 ; GENERAL INFORMATION:
 ; APPLICANT: Biomix, Inc.
 ; APPLICANT: Debe, Derek
 ; APPLICANT: Danzer, Joseph
 ; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
 ; FILE REFERENCE: 261/210
 ; CURRENT APPLICATION NUMBER: US/09/791,537
 ; CURRENT FILING DATE: 2001-02-22
 ; NUMBER OF SEQ ID NOS: 153055
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO: 117254
 ; LENGTH: 576
 ; TYPE: PRT
 ; ORGANISM: Moraxella catarrhalis
 US-09-791-537-117254

Query Match 10.1%; Score 87.5; DB 9; Length 576;
 Best Local Similarity 25.1%; Pred. No. 2.8;
 Matches 43; Conservative 28; Mismatches 59; Indels 41; Gaps 9;

19 AEGASGEVQDA-----AHAKASSIGS-AKGFSPRIS-GYRINDLRPAVDYRK 67
 Db 432 ASADTKFPAATDAITKGNALITKNAKSTITDGLGVDFDGRVTLALDTKRNAL----- 483

QY 68 YKNYKASTDEKLYSIGASYIDPDTSPPV---KPYFGARLSINRAHLLGSGDSFSRKT 123
 Db 484 --DKRVNAFDRIITALDSKVENGAQAALSGLFQPSYCKFN---ATAALGGYGSASAV 538

QY 124 SAGIGVLAGSYAVTPNVDLDAGTRINVTGKRVNTVKNVSGELSGAYRVKPF 174
 Db 539 AIGAG-----YRVNPMIAFKAG-----AALNTSGN-KKGSYNIGVNYEEF 576

RESULT 13
 US-09-684-883-15
 ; Sequence 15, Application US/09684883
 ; GENERAL INFORMATION:
 ; APPLICANT: Brodeur, Bernard R
 ; Hamel, Josee
 ; Rioux, Clement
 ; TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
 ; NUMBER OF SEQUENCES: 30
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: Foley & Lardner
 ; STREET: 3000 K Street, N.W., Suite 500
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20007-5109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/684,883
 ; FILING DATE: 06-Oct-2000
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/913,362
 ; FILING DATE: 13-NOV-1997
 ; APPLICATION NUMBER: US 08/406,362
 ; FILING DATE: 17-MAR-1995
 ; APPLICATION NUMBER: US 60/001,983
 ; FILING DATE: 04-AUG-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Bent, Stephen A.
 ; REGISTRATION NUMBER: 29,768
 ; REFERENCE/DOCKET NUMBER: 047998/0128
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202)672-5300
 ; TELEFAX: (202)672-5399
 ; INFORMATION FOR SEQ ID NO: 15:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 16 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; ORIGIN: SOURCE:
 ; ORGANISM: Neisseria meningitidis
 ; STRAIN: 608B
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
 ; US-09-684-883-15

Query Match 10.0%; Score 87; DB 9; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.032;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 FAVDYTRYKRYKAPST 76
 Db 1 FAVDYTRYKRYKAPST 16

RESULT 14
 US-09-791-537-112202
 ; Sequence 112202, Application US/09791537
 ; GENERAL INFORMATION:
 ; APPLICANT: Biomolix, Inc.
 ; APPLICANT: Dede, Derek
 ; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
 ; FILE REFERENCE: 261/210
 ; CURRENT APPLICATION NUMBER: US/09/791,537
 ; CURRENT FILING DATE: 2001-02-22
 ; NUMBER OF SEQ ID NOS: 153055
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 112202
 ; LENGTH: 213
 ; TYPE: PRT
 ; ORGANISM: Brucella canis
 ; US-09-791-537-112202

Query Match 10.0%; Score 87; DB 9; Length 213;
 Best Local Similarity 26.1%; Pred. No. 0.87;
 Matches 48; Conservative 30; Mismatches 72; Indels 34; Gaps 9;

QY 14 PAAALAEASGEVQDAHAHAKASSLSGAKGFSRISA---GYRINDLRPAVDYTRYK 69
 Db 41 PYSWAGGYTGLYLGYGNMKAK-TSTVGSIKPDMDKAGAFAGWNFQKDIYVGEAGDAGY 99

QY 70 NYKAPSTD-----FKLYSIGASYIDPDTSPPVYPF-----GARLSINRAHLLGS 117
 Db 100 SWAKSKSDLEVKQGF-EGLRARVGYDL--NPVMPYLTGAGIASQIKLN-----NGL 149

QY 118 DSEKTSAGIGVLAGSYAVTPNVDLDAGYRY-----NYGKVTYVKN-VRSGLSAGV 170
 Db 150 DGSKFRVGMWTAGAGLEKLTIDNIIIGRYEYRTQYSSNNNYDLAGTTVANKKIDQDIRGI 209

QY 171 RYKF 174
 Db 210 GYKF 213

RESULT 15
 US-09-540-209B-9349
 ; Sequence 9349, Application US/09540209B
 ; GENERAL INFORMATION:
 ; APPLICANT: GARY L. Breton
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTERIOIDES
 ; FILE REFERENCE: 2709.1001-001
 ; CURRENT APPLICATION NUMBER: US/09/540,209B
 ; CURRENT FILING DATE: 2000-04-04
 ; NUMBER OF SEQ ID NOS: 10444
 ; SEQ ID NO 9349
 ; LENGTH: 250
 ; TYPE: PRT
 ; ORGANISM: B. fragilis
 ; US-09-540-209B-9349

Query Match 9.8%; Score 85; DB 9; Length 250;
 Best Local Similarity 27.3%; Pred. No. 1.7;
 Matches 44; Conservative 20; Mismatches 57; Indels 40; Gaps 9;

QY 1 MKK-ALMALIALPAA-----ALAEASG--FYVQA-----DAHAKASSS 39
 Db 32 MKKVTVALVALALSSCNSDPKFNKGVSGADGKMLYLEASGLEGIYPLDSIKLKGDGS 91
 QY 40 LGSAGFSRISAGYRI-----NDLRPAVDYTRYKRYKAPSTDFK-LYSIGASYIYDPTQ 94

Tue Oct 29 09:23:24 2002

us-09-684-883-8.rapn

Page 7

Db 92 F-SFKOLRPESEPFYRLVLEDKXVINEFSVDSTETVSIQAPYTDSTATVEGS-----ENS 145
OY 95 SPVKPYFGARLSLNR-----ASAHLGSDSFSKTSAGL 127
Db 146 AKIKELTLKQVRLQKVDALVKAAQAHQIGNDYFEDSLAVL 186

Search completed: October 28, 2002, 16:13:53
Job time : 36.6987 secs

